

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:04:25 ; Search time 3588.29 Seconds
(without alignments)
19096.316 Million cell updates/sec

Title: US-09-647-140A-1
Perfect score: 4231
Sequence: 1 gacagcggtgcgcgcgga.....ttcatttgaaattttctccc 4231

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
1: em_estba.*
2: em_esthum.*
3: em_estmu.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pin.*
21: em_gss_vit.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_Other.*
26: em_gss_pro.*
27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	734	17.3	1084	13	BM462073
2	706.6	16.7	1139	14	BQ069612
3	664.8	15.7	896	14	BQ889997
4	636.4	15.0	682	12	BE879353
5	612.4	14.5	727	12	BE879718
6	582.8	13.8	689	13	BI771442

7	546	12.9	926	12	BE885514
8	483.4	11.4	497	9	AL701816
c	467.4	11.0	478	10	BE674208
9	454.8	10.7	639	10	BE225682
c	433.4	10.2	435	10	BE327296
12	433	10.2	465	9	AU126646
13	431.4	10.2	734	10	BB643073
14	429.2	10.1	628	10	BB623281
15	404.8	9.6	777	9	AJ454714
16	399.6	9.4	743	9	AJ453358
17	395.6	9.4	515	9	AJ453358
18	391.8	9.3	743	9	AJ453340
19	384	9.1	387	9	AA305627
20	374.4	8.8	887	13	BM048029
21	373.8	8.8	1002	13	BM553694
22	371.2	8.8	708	10	AW421943
23	366.6	8.7	593	10	AV607181
24	365.4	8.6	728	9	AJ451452
25	363.2	8.6	472	14	W54702
26	362	8.6	635	9	AU130197
27	357.2	8.4	720	9	AJ447590
28	350.8	8.3	610	10	BB637723
29	349	8.2	498	13	BM430372
30	334.8	7.9	474	13	BM256142
c	321.6	7.6	415	12	BF836367
32	319	7.5	383	14	R35797
33	317.6	7.5	652	10	BB661649
34	312.6	7.4	487	12	BF231451
35	308.6	7.3	486	12	BF889744
36	294.8	7.0	510	11	U66686
37	288.6	6.8	475	12	BF889748
38	284	6.7	514	14	R35798
39	281.4	6.7	455	10	BB859454
c	281.2	6.6	326	12	BE769242
41	270.6	6.4	841	13	BM451958
42	266.8	6.3	465	13	BI540773
43	260.6	6.2	591	13	BI540698
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c	250.6	5.9	406	13	BI403742

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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5', mRNA sequence.
BM462073
BM462073.1 GI:18511113
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL2111 row: c column: 19
High quality sequence stop: 657.
Location/Qualifiers
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BE225682 BB225582
BE327296 hwi0b05.x
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BB643073 BB643073
BB623281 BB623281
AJ454714 AJ454714
AJ453358 AJ453358
AJ453340 AJ453340
AA305627 AA305627
BM048029 BM048029
BM553694 AGENCOURT
AW421943 f188g10.y
AV607181 AV607181
AJ451452 AJ451452
W54702 md07d11.r1
AU130197 AU130197
AJ447590 AJ447590
BB637723 BB637723
BM430372 IDUO33E1.
BM256142 518435.WA
BF836367 RC3-HT023
R35797 YG66a11.r1
BB661649 BB661649
BF231451 233864.BA
BF889744 289315.WA
U66686 Homo sapien
BF889748 289319.WA
R35798 YG66a12.r1
BB859454 BB859454
BE769242 PM4-FT002
BM451958 AGENCOURT
BI540773 454162.MA
BI540698 454067.MA
AA375392 EST87662
BI403742 MI-P-CPI-

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/clone_lib="NIH_MGC_67"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 Kb. Library constructed by Life
Technologies."
BASE COUNT 258 a 340 c 190 g 295 t 1 others
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Best Local Similarity 100.0%; Pred. No. 3e-196;
Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2178 AGGAGAACCCCTCTGAAGGAAAGTTGGTTTCAGGCTTATAAGAAATTAATTCAGAGCTG 2237
Db 61 AGGAGAACCCCTCTGAAGGAAAGTTGGTTTCAGGCTTATAAGAAATTAATTCAGAGCTG 120
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Db 121 GTGCTCACTGGATGTTCTCAATTTTCCTTATTCCTTAAACACTGCAGCTGGCT 180
QY 2298 ATGTGCTTCAAGATGGTGGCTTTCATCTGAGGCAACAAACAAAGATGCTAATGTCA 2357
Db 181 ATGTGCTTCAAGATGGTGGCTTTCATCTGAGGCAACAAACAAAGATGCTAATGTCA 240
QY 2358 CTGTAATGAGGAGGAAATGTAACCGAGAGCTAGATCTTAACCTGGTACTTAGGAATTT 2417
Db 241 CTGTAATGAGGAGGAAATGTAACCGAGAGCTAGATCTTAACCTGGTACTTAGGAATTT 300
QY 2418 ATTCAAGTTTAACGTAGCTACCGTTCTTTTGGCATAGCAAGATCTATGTTATCT 2477
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QY 2538 CTCGGTATTATTTTGTATAGAAATCCAATAGGAAGAAATTTAAATCGTTTCTCCAAAG 2597
Db 421 CTCGGTATTATTTTGTATAGAAATCCAATAGGAAGAAATTTAAATCGTTTCTCCAAAG 480
QY 2598 ACATTGACACTTGGATGATTTGTCGCCGTGACGTTTGTAGATTTCAATCCAGACATTGC 2657
Db 481 ACATTGACACTTGGATGATTTGTCGCCGTGACGTTTGTAGATTTCAATCCAGACATTGC 540
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Db 541 TACAAGTGGTTGGTGTCTGTGCTGTGCGCGTGATTCCTTGGATCGCAATACCT 600
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Db 601 TGGTTCCTTGGAAATCATTTTCTTCTGGCGGATATTTTGGAAACGCTCAAGAG 660
QY 2778 ATGTGAAGCCCTGGAAATCTACAACTCGGAGTCAGTGTGTTTCCCACTTGTCACTCTC 2837
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Db 721 TCAGGGGCTCTGG 734
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LOCUS BQ069612
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DEFINITION AGENCOURT_6796693 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5812052
5', mRNA sequence.
ACCESSION BQ069612
VERSION BQ069612.1 GI:19898658
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1139)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2061 row: n column: 21
High quality sequence start: 10
High quality sequence stop: 618.
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/db_xref="taxon:9606"
/clone="IMAGE:5812052"
/clone_lib="NIH_MGC_47"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 314 a 259 c 280 g 285 t 1 others
ORIGIN
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Query Match 16.7%; Score 706.6; DB 14; Length 1139;
Best Local Similarity 98.4%; Pred. No. 1.8e-188;
Matches 745; Conservative 0; Mismatches 9; Indels 3; Gaps 3;
QY 12 GCGCGCGAGCCCGCAGCATCCCTGCTTGAGGTCCAGGAGCGGCGCCGCGCCGCG 71
Db 23 GGGCGCGAGCCCGCAGCATCCCTGCTTGAGGTCCAGGAGCGGCGCCGCGCCGCG 82
QY 72 CCTGATCAGCGGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 131
Db 83 CCTGATCAGCGGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 142
QY 132 AGGAGGTGAACCCCAACCCCGCTGCGAGGACGCGAACATCTGCTCAGCGCTGTTCTTGTGT 191
Db 143 AGGAGGTGAACCCCAACCCCGCTGCGAGGACGCGAACATCTGCTCAGCGCTGTTCTTGTGT 202
QY 192 GGCTCAATCCCTTGTGTTTAAATTTGGCCATAAACGGAGATTAGAGGAAGATGATGTATT 251
Db 203 GGCTCAATCCCTTGTGTTTAAATTTGGCCATAAACGGAGATTAGAGGAAGATGATGTATT 262
QY 252 CAGTGTCTCCAGAGAGCCGCTCACAGCACCTTGGAGAGAGTTGCAAGGTTCTGGGATA 311
Db 263 CAGTGTCTCCAGAGAGCCGCTCACAGCACCTTGGAGAGAGTTGCAAGGTTCTGGGATA 322
QY 312 AAGAAGTTTTTAAGAGCTGAGAAATGACGACACAGACCCCTTCTTTAAACAGAGCAATATAA 371
Db 323 AAGAAGTTTTTAAGAGCTGAGAAATGACGACACAGACCCCTTCTTTAAACAGAGCAATATAA 382
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QY 372 AGTGTACTGGAAATCTTATTTAGTTTGGGAATTTTACGTTAATTTAGGAAAGTGCCA 431
 Db 383 AGTGTACTGGAAATCTTATTTAGTTTGGGAATTTTACGTTAATTTAGGAAAGTGCCA 442
 QY 432 AAGTAATCAGGCCATATTTTGGGAAATATTTAATTTTGAATATTTATGATCCCA 491
 Db 443 AAGTAATCAGGCCATATTTTGGGAAATATTTAATTTTGAATATTTATGATCCCA 502
 QY 492 TGGATCTCTGGCTTTGAACACAGCGTAGCCATATGACCGGTGCTGACTTTTTCACGC 551
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 Db 742 GATCAGGTGAACATGGTTCTTAACTTCCTGTGGGGA 778

RESULT 3
 BQ889997
 LOCUS
 DEFINITION BQ889997 896 bp mRNA linear EST 16-AUG-2002
 5', mRNA sequence. AGENCOURT_8730208 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6339494

ACCESSION BQ889997
 VERSION BQ889997.1 GI:22282011
 KEYWORDS EST.

SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 896)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: egapbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2534 row: g column: 15
 High quality sequence stop: 599.

FEATURES
 source

1. .896
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 /lab_host="DH10B (phage-resistant)"
 /note="Organ: brain; Vector: pORF7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAAGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT 223 a 228 c 226 g 218 t 1 others
 ORIGIN

Query Match 15.7%; Score 664.8; DB 14; Length 896;
 Best Local Similarity 97.1%; Pred. No. 1.2e-176;
 Matches 699; Conservative 0; Mismatches 17; Indels 4; Gaps 2;

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 QY 75 GATCAGCGGACCCCGGCCCGGCCCGGCCCGGCCGGAAGATGCTGCCGCTGATACAGG 134
 Db 61 GATCAGCGGACCCCGGCCCGGCCCGGCCCGGCCGGAAGATGCTGCCGCTGATACAGG 120
 QY 135 AGGTGAAGCCCAACCCGCTGCGAGCGCGAACAATCTGCTCACGCTGCTTCTCTGGTGGC 194
 Db 121 AGGTGAAGCCCAACCCGCTGCGAGCGCGAACAATCTGCTCACGCTGCTTCTCTGGTGGC 180
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 QY 315 AAGTTTTAAGAGCTGAGAATGAGCGACAGCAAGCCCTTCTTTAAACAAGCAATCATAAAGT 374
 Db 301 AAGTTTTAAGAGCTGAGAATGAGCGACAGCAAGCCCTTCTTTAAACAAGCAATCATAAAGT 360
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 QY 615 GAGTAGCCATGCTCCATATGATTTATCGGAAGCACTTCGCTTAGTACATGGCCATGG 674
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 QY 675 GG-AAGACAACACAGGCGCAGATAGTCAATCT--GCTGTCCAATCATGTGAACAAGTTT 730
 Db 661 GGAAGACACCAACCAAGCCAGCATAGTCAATCTTGTGTTCCAATCATGTGAACAAGTTT 720

RESULT 4
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 601484613F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887306 5',
 mRNA sequence.
 ACCESSION BQ879353
 VERSION BQ879353
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 682)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Prepared by: Life Technologies, Inc.
CDNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9665 row: i column: 03
High quality sequence stop: 682.
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/db_xref="taxon:9606"
/clone_lib="NIH_MGC_69"
/tissue_type="large cell carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.1 kb. Library constructed by Life Technologies."
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ORIGIN

Query Match 15.0%; Score 636.4; DB 12; Length 682;
Best Local Similarity 99.3%; Pred. No. 1.2e-168;
Matches 681; Conservative 0; Mismatches 1; Indels 4; Gaps 4;
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DB 1 AAGGCTTTCCTTACTGTGACAGCTGGCGAATTTAGTGTGGTGGCCCGTGGGAG 60
QY 1461 CAGGGAAGTCATCATTGTTAAGTGGCGTGTCTCGGGAATTTGGCCCAAGTCACGGGCTGG 1520
DB 61 CAGGGAAGTCATCATTGTTAAGTGGCGTGTCTCGGGAATTTGGCCCAAGTCACGGGCTGG 120
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DB 181 TCAGGAGTAATATTTTATTTGGGAAGAAATATGAAAGGAACCATATGAAAGAGTCATAA 240
QY 1641 AGGCTTGTCTCTGAAAAAGGATTTACAGCTGTGTGAGGATGGTGATCTGACTGTGATAG 1700
DB 241 AGGCTTGTCTCTGAAAAAGGATTTACAGCTGTGTGAGGATGGTGATCTGACTGTGATAG 300
QY 1701 GAGATCGGGGAACCGCTGAGTGGAGGCGAGAAACGACGGGTAAACCTTGCAAGAGCAG 1760
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DB 481 TAGTGACTCATCAGTTGCAGTACCTCAAGCTGCAAGTCAGATCTTGATATGCAAGATG 540
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DB 541 GTAAATGTGTCAGAGGGGACTTACACTGAGTTCTTAAATCTGCTATAGATTTTGGCT 600
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DB 601 CCCTTTTAAAGAGGAT-ATGAGGAAGTGACAA-CTCCAGTTCAGGAACTCCCAACAC- 657

QY 2061 TAAGGAATCGTACCTTCTCAGAGTCT 2086
DB 658 TAAGGAATCGTA-CTTCTCAGAGTCT 682
RESULT 5
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LOCUS
DEFINITION
601491617F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893669 5',
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BE879718
ACCESSION
BE879718.1 GI:10328494
VERSION
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 727)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9682 row: b column: 06
High quality sequence stop: 571.
Location/Qualifiers
1. 727
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_69"
/tissue_type="large cell carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.1 kb. Library constructed by Life Technologies."
BASE COUNT 235 a 179 c 162 g 151 t
ORIGIN
Query Match 14.5%; Score 612.4; DB 12; Length 727;
Best Local Similarity 96.8%; Pred. No. 7.7e-162;
Matches 647; Conservative 0; Mismatches 21; Indels 2; Gaps 2;
QY 3178 AGAAGACCTTGGGAATATCAGAAACCCACACACCGCTGGCCCATGAAGAGTGAT 3237
DB 1 AGAAGACCTTGGGAATATCAGAAACCCACACACCGCTGGCCCATGAAGAGTGAT 60
QY 3238 AATCTTTGACAAATGTGAATTCATGTACAGTCCAGGTGGGCCCTCTGGTACTGAAGCATCT 3297
DB 61 AATCTTTGACAAATGTGAATTCATGTACAGTCCAGGTGGGCCCTCTGGTACTGAAGCATCT 120
QY 3298 GACAGCACTATTAAATCACAAGAAAGTTGGCATTTGTGGGAAGACCGGAGCTGGAA 3357
DB 121 GACAGCACTATTAAATCACAAGAAAGTTGGCATTTGTGGGAAGACCGGAGCTGGAA 180
QY 3358 AAGTCCCTCATCTCAGCCCTTTTGTAGATTGTGACAGCCGAGGTAATTTGGATTGA 3417
DB 181 AAGTCCCTCATCTCAGCCCTTTTGTAGATTGTGACAGCCGAGGTAATTTGGATTGA 240
QY 3418 TAAGATCTTTGACAACTGAAATTTGGACTTTCAGATTTTAAAGGAAGAAATGTCAATATACC 3477
DB 241 TAAGATCTTTGACAACTGAAATTTGGACTTTCAGATTTTAAAGGAAGAAATGTCAATATACC 300
QY 3478 TCAGGAACCTGTTTGTCTACTGGAACAATGAGGAAACCTGGATCCCTTTAAGGAGCA 3537
DB 1 TCAGGAACCTGTTTGTCTACTGGAACAATGAGGAAACCTGGATCCCTTTAAGGAGCA 657

```

Db 301 TCAGGAACCTGTTTGTTCACCTGGACAACTGAGGAAACCTGGATCCCTTTAATGAGCA 360
QY 3538 CACGATGAGGAAGTGGTGAATGCTTACAGAGGTACAACACTTAAAGAAACATTGAAGA 3597
Db 361 CACGATGAGGAAGTGGTGAATGCTTACAGAGGTACAACACTTAAAGAAACATTGAAGA 420
QY 3598 TCTTCTCGTAAATGGATGCTGAATAGCAGATCAAGATCCCAATTTAGTGTGGACA 3657
Db 421 TCTTCTCGTAAATGGATGCTGAATAGCAGATCAAGATCCCAATTTAGTGTGGACA 480
QY 3658 AAGACAACCTGGTGTGCTTCCAGGCGCAATCTCAGGAAATATCAGATATTCATTATTGA 3717
Db 481 AAGACAACCTGGTGTGCTTCCAGGCGCAATCTCAGGAAATATCAGATATTCATTATTGA 540
QY 3718 TGAAGCGACGGCAATGTGGATCAAGAACTG-ATGAGTTTAAATACAAAAAATCCGGG 3776
Db 541 TGAAGCGACGGCAATGTGGATCAAGAACTG-ATGAGTTTAAATACAAAAAATCCGGG 600
QY 3777 AGAAATTTGCCACTGCACCGCTGCTAACCATTGCACACAGA-TTGAACACCATTTATTCAC 3835
Db 601 AGAAATTTGCCACTGCACCGCTGCTAACCATTGCACACAGA-TTGAACACCATTTATTCAC 660
QY 3836 AGCGACAAGA 3845
Db 661 CGCGACAAGA 670

RESULT 6
LOCUS BI771442 689 bp mRNA linear EST 25-SEP-2001
DEFINITION 603059489F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5208502 5',
mRNA sequence.
ACCESSION BI771442
VERSION BI771442.1 GI:15763020
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 689)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1523 row: b column: 23
High quality sequence stop: 689.
FEATURES
Location/Qualifiers
1..689
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5208502"
/clone_lib="NIH_MGC_122"
/lab_host="PH10B"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site: 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."
BASE COUNT 201 a 135 c 155 g 198 t
ORIGIN

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Query Match 13.8%; Score 582.8; DB 13; Length 689;
Best Local Similarity 97.0%; Pred. No. 1.9e-153;
Matches 669; Conservative 0; Mismatches 12; Indels 9; Gaps 7;

QY 1797 CTCTCAGTGCAGTGCAGGAAAGTTAGCAGACACACTTGTTCGAACTGTGTATTGTCAA 1856
Db 1 CTCTCAGTGCAGTGCAGGAAAGTTAGCAGACACACTTGTTCGAACTGTGTATTGTCAA 60
QY 1857 T-TTTCATGAGAGATCACAATTTTAGTGACTCATCAGTTGAGTACCTCAAAAGTCGA 1915
Db 61 TGATTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGAGTACCTCAAAAGTCGA 120
QY 1916 AGTCAGATTCTGATATTGAAAGATGTAATAA-TGGTGCGAAGGGGACTTACACTGAGTT 1974
Db 121 AGTCAGATTCTGATATTGAAAGATGTAATAAAGTGGTGCAGAGGGGACTTACACTGAGTT 180
QY 1975 CCTAA-AATCTCGTATAGATTTTGGCTCCCTTTTAAAGAGAGGATAA--TGAGGAAAGTGA 2031
Db 181 CCTAAGAACTCGTATAGATTTTGGCTCCCTTTTAAAGAGAGGATAAAGTGCAGGACAACTGA 240
QY 2032 ACAACCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGT 2091
Db 241 ACAACCTCCAGTTCAGGAACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGT 300
QY 2092 TTGGTCTCAA-CAATCTTCTAGACCTCCCTTGAAGATGGTCTCTGGAGAGCCAAAGATA 2150
Db 301 TTGGTCTCAA-CAATCTTCTAGACCTCCCTTGAAGATGGTCTCTGGAGAGCCAAAGATA 360
QY 2151 CAGAGAAATGTCCTCAGTATACACTATCAGAGGAAACCGTCTCTGAAGAAAGTTGGTTTC 2210
Db 361 CAGAGAAATGTCCTCAGTATACACTATCAGAGGAAACCGTCTCTGAAGAAAGTTGGTTTC 420
QY 2211 AGGCTATAAGAAATTAATTCAGAGTGGTGTCTCAGTGGATGTCTTCAATTTTCCCTTATTC 2270
Db 421 AGGCTATAAGAAATTAATTCAGAGTGGTGTCTCAGTGGATGTCTTCAATTTTCCCTTATTC 480
QY 2271 TCCTAAACACTGCAGCTCAGGTTGCTATGTCTTCAAGATGGTGGCTTTCATCTACTGGG 2330
Db 481 TCCTAAACACTGCAGCTCAGGTTGCTATGTCTTCAAGATGGTGGCTTTCATCTACTGGG 540
QY 2331 CAACAAACAAAGTATGCTAAATGTCACTGTAACTGGCAGGAGGAAATGTAAACCGAGAA 2388
Db 541 CAACAAACAAAGTATGCTAAATGTCACTGTAACTGGCAGGAGGAAATGTAAACCGAGAA 600
QY 2389 GCTAGATCTTAAGTGGTACTTAGGAAATTAATTCAGGTTTAAGTACCTGACCTGTTCTTTT 2448
Db 601 GCTAGATCTTAAGTGGTACTTAGGAAATTAATTCAGGTTTAAGTACCTGACCTGTTCTTTT 659
QY 2449 TGGCATAGCAAGATCTCTATTGGTATTCTA 2478
Db 660 AGGCATAGCCAGATCTCTATTGGTATTCTA 689

RESULT 7
LOCUS BE885514 926 bp mRNA linear EST 20-OCT-2000
DEFINITION 601508707F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910441 5',
mRNA sequence.
ACCESSION BE885514
VERSION BE885514.1 GI:10334290
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 926)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC

```

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM9725 row: m column: 02
High quality sequence stop: 590.
Location/Qualifiers
1. 926
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3910441"
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/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."
BASE COUNT 318 a 188 c 224 g 196 t
ORIGIN

Query Match 12.9%; Score 546; DB 12; Length 926;
Best Local Similarity 90.0%; Pred. No. 5.8e-143;
Matches 657; Conservative 0; Mismatches 55; Indels 18; Gaps 6;
QY 1718 CTGAGTGGAGGGGAGAAAGCAGCGGTAAACCTTGCAGAGACAGTGTATCAAGATGCTGAC 1777
DB 1 CTGAGTGGAGGGGAGAAAGCAGCGGTAAACCTTGCAGAGACAGTGTATCAAGATGCTGAC 60
QY 1778 ATCTATCTCTGACGATCCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTGTTTC 1837
DB 61 ATCTATCTCTGACGATCCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTGTTTC 120
QY 1838 GAACCTGTGATTTGTCAAAATTTGCGATGAGAGATCACAAATTTAGTGACTCATCAGTTG 1897
DB 121 GAACCTGTGATTTGTCAAAATTTGCGATGAGAGATCACAAATTTAGTGACTCATCAGTTG 180
QY 1898 CAGTACTCTAAAGCTCAAGTCAAGTCTGTATTTGAAAGATGTTAAATGGTGCAGAA 1957
DB 181 CAGTACTCTAAAGCTCAAGTCAAGTCTGTATTTGAAAGATGTTAAATGGTGCAGAA 240
QY 1958 GGCACCTTACACTAGTCTCTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGAT 2017
DB 241 GGCACCTTACACTAGTCTCTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGAT 300
QY 2018 AATGAGGAAAGTGAACAACCTCCAGTTCCAGGAACTCCACACTAAGGAATCGTACTTC 2077
DB 301 AATGAGGAAAGTGAACAACCTCCAGTTCCAGGAACTCCACACTAAGGAATCGTACTTC 360
QY 2078 TCAGAGTCTTGGTCTCAACAATCTCTAGACCCCTCCCTTGAAGATGCTGCTG 2137
DB 361 TCAGAGTCTTGGTCTCAACAATCTCTAGACCCCTCCCTTGAAGATGCTGCTG 420
QY 2138 GAGAGCCAGATACAGAGATGTCACAGTACACTATCAG-AGGAGACCGTTCTGAAG 2196
DB 421 GAGAGCCAGATACAGAGATGTCACAGTACACTATCAGAGAGAACCGTTCTGAAG 480
QY 2197 AAAAGTTGGTTTTCAGGCTTATAAGAAATTAATCTCA--GAGCTGGTCTCACTGGATTGTC 2254
DB 481 ACAGTAGGCTCAAGGCTTATAAGAAATTAATCTCAAGAGAGCTGGTCTCACTGGATTGTC 540
QY 2255 TTCAATTTCTTATCTCC--TAAACACTGCAGCTCAGGTGGCTATGCTGCTTCAAGATT 2312
DB 541 TTCAATTTCTTATCTCC--TAAACACTGCAGCTCAGGTGGCTATGCTGCTTCAAGAT 600
QY 2313 GTTGGCTTTCATCT-----GGGCAACAAACAAGATAT-----GCTAATGTCACTGTA 2362
DB 601 TCGGGCTTATCATCAACTACCTGGGGGAGAGAAAGATATGCTAAATGTTTCACTGTA 660
QY 2363 AATG---GAGGAGGAATGTAAACCGAGAGAGCTAGATCTTAACTGGTACTTAGGAATTTAT 2419
DB 661 AATGGAGGGAGGAAAGTGTACCGAGAAAGTAGAGTTTAAACGGGGACCTTAGGAATACAT 720

QY 2420 TCAGGTTTAA 2429
DB 721 TCAGGTTTAA 730
RESULT 8
LOCUS AL701816 497 bp mRNA linear EST 22-MAR-2002
DEFINITION DKFZp686F08149_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
ACCESSION AL701816
VERSION AL701816.1 GI:19685172
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 497)
Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.)
Unpublished (1999)
Contact: Wambutt R
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No sl sequence available.
This clone (DKFZp686F08149) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source
1. 497
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp686F08149"
/clone_lib="686 (synonym: hlcc3)"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"
BASE COUNT 159 a 84 c 126 g 128 t
ORIGIN

Query Match 11.4%; Score 483.4; DB 9; Length 497;
Best Local Similarity 99.6%; Pred. No. 2.5e-125;
Matches 495; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1581 TGAGGAGTAATATTTTATTTGGGAAGAAATATGAAAGGACGATATCAAAAGCTCATAA 1640
DB 1 TGAGGAGTAATATTTTATTTGGGAAGAAATACGAAAGGACGATATCAAAAGCTCATAA 60
QY 1641 AGGCTTGCTCTGAAAAGGATTTACAGCTGTTGGAGGATGGTGATCTGCTGATAG 1700
DB 61 AGGCTTGCTCTGAAAAGGATTTACAGCTGTTGGAGGATGGTGATCTGCTGATAG 120
QY 1701 GAGATCGGGGAACACCTCAGTGGAGGCGAGAAAGCACGGGTAAACCTTGCAGAGCAG 1760
DB 121 GAGATCGGGGAACACCTCAGTGGAGGCGAGAAAGCACGGGTAAACCTTGCAGAGCAG 180
QY 1761 TGTATCAAGATGCTGACATCTATCTCTGACGATCTCTCAGTGCAGTAGATCGGGAAG 1820
DB 181 TGTATCAAGATGCTGACATCTATCTCTGACGATCTCTCAGTGCAGTAGATCGGGAAG 240
QY 1821 TTAGCAGACACTTGTTCGAACTGTGATTTTGCATAATTTTCCATGAGAAGATCACAATTT 1880
DB 241 TTAGCAGACACTTGTTCGAACTGTGATTTTGCATAATTTTGCATGAGAAGATCACAATTT 300
QY 1881 TAGTGACTCATCAGTTGTCAGTACCTCAAGCTCGCAAGTCAGATTTCTGATATTGAAGATG 1940

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|||||
Db 301 TAGTGACTCAGTTGCGAGTACCTCAAGCTGCAAGTCAGATTCGATTTGAAAGATG 360
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QY 1941 GTAAATGGTGAGAGGGGACTTACACTGAGTTCCTAAATCTGATATAGATTTGGCT 2000
|||||
Db 361 GTAAATGGTGAGAGGGGACTTACACTGAGTTCCTAAATCTGATATAGATTTGGCT 420
|||||
QY 2001 CCCTTTTAAAGAGGATATAGAGGAAGTGAACAACCTCCAGTTCAGGAA-CTCCACA 2059
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Db 421 CCCTTTTAAAGAGGATATAGAGGAAGTGAACAACCTCCAGTTCAGGAACTCCACA 480
|||||
QY 2060 CTAAGGAATCGTACCTT 2076
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Db 481 CTAAGGAATCGTACCTT 497

RESULT 9
BE674208/c
LOCUS BE674208 478 bp mRNA linear EST 08-SEP-2000
DEFINITION 7076907.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278940 3'
similar to FR:075555 075555 ABC TRANSPORTER MOAT-B ISOFORM ;, mRNA
sequence.
ACCESSION BE674208
VERSION BE674208.1 GI:10034749
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 478)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: rcapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares (Pharmacica) with a
modified polylinker; Plasmid DNA from the normalized
library NCI_CGAP_Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clonoids
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo.
BASE COUNT 122 a 107 c 80 g 168 t 1 others
ORIGIN

Query Match 11.0%; Score 467.4; DB 10; Length 478;
Best Local Similarity 98.5%; Pred. No. 8.5e-121;
Matches 471; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3287 CTGAGCATCTGACGAGCACTCATTAATCAACAAGAAAGTTGGCATTTGGGAAGAAC 3346
|||||
Db 478 CTGAGCATTTGACGAGCACTCATTAATCAACAAGAAAGTTGGCATTTGGGAAGAACT 419

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QY 3347 GGAGCTGGAAGAAAGTTCCTCATCTCAGCCCTTTTAGATTGTCAGAACCCGAGGTAAA 3406
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Db 418 GGAGNTGGAAGAAAGTTCCTCATCTCAGCCCTTTTAGATTGTCAGAACCTGAAGGTAAA 359
|||||
QY 3407 ATTTGGATTGATAAGATCTTTGACAACCTGAAATTTGGACTTCACGATTTTAAAGGAAGAAATG 3466
|||||
Db 358 ATTTGGATTGATAAGATCTTTGACAACCTGAAATTTGGACTTCACGATTTTAAAGGAAGAAATG 299
|||||
QY 3467 TCAATCATACCTCAGGAACCTGTTTGTCTCACTGGAAACAATGAGGAAAAAACCCTGGATCCC 3526
|||||
Db 298 TCAATCATACCTCAGGAACCTGTTTGTCTCACTGGAAACAATGAGGAAAAAACCCTGGATCCC 239
|||||
QY 3527 TTTAAGGAGCACACGCGATGAGGAACCTGTGGAATGCCCTTACAAGAGGTACAACTTAAAGAA 3586
|||||
Db 238 TTTAATGAGCACACGCGATGAGGAACCTGTGGAATGCCCTTACAAGAGGTACAACTTAAAGAA 179
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QY 3587 ACCATTGAAGATCTTCTCGTAAATGGATGACTGAATTAGCAGAATCAGGATCCAAATTTT 3646
|||||
Db 178 ACCATTGAAGATCTTCTCGTAAATGGATGACTGAATTAGCAGAATCAGGATCCAAATTTT 119
|||||
QY 3647 AGTGTGGACAACAAGAACCTGGTGTGCTCCAGGCAATTCACGAAAAAATCAGATA 3706
|||||
Db 118 AGTGTGGACAACAAGAACCTGGTGTGCTCCAGGCAATTCACGAAAAAATCAGATA 59
|||||
QY 3707 TTGATTATTGATGAAGCGAGCGCAAAATGTGGATCCAGAACTGATGATTAATACAAA 3764
|||||
Db 58 TTGATTATTGATGAAGCGAGCGCAAAATGTGGATCCAGAACTGATGATTAATACAAA 1

RESULT 10
LOCUS BB225682 639 bp mRNA linear EST 23-OCT-2001
DEFINITION BB225682 RIKEN full-length enriched, adult male aorta and vein Mus
musculus cDNA clone A530093r19 3' similar to U83660 Human multidrug
resistance-associated protein homolog (MRP4) mRNA, mRNA sequence.
ACCESSION BB225682
VERSION BB225682.2 GI:16353983
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 639)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda,
M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki,
D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
On Jul 3, 2000 this sequence version replaced gi:8896327.
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Muramatsu, M. and Hayashizaki, Y.
M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura,
S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format

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Best Local Similarity 99.8%; Pred. No. 3.6e-111;
Matches 434; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3326 GTTGCCATTGTGGGAGAACCGGAGCTGGAAAAAGTTCCCTCATCTCAGCCCTTTTATGA 3385
Db 435 GTTGGCATTGTGGGAGAACCGGAGCTGGAAAAAGTTCCCTCATCTCAGCCCTTTTATGA 376
QY 3386 TTGTCAGAACCCGAGGTTAAATTTGGATTGATGATGATCTTGACAACTGAAATTTGGACTT 3445
Db 375 TTGTCAGAACCCGAGGTTAAATTTGGATTGATGATGATCTTGACAACTGAAATTTGGACTT 316
QY 3446 CACGATTTAAGGAAGAAATGTCATATCATCTCAGAACCTGTTTGTCTACTGGAACA 3505
Db 315 CACGATTTAAGGAAGAAATGTCATATCATCTCAGAACCTGTTTGTCTACTGGAACA 256
QY 3506 ATGAGGAAAACTGGATCCCTTTAAGGAGCACACGCGATGAGAACTGTGGAAATGCTTTA 3565
Db 255 ATGAGGAAAACTGGATCCCTTTAAGGAGCACACGCGATGAGAACTGTGGAAATGCTTTA 196
QY 3566 CAAGAGGTACAACTTAAAGAAACCAATTTGAAGATCTTCTGTTGTTAAATGATGATCTGAATTA 3625
Db 195 CAAGAGGTACAACTTAAAGAAACCAATTTGAAGATCTTCTGTTGTTAAATGATGATCTGAATTA 136
QY 3626 GCAGAAATCAGGATCAATTTAGTCTGTCGACAAACACAACTGCTGCTTCCAGGGCA 3685
Db 135 GCAGAAATCAGGATCAATTTAGTCTGTCGACAAACACAACTGCTGCTTCCAGGGCA 76
QY 3686 ATTCTCAGGAAAAATCAGATATTGATTTAGTGAAGCGACGCAAAATGTGGATCCAAGA 3745
Db 75 ATTCTCAGGAAAAATCAGATATTGATTTAGTGAAGCGACGCAAAATGTGGATCCAAGA 16
QY 3746 ACTGATGAGTTAATA 3760
Db 15 ACTGATGAGTTAATA 1

RESULT 12
AUI26646
LOCUS AUI26646 NT2RP1 Homo sapiens cDNA clone NT2RP1001350 5', mRNA
DEFINITION AUI26646 465 bp mRNA linear EST 01-AUG-2002
sequence.
ACCESSION AUI26646
VERSION AUI26646.1 GI:10951362
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 465)
Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.
HRI human cDNA project (Ota, T., Nishikawa, T., Suzuki, Y., Kawai, Y.,
Ishii, S., Saito, K., Nakamura, Y., Nagai, T., Sugano, S., Isogai, T.)
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
source Location/Qualifiers
1. .465
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/clone="NT2RP1001350"
/clone_lib="NT2RP1"
/cell_type="teratocarcinoma"
/cell_line="NT2"

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/Note="Vector: pUC19FL3; mRNA from NT2 neuronal precursor
cells after 48-hours retinoic acid (RA) induction"
BASE COUNT 161 a 80 c 106 g 115 t 3 others
ORIGIN
Query Match 10.2%; Score 433; DB 9; Length 465;
Best Local Similarity 98.6%; Pred. No. 4.8e-111;
Matches 436; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3480 AGAACTCTGTTTGTCTACATGGAACATGAGGAAAAACCTGGATCCCTTTAAGGAGCACA 3539
Db 14 AGAACTCTGTTTGTCTACATGGAACATGAGGAAAAACCTGGATCCCTTTAAGGAGCACA 73
QY 3540 CGGATGAGGAACGTGGAATGCTTACAAGAGGTACAACTTAAAGAAACCACTTGAAGATC 3599
Db 74 CGGATGAGGAACGTGGAATGCTTACAAGAGGTACAACTTAAAGAAACCACTTGAAGATC 133
QY 3600 TTCTCTGTAATGATGATCTGAATTTAGCAGAATCAGGATCCCAATTTTAGTGTTCGACAAA 3659
Db 134 TTCTCTGTAATGATGATCTGAATTTAGCAGAATCAGGATCCCAATTTTAGTGTTCGACAAA 193
QY 3660 GACAACTGTTGCTTGTCCCTTGCAGGGCAATTTCTCAGGAAAAATCAGATATTGATTATGATG 3719
Db 194 GACAACTGTTGCTTGTCCCTTGCAGGGCAATTTCTCAGGAAAAATCAGATATTGATTATGATG 253
QY 3720 AAGCGACGCAAAATGTTGATCCCAAGAACTGATGATTAACAAAAAATCCGGGAGA 3779
Db 254 AAGCGACGCAAAATGTTGATCCCAAGAACTGATGATTAACAAAAAATCCGGGAGA 313
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QY 3840 ACAAGATATGTTTGTAGATTCAGGAAGACTGAAAGAAATATGATGACCGCTATGTTTTCG 3899
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Db 434 GGCATAAATAAGAGAGCCCTTTT 455

RESULT 13
BB643073
LOCUS BB643073 734 bp mRNA linear EST 26-OCT-2001
DEFINITION BB643073 RIKEN full-length enriched, 9.5 days embryo parthenogenote
Mus musculus cDNA clone B130008G09 5', mRNA sequence.
ACCESSION BB643073
VERSION BB643073.1 GI:16477826
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 734)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki
D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:00:25 ; Search time 529.063 Seconds
(without alignments)
18009.573 Million cell updates/sec

Title: US-09-647-140A-1

Perfect score: 4231

Sequence: 1 gacaggcgctggcgccgga.....ttcattgaattattctccc 4231

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4231	100.0	4231	20	AAZ30078
2	4231	100.0	4231	22	AAH81778
3	4211	99.5	6082	22	AAS63921
4	4211	99.5	6082	22	AAH93828
5	4211	99.5	6082	22	AAH85142
6	4211	99.5	6082	24	ABL95292
7	4196.6	99.2	4515	23	ABV20669
8	4196.6	99.2	4515	23	ABV22410
9	4196.6	99.2	4515	23	ABV24188

10	4196.6	99.2	4515	23	ABV24580
11	4196.6	99.2	4515	23	ABV26511
12	4196.6	99.2	4515	23	ABV28224
13	3973.2	93.9	3978	24	AAK92135
14	3910.2	92.4	6140	22	AAS63922
15	3910.2	92.4	6140	22	AAH93829
16	3910.2	92.4	6140	22	AAH85143
17	3910.2	92.4	6140	24	ABL95293
18	1218	28.8	1427	21	AAF16178
19	1045.4	24.7	1074	22	AAS64134
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21	1045.4	24.7	1074	24	ABL95505
22	796	18.8	888	23	ABV24259
23	707.4	16.7	768	23	ABV12837
24	655.4	15.5	3391	23	ABL02707
25	655	15.5	2275	21	AAC63519
26	621	14.7	684	23	ABV33965
27	611.8	14.5	5504	23	ABL02706
28	589.8	13.9	633	23	ABV03668
29	569.4	13.5	4507	23	ABL25801
30	563.6	13.3	12059	23	ABL18886
31	551.6	13.0	7743	23	ABL18887
32	546.6	12.9	4351	23	ABL13149
33	541.6	12.8	643	23	ABV42833
34	528.8	12.5	4047	23	ABL07889
35	512.6	12.1	3720	23	ABL09969
36	491.8	11.6	4035	23	ABL04815
37	489.4	11.1	8496	23	ABL25800
38	480.2	10.9	486	18	AAT94053
39	450.4	10.6	4918	24	ABK63671
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ALIGNMENTS

RESULT 1

AAZ30078

ID AAZ30078 standard; cDNA; 4231 bp.

AC AAZ30078;

XX 26-JAN-2000 (first entry)

XX cDNA encoding a human MPR-related ABC transporter designated MOAT-B.

DE Human; MPR-related ABC transporter; MOAT protein; MOAT-B;

XX MOAT mediated transport; anticancer drug sensitivity;

KW transporter mediated cellular efflux; anticancer; ss.

XX Homo sapiens.

OS Key Location/Qualifiers

XX CDS 116..4093

FT /*tag= a

FT /product= "MOAT-B"

FT /transl_except= (pos: 1715..1717, aa: Pro)

FT /transl_except= (pos: 3566..3568, aa: Arg)

FT /note= "MPR-related ABC transporter"

XX WO9949735-A1.

XX 07-OCT-1999.

XX 26-MAR-1999;

XX 27-MAR-1998;

XX 03-AUG-1998;

PR 98US-0079759.

PR 98US-0095153.

Human prostate exp
Human prostate exp
Human prostate exp
Prostate cancer-as
Human prostate cDN
Human prostate-spe
Human prostate-spe
Human P510S cDNA s
Human prostate can
Human cDNA encodin
P510S-E3 construct
P510S-E3 construct
Human prostate exp
Human prostate exp
Human prostate exp
Drosophila melanog
Multi-drug resista
Human prostate exp
Drosophila melanog
Human prostate exp
Drosophila melanog
Drosophila melanog
Drosophila melanog
Drosophila melanog
Drosophila melanog
Drosophila melanog
Partial human mult
Rat sequence diffe
Rat canalicular mu
Drosophila melanog
Multidrug-resistan
Human multidrug re
Human MRP-beta cDN
cDNA encoding a hu

XX	PA	(FOXK-) FOX CHASE CANCER CENT.
XX	Kruh G, Lee K, Belinsky M, Bain L;	
XX	WPI: 1999-610812/52.	
XX	P-PSDB; AAY43541.	
XX	New transporter gene useful for screening for anti-cancer drugs -	
XX	Claim 1; Page 130-131; 153pp; English.	
XX	The present sequence encodes a human MPR-related ABC transporter (MOAT)	
XX	protein, designated MOAT-B. The protein comprises a multi-domain	
XX	structure including a tandem repeat of nucleotide binding folds	
XX	appended C-terminal to a hydrophobic domain, having Walker A and B ATP	
XX	binding sites and several potential membrane spanning domains. The MOAT	
XX	nucleic acids are useful for screening a test compound for inhibition of	
XX	MOAT mediated transport, indicated by restoration of anticancer drug	
XX	sensitivity, which in turn causes a reduction of transporter mediated	
XX	cellular efflux of anticancer agents. MOAT DNA or RNA may be used as	
XX	probes to detect the presence or expression of genes encoding MOAT	
XX	proteins. Anti-MOAT antibodies are useful for detecting and quantitating	
XX	MOAT proteins.	
XX	Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 other;	
XX	Query Match 100.0%; Score 4231; DB 20; Length 4231;	
XX	Best Local Similarity 100.0%; Pred. No. 0;	
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RESULT 2

AAH81778
ID AAH81778 standard; DNA; 4231 BP.
XX
AC AAH81778;
XX
DT 21-SEP-2001 (first entry)
XX
DE Human differential transcription-associated cDNA SEQ ID 287.
XX
KW Differential transcription; human; rat; tumour cell; cytostatic;
KW Ras modulator; Class II tumour suppressor gene; gene therapy; ss.
XX
XX Homo sapiens.
OS
PN WO200157058-A2.
XX
PD 09-AUG-2001.
XX
PF 31-JAN-2001; 2001WO-EP01003.
XX
PR 31-JAN-2000; 2000DE-1004102.
XX
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI Rosenthal A, Hinzmann B, Schaefer R, Zuber J, Tchernitsa O;
PI Grips M, Hellriegel M, Schmitz A, Sers C;
XX
WPI; 2001-483415/52.

Nucleic acids differentially expressed between tumor and normal cells,
useful for diagnosis or therapy of tumors and for screening active
agents

Disclosure; Page 442-443; 579pp; German.

This invention describes a nucleic acid (I) with differential expression
between tumour and normal cells and which has cytostatic activity. (I)
work as modulators of Ras activity by inducing expression of tumour
suppressor genes. (I), and polypeptides encoded by them, are useful as
targets for diagnosis or therapy and in screening to determine the
effects of an active compound (potential pharmaceutical) on a cell line,
particularly for diagnosis and treatment of tumors, especially by
modulating expression of (I) (by gene therapy, antisense RNA or ribozyme
methods) or by modulating the amount and/or location of (I)-encoded
polypeptides (by administration of the polypeptide or its activator,
antibody (optionally as a conjugate) or inhibitor). The method allows
identification of many Class II tumour suppressor genes (i.e. genes that
are not primary targets for tumour-initiating mutations).

CC AAH81492-AAH82376 represent the human and rat derived nucleic acid
CC fragments described in the method of the invention.
XX
SQ Sequence 4231 BP; 1170 A; 895 C; 1015 G; 1151 T; 0 other;
Query Match 100.0%; Score 4231; DB 22; Length 4231;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGACAGCGTGGCGCGGAGCCCGCCAGCATCCCTGCTTGGAGTCCAGAGCGGAGCCCGC 60
Db 1 GGACAGCGTGGCGCGGAGCCCGCCAGCATCCCTGCTTGGAGTCCAGAGCGGAGCCCGC 60
QY 61 GGCACCGCGCCCTGATCAGCGGACCCCGCCGCGCCCGCCCGCCCGCCGCAAGATGCT 120
Db 61 GGCACCGCGCCCTGATCAGCGGACCCCGCCGCGCCCGCCCGCCCGCCGCAAGATGCT 120
QY 121 GCCCGTGTACAGAGGTGAAGCCCAACCCGCTGCGAGGCGCAACATCTGCTCACGGGT 180
Db 121 GCCCGTGTACAGAGGTGAAGCCCAACCCGCTGCGAGGCGCAACATCTGCTCACGGGT 180
QY 181 GTTCTTCTGCTGCTCAATCCCTTGTAAATTTGGCCATAAACCGAGATTAGAGGAAGA 240
Db 181 GTTCTTCTGCTGCTCAATCCCTTGTAAATTTGGCCATAAACCGAGATTAGAGGAAGA 240
QY 241 TGATATGTTATTCAGTGTGCGCAAGACCCGCTCACAGCACCTTTGGAGAGGAGTTGCAAGG 300
Db 241 TGATATGTTATTCAGTGTGCGCAAGACCCGCTCACAGCACCTTTGGAGAGGAGTTGCAAGG 300
QY 301 GTTCTGGGATAAAGAGTGTAAAGAGCTGAGATGAGCGCACAGAGCCCTCTTTAAACAAG 360
Db 301 GTTCTGGGATAAAGAGTGTAAAGAGCTGAGATGAGCGCACAGAGCCCTCTTTAAACAAG 360
QY 361 AGCAATCATAAAGTGTACTGGAAATCTTATTTAGTTTGGAAATTTTACGTTAAATGA 420
Db 361 AGCAATCATAAAGTGTACTGGAAATCTTATTTAGTTTGGAAATTTTACGTTAAATGA 420
QY 421 GGAAAGTGCCAAAGTAATCCAGCCCATATTTTGGGAAAAATTTAATTAATTTGAAAA 480
Db 421 GGAAAGTGCCAAAGTAATCCAGCCCATATTTTGGGAAAAATTTAATTAATTTGAAAA 480
QY 481 TTATGATCCCATGGATCTGTGGCTTTGAACACAGCGTACGCCCTATCCAGCGTGTGAC 540
Db 481 TTATGATCCCATGGATCTGTGGCTTTGAACACAGCGTACGCCCTATCCAGCGTGTGAC 540
QY 541 TTTTGTGACGCTCATTTTGGCTATCTGCTATCTATATTTTATCAGGTTTCAAGTGTGC 600
Db 541 TTTTGTGACGCTCATTTTGGCTATCTGCTATCTATATTTTATCAGGTTTCAAGTGTGC 600
QY 601 TGGGATGAGGTTACGAGTACGCCATGTGCCATATGATTTATCGGAAGGCACTTCGCTTAG 660
Db 601 TGGGATGAGGTTACGAGTACGCCATGTGCCATATGATTTATCGGAAGGCACTTCGCTTAG 660
QY 661 TACATGCGCATGGGGAAGACACACAGCCAGATAGTCAATCTGCTGCCAATGATGT 720
Db 661 TACATGCGCATGGGGAAGACACACAGCCAGATAGTCAATCTGCTGCCAATGATGT 720
QY 721 GAACAAGTTTGTATCAGGTGACAGTGTCTTACACTTCTGCGCAGGACCACTGCAGGC 780
Db 721 GAACAAGTTTGTATCAGGTGACAGTGTCTTACACTTCTGCGCAGGACCACTGCAGGC 780
QY 781 GATCGAGTGTGACGCTTCTGATGGAGATAGGAATATCGTCCCTGCTGGATGGC 840
Db 781 GATCGAGTGTGACGCTTCTGATGGAGATAGGAATATCGTCCCTGCTGGATGGC 840
QY 841 AGTTCTAATCATTTCTCTGCGCTTGCAGGCTGTTTGGGAAGTGTCTCATCACTGAG 900
Db 841 AGTTCTAATCATTTCTCTGCGCTTGCAGGCTGTTTGGGAAGTGTCTCATCACTGAG 900
QY 901 GAGTAAACTGCAACTTTCACGATGCCAGGATCAGGACCATGAATGAATTAATGAG 960
Db 901 GAGTAAACTGCAACTTTCACGATGCCAGGATCAGGACCATGAATGAATTAATGAG 960

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DB 1861 GCATGAGAGATCACAAATTTTAGTACTATCATAGTGTGACCTCAAAAGCTGCAAGTCA 1920
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DB 1921 GATTTCTGATATGAAAGATGTTAAATGTTGAGAGAGGATATGAGGAAAGTGAACACCTCC 1980
QY 1981 ATCTGTATAGATTTTGGTCCCTTTTAAAGAGGATATGAGGAAAGTGAACACCTCC 2040
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DB 3121 AGTTGAGAATATGATGATCTCAGTAGAAGGCTATTGAATACACAGACCTTTGAAAAAGA 3180


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3371 AGCACTCAATAATCACAAGAAAGGTTGGCAATTTGGGAAGAACCGGAGCTGGAAGAG 3430
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Db 4270 CAAGATGCTAGTTCAATTTGAATATTCTCCC 4300
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RESULT 4

AAH93828

ID AAH93828 standard; cdna; 6082 bp.

XX

AC AAH93828;

XX

DT 04-OCT-2001 (first entry)

XX

DE Human prostate-specific 1st full length cdna sequence for P510S.

XX

KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;

KW cytostatic; gene therapy; metastasis; ss.

XX

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OS Homo sapiens.
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US01574.
XX
PR 14-JAN-2000; 2000US-0483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Mesgher MJ;
XX WPI; 2001-425873/45.
DR
XX
XX New polynucleotide encoding a prostate-specific protein, for
XX diagnosing, monitoring and treating prostate cancer in a patient and
XX for use in vaccines -
XX
XX Claim 1; Page 411-412; 543pp; English.
XX
XX The present invention describes polynucleotide sequences (I) which encode
XX prostate-specific proteins (II). (I) and (II) have cytostatic activity,
XX and can be used in vaccine production and gene therapy. (I), (II),
XX antibodies to (II), fusion proteins comprising (II), and isolated
XX T cells prepared using (I) or (II) are used to treat cancer in a patient.
XX (I) and the antibodies are also used in the detection of cancer in a
XX patient. The cancer that is diagnosed or treated is particularly
XX prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
XX (I) can be used for monitoring the progression of cancer in a patient.
XX (I) and (II) can also be used to improve diagnostic and therapeutic
XX methods for prostate cancer. They can indicate the level of metastasis
XX as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
XX AAH01318 represent polynucleotide and amino acid sequences used in the
XX exemplification of the present invention.
XX
XX Sequence 6082 BP; 1721 A; 1249 C; 1357 G; 1755 T; 0 other;
XX
Query Match 99.5%; Score 4211; DB 22; Length 6082;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4225; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 1 GGACAGCGTGGCGCGGAGCCGCCAGCATCCCTGCTTGAGGTCAGGAGCGGAGCCCGC 60
DB 71 GGACAGCGTGGCGCGGAGCCGCCAGCATCCCTGCTTGAGGTCAGGAGCGGAGCCCGC 130
QY 61 GGCACCGCGCGCTGATCAGCGGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 120
DB 131 GGCACCTGCGCGCTGATCAGCGGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 190
QY 121 GCCCGGTACAGGAGTGAAGCCCAACCGCTGCGAGCGCGGACGATCTGCTACCGCGT 180
DB 191 GCCCGGTACAGGAGTGAAGCCCAACCGCTGCGAGCGCGGACGATCTGCTACCGCGT 250
QY 181 GTTCTTCTGCTGCTCAATCCCTTGTGTTAAATTTGGCCATAAAGCGGAGATTAGAGGA 240
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DB 311 TGATATGATATTCAGTCTGCCAGAGACCGCTCACAGCACCTTTGGAGAGAGTTGCAAGG 370
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DB 371 GTTCTGGGATAAAGAGTTTAAAGCTGAGATGAGCAGCAGACGCTTTTAAACAAG 430
QY 361 AGCAATCATAAAGTGTACTGGAAATCTTATTTAGTTTGGGAATTTTACGTTAATGA 420
DB 431 AGCAATCATAAAGTGTACTGGAAATCTTATTTAGTTTGGGAATTTTACGTTAATGA 490
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Db 2351 TGCAGCTCAGGTTGCCATGCTTCAAGATGGTGGCTTTTCATACCTGGGCAACAAACA 2410
Qy 2341 AAGTATGCTAAATGCTACTGTAAATGGAGGAGAAATGTAAACCGAGAGCTAGATCTTAA 2400
Db 2411 AAGTATGCTAAATGCTACTGTAAATGGAGGAGAAATGTAAACCGAGAGCTAGATCTTAA 2470
Qy 2401 CTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTCTTTTGGCATAGCAAG 2460
Db 2471 CTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTCTTTTGGCATAGCAAG 2530
Qy 2461 ATCTCTATTTGATTTCTACGTCCTGTTGTTAACTCTTCACAACTTTGCAACAAATGTT 2520
Db 2531 ATCTCTATTTGATTTCTACGTCCTGTTGTTTAACTCTTCACAACTTTGCAACAAATGTT 2590
Qy 2521 TGAGTCAATTTGAAAGCTCCCGGTATTTATTTCTTGATAGAAATCCAATAGGAAGATTTT 2580
Db 2591 TGAGTCAATTTGAAAGCTCCCGGTATTTATTTCTTGATAGAAATCCAATAGGAAGATTTT 2650
Qy 2581 AAATCGTTTCTCCAAAGACATTTGGACACTTGGATGATTTGCTGGCGTGTGAGTTTTTGA 2640
|||||

Db 2651 AAATCGTTTCTCCAAAGACATTTGGACACTTGGAGATGATTTGCTGCCGCTGACGTTTTTGA 2710
Qy 2641 TTTTATCCAGACATTTGCTACAAGTGGTGTGTGGTCTCTGTGGCTGTGTGCCGTGATTC 2700
Db 2711 TTTTATCCAGACATTTGCTACAAGTGGTGTGTGGTCTCTGTGGCTGTGTGCCGTGATTC 2770
Qy 2701 TTGGATCGCAATACCCCTTGGTTCCTTGGAAATCATTTTCAATTTTCTTCCGGGATATTT 2760
Db 2771 TTGGATCGCAATACCCCTTGGTTCCTTGGAAATCATTTTCAATTTTCTTCCGGGATATTT 2830
Qy 2761 TTTGGAAACGTCGAAGAGATGTGAAGCGCTTGGAAATCTACAACCTCGGAGTCCAGTGTTC 2820
Db 2831 TTTGGAAACGTCGAAGAGATGTGAAGCGCTTGGAAATCTACAACCTCGGAGTCCAGTGTTC 2890
Qy 2821 CCACCTTGTCTATCTTCTCTCCAGGGCTCTGGACCATCCGGGCATACAAACGACAAGAGAG 2880
Db 2891 CCACCTTGTCTATCTTCTCTCCAGGGCTCTGGACCATCCGGGCATACAAACGACAAGAGAG 2950
Qy 2881 GTGTCAAGAACTGTTTGTATGCACACAGAGATTTACATTCAGAGGCTTGGTCTTGTTTT 2940
Db 2951 GTGTCAAGAACTGTTTGTATGCACACAGAGATTTACATTCAGAGGCTTGGTCTTGTTTT 3010
Qy 2941 GACAACGTCCTCGCTGCTCGCGTCCCTGTGGATGCCATCTGTGCCATGTTTGTCTCAT 3000
Db 3011 GACAACGTCCTCGCTGCTCGCGTCCCTGTGGATGCCATCTGTGCCATGTTTGTCTCAT 3070
Qy 3001 CGTTGCCCTTGGTTCCTGATTTCTGCAAAAACCTCTGGATGCCGGCAGGCTTGGTTTGGC 3060
Db 3071 CGTTGCCCTTGGTTCCTGATTTCTGCAAAAACCTCTGGATGCCGGCAGGCTTGGTTTGGC 3130
Qy 3061 ACTGTCTATGCCCTCACGCTCATNGGGATGTTTTCAGTGGTGTGTTCGACAAAGTGTGA 3120
Db 3131 ACTGTCTATGCCCTCACGCTCATNGGGATGTTTTCAGTGGTGTGTTCGACAAAGTGTGA 3190
Qy 3121 AGTTGAGAATATGATCATCTCAGTGAAGAGGTCATTTGAATACACAGACCTTCAAAAAGA 3180
Db 3191 AGTTGAGAATATGATCATCTCAGTGAAGAGGTCATTTGAATACACAGACCTTCAAAAAGA 3250
Qy 3181 AGCACCTTGGGAATATCAGAAAGCCACACAGCCTGCCCCCATGAGGAGTGTGAAT 3240
Db 3251 AGCACCTTGGGAATATCAGAAAGCCACACAGCCTGCCCCCATGAGGAGTGTGAAT 3310
Qy 3241 CTTTGCATATGAACTTCAATGTACAGTCCAGTGGGCCCTCTGGTACTGAAGCATCTGAC 3300
Db 3311 CTTTGCATATGAACTTCAATGTACAGTCCAGTGGGCCCTCTGGTACTGAAGCATCTGAC 3370
Qy 3301 AGCACCTATTAATCAAGAAAGGTTGTCATTTGGGAAGAACCGAGCTGGAAGAG 3360
Db 3371 AGCACCTATTAATCAAGAAAGGTTGTCATTTGGGAAGAACCGAGCTGGAAGAG 3430
Qy 3361 TTTCCCTCATCTCAGCCCTTTTAGATTTGTCAAGAACCCGAGGTAAATTTGGATTGATA 3420
Db 3431 TTTCCCTCATCTCAGCCCTTTTAGATTTGTCAAGAACCCGAGGTAAATTTGGATTGATA 3490
Qy 3421 GATCTTGACAACTGAAATTTGGACTTCACAGTTTAAAGAGAAATATGTAATCATACCTCA 3480
Db 3491 GATCTTGACAACTGAAATTTGGACTTCACAGTTTAAAGAGAAATATGTAATCATACCTCA 3550
Qy 3481 GGAACCTGTTTGTTCACCTGGAACATGAGAAAACCTGGATCCCTTTAAAGGAGCACAC 3540
Db 3551 GGAACCTGTTTGTTCACCTGGAACATGAGAAAACCTGGATCCCTTTAAAGGAGCACAC 3610
Qy 3541 GGATGAGGAACCTGTGGAATGCTTACAAGAGGTACAACTTAAAGAAACCATTTGAAGATCT 3600
Db 3611 GGATGAGGAACCTGTGGAATGCTTACAAGAGGTACAACTTAAAGAAACCATTTGAAGATCT 3670
Qy 3601 TCCTGGTAAATGGATACCTGAAATTTAGCAAGATCAGGATCCAAATTTAGTGTGGACAAAG 3660
Db 3671 TCCTGGTAAATGGATACCTGAAATTTAGCAAGATCAGGATCCAAATTTAGTGTGGACAAAG 3730
Qy 3661 ACAACTGGTGTCCCTTGGCAGGCAATTTCTCAGGAAATATCAGATATTTGATTTTATGA 3720
Db 3731 ACAACTGGTGTCCCTTGGCAGGCAATTTCTCAGGAAATATCAGATATTTGATTTATGA 3790
|||||

Qy	781	GATCGAGTCAGTCGCCTACTCTGGATGGAGATAGGAATATCGTCCCTTGCTGGATGGC	840
Db	851		
Qy	841	AGTTCTAATCATTTCTCCTCCCTTGCAAAAGCTGTTTTGGGAAGTTGTTCTCATCACTGAG	900
Db	911	AGTTCTAATCATTTCTCCTCCCTTGCAAAAGCTGTTTTGGGAAGTTGTTCTCATCACTGAG	970
Qy	901	GAGTAAACATGCAACTTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATAACTGG	960
Db	971	GAGTAAACATGCAACTTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATAACTGG	1030
Qy	961	TATAAGGATATAAATAATGTACGCTCGGAAAGTCATTTTCAATCTATTACCAATTT	1020
Db	1031	TATAAGGATATAAATAATGTACGCTCGGAAAGTCATTTTCAATCTATTACCAATTT	1090
Qy	1021	GAGAAAGAAGGAGATTTCACAAGATTCTGAGAAGTTCTGCCTCAGGGGGATGAATTTGGC	1080
Db	1091	GAGAAAGAAGGAGATTTCACAAGATTCTGAGAAGTTCTGCCTCAGGGGGATGAATTTGGC	1150
Qy	1081	TTCGTTTTTCAGTGCAGCAAAATCATCGTTGTGACCTTACACACTACGTCGCTCT	1140
Db	1151	TTCGTTTTTCAGTGCAGCAAAATCATCGTTGTGACCTTACACACTACGTCGCTCT	1210
Qy	1141	CGGCACTGTGATCACAGCCAGCCGCGTGTGTGTCGCACTGACGCTGTATGGGCGTGGCG	1200
Db	1211	CGGCACTGTGATCACAGCCAGCCGCGTGTGTGTCGCACTGACGCTGTATGGGCGTGGCG	1270
Qy	1201	GCTGACGGTTACCTCTCTTCCCTCAGCCATTGAGAGGCTGTACAGAGCAATCGTCAG	1260
Db	1271	GCTGACGGTTACCTCTCTTCCCTCAGCCATTGAGAGGCTGTACAGAGCAATCGTCAG	1330
Qy	1261	CATCCCAAGATCCAGACTTTTTCCTACTTGATGAGATATCACAGCGCAACCGTCACT	1320
Db	1331	CATCCCAAGATCCAGACTTTTTCCTACTTGATGAGATATCACAGCGCAACCGTCACT	1390
Qy	1321	GCCGTGAGATGTTAAAGAGATGTCATGTGCAGGATTTTACTGCTTTTGGGATAGGC	1380
Db	1391	GCCGTGAGATGTTAAAGATGTCATGTGCAGGATTTTACTGCTTTTGGGATAGGC	1450
Qy	1381	ATCAGAGACCCCAACTCTACAAAGGCTTTTCCCTTACTGTACAGACTGGCGAATTTGTTAGC	1440
Db	1451	ATCAGAGACCCCAACTCTACAAAGGCTTTTCCCTTACTGTACAGACTGGCGAATTTGTTAGC	1510
Qy	1441	TGTGTCGTCGCCCGTGGAGCAGGGAAGTCATCTGTTAAGTCCCTGCTCGGGGAAT	1500
Db	1511	TGTGTCGTCGCCCGTGGAGCAGGGAAGTCATCTGTTAAGTCCCTGCTCGGGGAAT	1570
Qy	1501	GGCCCCAAGTCACGGCTGGTCAGGCTGCATGGAAGATTCSCCTATCTGTCTCAGCAGCC	1560
Db	1571	GGCCCCAAGTCACGGCTGGTCAGGCTGCATGGAAGATTCSCCTATCTGTCTCAGCAGCC	1630
Qy	1561	CTGGGTGTTCTCGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAAAGGA	1620
Db	1631	CTGGGTGTTCTCGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATACGAAAGGA	1690
Qy	1621	ACGATATGAAAAGTCATAAGGCTTTGTCCTGAAAAGAGATTTACAGCTGTTGAGGA	1680
Db	1691	ACGATATGAAAAGTCATAAGGCTTTGTCCTGAAAAGAGATTTACAGCTGTTGAGGA	1750
Qy	1681	TGGTGATCTGACTGTGATGAGAGATCGGGGAACACACGCTGAGTGGAGGGCAGAAACACG	1740
Db	1751	TGGTGATCTGACTGTGATGAGAGATCGGGGAACACACGCTGAGTGGAGGGCAGAAACACG	1810
Qy	1741	GGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGACGATCCTCT	1800
Db	1811	GGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGACGATCCTCT	1870
Qy	1801	CAGTCGATAGATCGGGAAGTTAGCAGACACTCTGTCGAACCTGTGTAATTTGTCAAATTT	1860
Db	1871	CAGTCGATAGATCGGGAAGTTAGCAGACACTCTGTCGAACCTGTGTAATTTGTCAAATTT	1930

QY	1861	GCATGAGAAGATCACAAATTTTAGTGACTCATCACTAGTTGCAGTAAGCTCAAAGCTCA	1920
DB	1931	GCATGAGAAGATCACAAATTTTAGTGACTCATCACTAGTTGCAGTAAGCTCAAAGCTCA	1990
QY	1921	GATTCTCATATTTCAAAGATGGTAAATGGTGCAGAAGGGGACATTACACTGAGTTCCCTAAA	1980
DB	1991	GATTCTCATATTTCAAAGATGGTAAATGGTGCAGAAGGGGACATTACACTGAGTTCCCTAAA	2050
QY	1981	ATCTGCTATAGATTTTGGCTCCCTTTTAAAGAAGGATAAATGAGGAAAGTCAACAACCTCC	2040
DB	2051	ATCTGCTATAGATTTTGGCTCCCTTTTAAAGAAGGATAAATGAGGAAAGTCAACAACCTCC	2110
QY	2041	AGTTCCAGGAACCTCCACACTAAGGAATCGTACCTCTTCAGAGTCTTCGGTTTGGTCTCA	2100
DB	2111	AGTTCCAGGAACCTCCACACTAAGGAATCGTACCTCTTCAGAGTCTTCGGTTTGGTCTCA	2170
QY	2101	ACAATCTTCTAGACCCTCCTTGAAAGATGGTGTCTCTGGAGAGCCAGATACAGAGAATGT	2160
DB	2171	ACAATCTTCTAGACCCTCCTTGAAAGATGGTGTCTCTGGAGAGCCAGATACAGAGAATGT	2230
QY	2161	CCAGGTTACACTATCAGAGGAGAACCGTCTGAAGGAAAAGTTGGTTTTCAGGCCCTATAA	2220
DB	2231	CCAGGTTACACTATCAGAGGAGAACCGTCTGAAGGAAAAGTTGGTTTTCAGGCCCTATAA	2290
QY	2221	GAATTACTTCAGAGCTGGTGCTCACTGGATGTCTTCATTCTTCCTTATCTCTCTAAACAC	2280
DB	2291	GAATTACTTCAGAGCTGGTGCTCACTGGATGTCTTCATTCTTCCTTATCTCTCTAAACAC	2350
QY	2281	TGCAGCTCAGGTTGCCATATGTGCTTCAAGATTTGGTGGCTTTTCATCTGGGCAACAACA	2340
DB	2351	TGCAGCTCAGGTTGCCATATGTGCTTCAAGATTTGGTGGCTTTTCATCTGGGCAACAACA	2410
QY	2341	AAAGTATGCTAAATGTCACTGCTAAATGGAGGAGGAAAATGTAACCGAGAAGCTAGACTCTAA	2400
DB	2411	AAAGTATGCTAAATGTCACTGCTAAATGGAGGAGGAAAATGTAACCGAGAAGCTAGACTCTAA	2470
QY	2401	CTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATAGCAAG	2460
DB	2471	CTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATAGCAAG	2530
QY	2461	ATCTCTATTTGGTATCTCACTAGCTCTGTAACTCTTCACAACTTTGCAACAACAAATGTT	2520
DB	2531	ATCTCTATTTGGTATCTCACTAGCTCTGTAACTCTTCACAACTTTGCAACAACAAATGTT	2590
QY	2521	TGAGTCAATTTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAAATAGGAAGAATTTT	2580
DB	2591	TGAGTCAATTTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAAATAGGAAGAATTTT	2650
QY	2581	AAATCGTTTCTCCAAAGACATTTGGACACTTGGATGATTTTGCCTGCCGCTGACGTTTTAGA	2640
DB	2651	AAATCGTTTCTCCAAAGACATTTGGACACTTGGATGATTTTGCCTGCCGCTGACGTTTTAGA	2710
QY	2641	TTTCATCCAGACATTTGCTACAGTGGTGGTGTCTCTGTGGCTGTGGCGGTGATTC	2700
DB	2711	TTTCATCCAGACATTTGCTACAGTGGTGGTGTCTCTGTGGCTGTGGCGGTGATTC	2770
QY	2701	TTGGATTCGAATACCCCTTGTTTCCCTTGGAAATCATTTTTCATTTTCTTCGGCGATATT	2760
DB	2771	TTGGATTCGAATACCCCTTGTTTCCCTTGGAAATCATTTTTCATTTTCTTCGGCGATATT	2830
QY	2761	TTTGGAAACGTCAAGAGATGTGAAGCGCTTGGAAATCTACAACCTCGGAGTCCAGTGTTC	2820
DB	2831	TTTGGAAACGTCAAGAGATGTGAAGCGCTTGGAAATCTACAACCTCGGAGTCCAGTGTTC	2890
QY	2821	CCACTTGTCACTTCTCTCCAGGGGCTCTGGACCATTCGGGGCATACAAAGCAGAGAGAG	2880
DB	2891	CCACTTGTCACTTCTCTCCAGGGGCTCTGGACCATTCGGGGCATACAAAGCAGAGAGAG	2950
QY	2881	GTGTCAGAACTGTTTGTATGACACACAGATTTACATTCAGAGGCTTGGTTCTTGT	2940
DB	2951	GTGTCAGAACTGTTTGTATGACACACAGATTTACATTCAGAGGCTTGGTTCTTGT	3010
QY	2941	GACAACGTCCCGCTGGTTGCTGCCGCTCGCTCTGGATGCCATCTGTGCCATGTGTTGCTATCAT	3000

(SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 XX
 Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedwick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
 XX
 WPI: 2002-255649/30.
 XX
 New prostate-specific polynucleotides for diagnosing and treating
 PT diseases, in particular prostate cancer, and as markers for the
 PT progression of cancer
 PT
 XX
 Claim 1; SEQ ID NO 535; 87pp; English.
 PS
 XX
 The present invention provides prostate-specific coding sequences and
 CC their encoded proteins. These can be used in the diagnosis and treatment
 CC of cancers, particularly prostate cancer. The present sequence is a CDNA
 CC described in the invention.
 XX
 SQ Sequence 6082 BP; 1721 A; 1249 C; 1357 G; 1755 T; 0 other;
 Query Match 99.5%; Score 4211; DB 24; Length 6082;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 4225; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
 QY 1 GGACAGGGGTGGCGCGGAGCCCGCAGCATCCCTGCTTGAGTCCAGGAGCGGACCCGCG 60
 DB 71 GGACAGGGGTGGCGCGGAGCCCGCAGCATCCCTGCTTGAGTCCAGGAGCGGACCCGCG 130
 QY 61 GGCCACCGCCGCTGATCAGCGCGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
 DB 131 GGCCACTGCCGCTGATCAGCGCGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 190
 QY 121 GCCCGTGACAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATGCTCAGCGGT 180
 DB 191 GCCCGTGACAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATGCTCAGCGGT 250
 QY 181 GTTCTTCTGGTGGCTCAATCCCTGTTTAAATTTGGCCATAAACCGAGATTAGAGGAAGA 240
 DB 251 GTTCTTCTGGTGGCTCAATCCCTGTTTAAATTTGGCCATAAACCGAGATTAGAGGAAGA 310
 QY 241 TGATATGTTATTCAGTGTGCCAGAGACCGCTCAGACACCTTGAGAGGAGTTCCAGG 300
 DB 311 TGATATGTTATTCAGTGTGCCAGAGACCGCTCAGACACCTTGAGAGGAGTTCCAGG 370
 QY 301 GTTCTGGGATAAAGAAGTTTAAAGAGCTGAGAAAGACGACAGAGCGCTCTTTAAACAAG 360
 DB 371 GTTCTGGGATAAAGAAGTTTAAAGAGCTGAGAAAGACGACAGAGCGCTCTTTAAACAAG 430
 QY 361 AGCAATCAATAAGTGTACTGGAATCTTATTTAGTTTGGGAAATTTTACGTTAATTA 420
 DB 431 AGCAATCAATAAGTGTACTGGAATCTTATTTAGTTTGGGAAATTTTACGTTAATTA 490
 QY 421 GGAAGTCCCAAGCTAATCCAGCCATATTTTGGGAAAATTTATTAATTTTGAAGA 480
 DB 491 GGAAGTCCCAAGCTAATCCAGCCATATTTTGGGAAAATTTATTAATTTTGAAGA 550
 QY 481 TTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCCTATGCCAGGTCGTCAC 540
 DB 551 TTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCCTATGCCAGGTCGTCAC 610
 QY 541 TTTTGGACCGCTCAATTTGGCTACTGCACTATTAATTTTATATTTTATACGTTCAAGTGGC 600
 DB 611 TTTTGGACCGCTCAATTTGGCTACTGCACTATTAATTTTATATTTTATACGTTCAAGTGGC 670
 QY 601 TGGGATGAGGTTACAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGTCCTTAG 660
 DB 671 TGGGATGAGGTTACAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGTCCTTAG 730
 QY 661 TAACATGCCATGGGAGAACCAACACAGGCCAGATAGTCAATCTGCTGCCAATGATGT 720
 DB 1811 GGTAAACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGGAGCTCTCT 1870

DB 731 TAACATGCCATGGGGAAGACAACACAGGCCAGATAGTCAATCTGCTGCCAATGATGT 790
 QY 721 GAACAAGTTTATCAGGTGACAGTGTCTTACACTTCTCTGGCAGGACCACTGCGAGGC 780
 DB 791 GAACAAGTTTATCAGGTGACAGTGTCTTACACTTCTCTGGCAGGACCACTGCGAGGC 850
 QY 781 GATCGCAGTACGTCCTACTCTGAGTGGAGATAGGAATATCGTCCCTGCTGGGATGGC 840
 DB 851 GATCGCAGTACGTCCTACTCTGAGTGGAGATAGGAATATCGTCCCTGCTGGGATGGC 910
 QY 841 AGTTCTAATCATCTCTGCTCCCTTGCAGAACTCTTTTGGGAAGTGTCTCTCATCAGTGA 900
 DB 911 AGTTCTAATCATCTCTGCTCCCTTGCAGAACTGTTTTGGGAAGTGTCTCTCATCAGTGA 970
 QY 901 GAGTAAACCTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATAACTGG 960
 DB 971 GAGTAAACCTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATAACTGG 1030
 QY 961 TATAAGATTAATAAATGATGACCCCTGGGAAAAGTCAATTTTCAAAATCTTATACCAATTT 1020
 DB 1031 TATAAGATTAATAAATGATGACCCCTGGGAAAAGTCAATTTTCAAAATCTTATACCAATTT 1090
 QY 1021 GAGAAAGAGGAGATTTCCAAGATTTCTGAGAACTTCTGCTCAGGGGATGAATTTGGC 1080
 DB 1091 GAGAAAGAGGAGATTTCCAAGATTTCTGAGAACTTCTGCTCAGGGGATGAATTTGGC 1150
 QY 1081 TTGCTTTTTCAGTGCAAGCAAAATCATCTGTTTGTGACCTTCCACCACCTACGCTGCTCCT 1140
 DB 1151 TTGCTTTTTCAGTGCAAGCAAAATCATCTGTTTGTGACCTTCCACCACCTACGCTGCTCCT 1210
 QY 1141 CGGCATGTGATCACAGCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGCTGTGCG 1200
 DB 1211 CGGCATGTGATCACAGCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGCTGTGCG 1270
 QY 1201 GCTGACGTTACCTCTCTTCCCTCAGCCATTTGAGAGGCTGTACAGGCAATTCGTCAG 1260
 DB 1271 GCTGACGTTACCTCTCTTCCCTCAGCCATTTGAGAGGCTGTACAGGCAATTCGTCAG 1330
 QY 1261 CATCCGAAGATTCAGACCTTTTGTGCTGATGAGATATCACAGCAACCGTCAGCT 1320
 DB 1331 CATCCGAAGATTCAGACCTTTTGTGCTGATGAGATATCACAGCAACCGTCAGCT 1390
 QY 1321 GCGCTCAGATGTTAAAGATGGTGCATGTGAGGATTTTACTGCTTTTGGGATAAGGC 1380
 DB 1391 GCGCTCAGATGTTAAAGATGGTGCATGTGAGGATTTTACTGCTTTTGGGATAAGGC 1450
 QY 1381 ATCAGAGACCCCAACTCTACAGGCTTTTCTTACTGTGACACCTTGGCGAATTTGTAGC 1440
 DB 1451 ATCAGAGACCCCAACTCTACAGGCTTTTCTTACTGTGACACCTTGGCGAATTTGTAGC 1510
 QY 1441 TGTGCTCGCCCGCTGGGAGCAGGGAAGTCACTCTGTTAAAGTGGCGTCTCGGGGAAT 1500
 DB 1511 TGTGCTCGCCCGCTGGGAGCAGGGAAGTCACTCTGTTAAAGTGGCGTCTCGGGGAAT 1570
 QY 1501 GCGCCCAAGTCAGGCGCTGGTGCAGCGTGCATGGAAGATTTGCTGTCTCAGCAGCC 1560
 DB 1571 GCGCCCAAGTCAGGCGCTGGTGCAGCGTGCATGGAAGATTTGCTGTCTCAGCAGCC 1630
 QY 1561 CTGGGTGTTCTCGGAACTCTCAGGAGTAAATTTTATTTGGGAAGAAATATGAAAAGGA 1620
 DB 1631 CTGGGTGTTCTCGGAACTCTCAGGAGTAAATTTTATTTTGGGAAGAAATATGAAAAGGA 1690
 QY 1621 AGGATATGAAAAGTCAATAAAGCTTGTCTCTGAAAAAGGATTTACAGCTGTTGGAGGA 1680
 DB 1691 AGGATATGAAAAGTCAATAAAGCTTGTCTCTGAAAAAGGATTTACAGCTGTTGGAGGA 1750
 QY 1681 TGGTGTCTGACTGTAGGAGATCGGGGAACCAAGCTGAGTGGAGGCGAGAAAGCAGC 1740
 DB 1751 TGGTGTCTGACTGTAGGAGATCGGGGAACCAAGCTGAGTGGAGGCGAGAAAGCAGC 1810
 QY 1741 GGTAAACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGGAGATGCTCT 1800
 DB 1811 GGTAAACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGGAGATGCTCTCT 1870

1801 CAGTCAGTAGATGCGGAAGTTAGCAGACACTGTTGTCGAACCTGTGATTTGTCAAATTTT 1860
1871 CAGTCAGTAGATGCGGAAGTTAGCAGACACTGTTGTCGAACCTGTGATTTGTCAAATTTT 1930
1861 GCATGAGAAGATCACAAATTTTAGTGACTCATCAGTTGCGAGTACCTCAAAGCTGCAAGTCA 1920
1931 GCATGAGAAGATCACAAATTTTAGTGACTCATCAGTTGCGAGTACCTCAAAGCTGCAAGTCA 1990
1921 GATTCGTATATTGAAGATGTTAAATGTTGAGAGGGGACTTACACTGAGTTCCTATAA 1980
1991 GATTCGTATATTGAAGATGTTAAATGTTGAGAGGGGACTTACACTGAGTTCCTATAA 2050
1981 ATCTGGTATAGATTTTGGTCCCTTTTAAAGAGGATTAATGAGGAAGTGAACAACTCC 2040
2051 ATCTGGTATAGATTTTGGTCCCTTTTAAAGAGGATTAATGAGGAAGTGAACAACTCC 2110
2041 AGTTCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCA 2100
2111 AGTTCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCA 2170
2101 ACAATCTTCTAGAACCTCTCTGAAAGATGGTGCTCTGGAGAGCCAAAGATACAGAGAATCT 2160
2171 ACAATCTTCTAGAACCTCTCTGAAAGATGGTGCTCTGGAGAGCCAAAGATACAGAGAATCT 2230
2161 CCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCCCTATAA 2220
2231 CCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCCCTATAA 2290
2221 GAATTTACTTCAGAGCTGGTCTACCTGGATGCTCTTCATTTTCCTTATTTCTCCTTAAACAC 2280
2291 GAATTTACTTCAGAGCTGGTCTACCTGGATGCTCTTCATTTTCCTTATTTCTCCTTAAACAC 2350
2281 TGCAGCTCAGGTTGGCTATGCTTCAAGATGGTGCTCTCATCTGGGCAAAACAAACA 2340
2351 TGCAGCTCAGGTTGGCTATGCTTCAAGATGGTGCTCTCATCTGGGCAAAACAAACA 2410
2341 AAGTATGCTAAATGTCACCTGTAATGAGGAGGAGAAATGTAAACGAGAGCTAGATCTTAA 2400
2411 AAGTATGCTAAATGTCACCTGTAATGAGGAGGAGAAATGTAAACGAGAGCTAGATCTTAA 2470
2401 CTGGTACTTAGGAATTTTACAGTTTAACTGACTACCTACCGTTCCTTTTGGCATAGCAAG 2460
2471 CTGGTACTTAGGAATTTTACAGTTTAACTGACTACCTACCGTTCCTTTTGGCATAGCAAG 2530
2461 ATCTCTATTGGTATTTCTACGCTCTGTTAACTCTTCAACAACTTTCGCAACAAATAATGTT 2520
2531 ATCTCTATTGGTATTTCTACGCTCTGTTAACTCTTCAACAACTTTCGCAACAAATAATGTT 2590
2521 TGAGTCAATTCGAAAGCTCCGGTATTAATCTTTTGATAGAAATCCAATAGGAAGAATTTT 2580
2591 TGAGTCAATTCGAAAGCTCCGGTATTAATCTTTTGATAGAAATCCAATAGGAAGAATTTT 2650
2581 AAATCGTTTCTCCAAAGACATTTGNACATTTGGATGATTTGCTGCGCGTGCATTTTGA 2640
2651 AAATCGTTTCTCCAAAGACATTTGNACATTTGGATGATTTGCTGCGCGTGCATTTTGA 2710
2641 TTTTCATCCAGACATTTGCTACAAAGTGGTTGGTGCTCTCTGTGGCTGTGGCGCTGATTTCC 2700
2711 TTTTCATCCAGACATTTGCTACAAAGTGGTTGGTGCTCTCTGTGGCTGTGGCGCTGATTTCC 2770
2701 TTGGATCGCAATACCTTTGGTTCCCTTTGGAATCATTTTTCATTTTCTTCGCGCATATTT 2760
2771 TTGGATCGCAATACCTTTGGTTCCCTTTGGAATCATTTTTCATTTTCTTCGCGCATATTT 2830
2761 TTTTGGAAACGTCAGAGATGTAAGCGGCTGGAATCTCAACTCGGAGTCCAGTGTTC 2820
2831 TTTTGGAAACGTCAGAGATGTAAGCGGCTGGAATCTCAACTCGGAGTCCAGTGTTC 2890
2821 CCACCTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAGAGAG 2880
2891 CCACCTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAGAGAG 2950

2881 GTGTCAAGAACTGTTGATGCACACCAGGATTTACATTCAGAGGCTGGTTCTTGTGTTTTT 2940
2951 GTGTCAAGAACTGTTGATGCACACCAGGATTTACATTCAGAGGCTGGTTCTTGTGTTTTT 3010
2941 GACAACCTCCCGTGGTTGCGCGTCTGCTGAGTGCATCTGTGCCATCTGTTGTGTCATCAT 3000
3011 GACAACCTCCCGTGGTTGCGCGTCTGCTGAGTGCATCTGTGCCATCTGTTGTGTCATCAT 3070
3001 CGTTCCTTTTGGTCCCTGATTTCTGGCAAAACTCTGATGTCGCCGGGAGGTTGGTTGGC 3060
3071 CGTTCCTTTTGGTCCCTGATTTCTGGCAAAACTCTGATGTCGCCGGGAGGTTGGTTGGC 3130
3061 ACTGTCTATGCCCTCACGCTCATGGGATGTTTTCAGTGGTGCTTCTGCACAAAGTGTGTA 3120
3131 ACTGTCTATGCCCTCACGCTCATGGGATGTTTTCAGTGGTGCTTCTGCACAAAGTGTGTA 3190
3121 AGTTGAGAATATGATGATCTCAGTAGAAGGGTCAATTTGAATACACAGACCTTTGAAAAGA 3180
3191 AGTTGAGAATATGATGATCTCAGTAGAAGGGTCAATTTGAATACACAGACCTTTGAAAAGA 3250
3181 AGCACCTTTGGGAATATCAGAAACGCCACCACAGCCCTGGCCCATGAAGAGTGAATA 3240
3251 AGCACCTTTGGGAATATCAGAAACGCCACCACAGCCCTGGCCCATGAAGAGTGAATA 3310
3241 CTTTTCAGAAATGTAACCTTCATGTACAGTCCAGGTGGGCCCTCTGTACTGAAGCATCTGAC 3300
3311 CTTTTCAGAAATGTAACCTTCATGTACAGTCCAGGTGGGCCCTCTGTACTGAAGCATCTGAC 3370
3301 AGCACTCAATTAATACAGAAAGGTTGGCATTTGGGGAAGAACCGGAGCTGGAAAAG 3360
3371 AGCACTCAATTAATACAGAAAGGTTGGCATTTGGGGAAGAACCGGAGCTGGAAAAG 3430
3361 TTCCTCTACTCAGCCCTTTTAGATGTTGTCAGAACCCGAGGTAAATTTTGGATTGATA 3420
3431 TTCCTCTACTCAGCCCTTTTAGATGTTGTCAGAACCCGAGGTAAATTTTGGATTGATA 3490
3421 GATCTTTGACAACCTGAAATTTGGACTTTCAGCATTTTAAAGGAAGAAATGTCAATTCATCTCA 3480
3491 GATCTTTGACAACCTGAAATTTGGACTTTCAGCATTTTAAAGGAAGAAATGTCAATTCATCTCA 3550
3481 GGNACCTGTTTGTTCACCTGGAACATGAGGAAAACCTGGATCCCTTTTAAAGGAGCAC 3540
3551 GGAACCTGTTTGTTCACCTGGAACATGAGGAAAACCTGGATCCCTTTTAAAGGAGCAC 3610
3541 GGATGAGGAACCTGTGGAATGCCCTTACAAGAGGTACAACTTAAAGAAACCACTGAAGATCT 3600
3611 GGATGAGGAACCTGTGGAATGCCCTTACAAGAGGTACAACTTAAAGAAACCACTGAAGATCT 3670
3601 TCCTGTAAAAATGATGATGAAATTTAGCAGAAATCAGGATCCAAATTTTAGTCTTGCACAAAG 3660
3671 TCCTGTAAAAATGATGATGAAATTTAGCAGAAATCAGGATCCAAATTTTAGTCTTGCACAAAG 3730
3661 ACACCTGTTGTCCTTCCAGGCAATTTCTCAGGAAAATTCAGATATTTGATTTGATGA 3720
3731 ACAACCTGTTGTCCTTCCAGGCAATTTCTCAGGAAAATTCAGATATTTGATTTGATGA 3790
3721 AGCAGCGCAAAATGTCGATCCAAAGAACTGATGAGTTAAATACAAAANAATTCGGGAGAA 3780
3791 AGCAGCGCAAAATGTCGATCCAAAGAACTGATGAGTTAAATACAAAANAATTCGGGAGAA 3849
3781 ATTTGCCCACTGCAACCTGCTACCAATTTGCACACAGATTTGAACACCACTTATTCACAGCGA 3840
3850 ATTTGCCCACTGCAACCTGCTACCAATTTGCACACAGATTTGAACACCACTTATTCACAGCGA 3909
3841 CAAGATAATGTTTATGATTCAGGAAGACTGAAAAGAAATATGATGAGCCGTATGTTTGTCT 3900
3910 CAAGATAATGTTTATGATTCAGGAAGACTGAAAAGAAATATGATGAGCCGTATGTTTGTCT 3969
3901 GCAAAATAAGAGAGCCTATTTTACAAGATGGTGCACAACTGGGCAAGGCAAGCCGC 3960
3970 GCAAAATAAGAGAGCCTATTTTACAAGATGGTGCACAACTGGGCAAGGCAAGCCGC 4029
3961 TGCCCTCTACTGAAACAGCAAAACAGCTATATCTTCAAAAAGAAATTTATCCACATATTTGCTCA 4020

Db	4030	TGCCCTCACTGAACAGCAAAACAGGTACTTCAAAAGAAATATTCCACATATTGTCGA	4089
Qy	4021	CAC TGACACATGGTTACAAACACACTTCCAAATGGACAGCCCTCGACCTTAACATATTTTCGA	4080
Db	4090	CAC TGACACATGGTTACAAACACACTTCCAAATGGACAGCCCTCGACCTTAACATATTTTCGA	4149
Qy	4081	GACAGCACGTGTGAATCCAAACACAAAATGTCAAATCCGTTCCGAAGGCGATTTTCCACATAGTT	4140
Db	4150	GACAGCACGTGTGAATCCAAACACAAAATGTCAAATCCGTTCCGAAGGCGATTTTCCACATAGTT	4209
Qy	4141	TTTGGCATATGTAACACCATTTGTACTTTTTTTTACTTTTGGCAACAATAATTTATACATA	4200
Db	4210	TTTGGCATATGTAACACCATTTGTACTTTTTTTTACTTTTGGCAACAATAATTTATACATA	4269
Qy	4201	CAAGATGCTAGTTTCATTTGAATATTTCTCCC	4231
Db	4270	CAAGATGCTAGTTTCATTTGAATATTTCTCCC	4300

RESULT 7

ABV20669

ABV20003
ID ABV20669 standard; CDNA; 4515 BP.

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CONTACT

AC ABV20669:

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DT 13-SEP-2002 (first entry)

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DE Human prostat

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KW Human; prost:

KW pharmacogenomic marker; gene

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OS Homo sapiens.

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PN WO200160860-A2.

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PD 23-AUG-2001.

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DE 20-FEB-2001. 2001WC-UC05171

PF 20-FEB-2001; 2001W0-US03171.
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17-FEB-2000 2000NS-

17 FEB 2000, 2000US-189862P.
PR 16-MAR-2000: 2000US-189862P.

PR 25-MAY-2000: 2000US-207454P.
TO XMM 2000: 2000US 103002Z.

PR 09-JUN-2000; 2000US-211314P.

PR 18-JUL-2000; 2000US-219007P.

PR 13-DEC-2000; 2000US-255281P.

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PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

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PI Schlegel R, Endege WO, Monahan JE;

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DR WPI; 2001-662795/76.

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PT Novel isolated nucleic acid molecule associated with cancerous state of

prostate cells and correlating with presence of prostate cancer, useful

PT for detecting presence of prostate cancer, stage of prostate cancer

[illegible]

PS Claim I; Page 3388; 11/30pp; English.
v v

CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 4515 BP; 1253 A; 942 C; 1059 G; 1261 T; 0 other;

Query Match 99.2%; Score 4196.6; DB 23; Length 4515;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4210; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Db	3121	ATCTCAGTAGAAGGGTCATTGAATACACAGACCTTTGAAAAAGACGACCTTGGGGAAATAT	3180
Qy	3197	CAGAAACGCCACCACCCAGCCCTGGCCCCATGAAGAGTGTATATCTTTGACAAATGTGAAC	3256
Db	3181	CAGAAACGCCACCACCCAGCCCTGGCCCCATGAAGAGTGTATATCTTTGACAAATGTGAAC	3240
Qy	3257	TTTCATGTACAGTCCAGGTGGGGCCTCTGGTACTGAAGCACTCTGACAGCACTCATATAATCA	3316
Db	3241	TTTCATGTACAGTCCAGGTGGGGCCTCTGGTACTGAAGCACTCTGACAGCACTCATATAATCA	3300
Qy	3317	CAAGAAAAAGTTGGCATTTGTGGGAAGAACCCGAGCTGGAAAAAGTTCCCTCATCTCAGCC	3376
Db	3301	CAAGAAAAAGTTGGCATTTGTGGGAAGAACCCGAGCTGGAAAAAGTTCCCTCATCTCAGCC	3360
Qy	3377	CTTTTTAGATTGTCAGAACCCCAAGGTAAAAATTTGGATTGATAAGATCTTTGACAACTGAA	3436
Db	3361	CTTTTTAGATTGTCAGAACCCCAAGGTAAAAATTTGGATTGATAAGATCTTTGACAACTGAA	3420
Qy	3437	ATTGGACTTCAGGATTTTAAGGAAGAAAATGTCAATCATACCTTCAGGAACCTCTTTTGTTTC	3496
Db	3421	ATTGGACTTCAGGATTTTAAGGAAGAAAATGTCAATCATACCTTCAGGAACCTCTTTTGTTTC	3480
Qy	3497	ACTGGAACAATCAGGAAAAACCTGGATCCCTTTAAGGAGCACACGGATGAGCACTGTGG	3556
Db	3481	ACTGGAACAATCAGGAAAAACCTGGATCCCTTTAAGGAGCACACGGATGAGCACTGTGG	3540
Qy	3557	AATGCCCTTACAAGAGGTACAACCTTAAGAAACCACTTGAAGATCTCTCGTGAATAATGGAT	3616
Db	3541	AATGCCCTTACAAGAGGCACACTTAAGAAACCACTTGAAGATCTCTCGTGAATAATGGAT	3600
Qy	3617	ACTGAATTAGCAGAAATCAGGATCCAATTTTAGTGTGGACAAAGACAACTGGTGTGCCCTT	3676
Db	3601	ACTGAATTAGCAGAAATCAGGATCCAATTTTAGTGTGGACAAAGACAACTGGTGTGCCCTT	3660
Qy	3677	GCCAGGGCAATCTCAGGAAAAATCAGATATTGATTATTTGATGAGCGACGCGCAATGTG	3736
Db	3661	GCCAGGGCAATCTCAGGAAAAATCAGATATTGATTATTTGATGAGCGACGCGCAATGTG	3720
Qy	3737	GATCCAGAACTGATGAGTTAATACAAAAAAAATCCGGGAGAAATTTGCCACATGCACCC	3796
Db	3721	GATCCAGAACTGATGAGTTAATACAAAAAAAATCCGGGAGAAATTTGCCACATGCACCC	3780
Qy	3797	GTGCTAACCATTTGCACACAGATTGAACACCATTAATTGACAGCGACAAGATAATGGTTTTA	3856
Db	3781	GTGCTAACCATTTGCACACAGATTGAACACCATTAATTGACAGCGACAAGATAATGGTTTTA	3840
Qy	3857	GATTTCAGGAAGACTGAAGAATATGATGAGCGGTATGTTTGCTGCAGAAATAAAGAGAGC	3916
Db	3841	GATTTCAGGAAGACTGAAGAATATGATGAGCGGTATGTTTGCTGCAGAAATAAAGAGAGC	3900
Qy	3917	CTATTTTACAAGATGGTGCACAACTGGGCAAGGACAGCGCTGCCTCTCACTGAAACA	3976
Db	3901	CTATTTTACAAGATGGTGCACAACTGGGCAAGGACAGCGCTGCCTCTCACTGAAACA	3960
Qy	3977	GCAAAACAGGTTATCTTCAAAAAGAAATTTATCCACATATTTGGTTCACACTGACCACATGTT	4036
Db	3961	GCAAAACAGGTTATCTTCAAAAAGAAATTTATCCACATATTTGGTTCACACTGACCACATGTT	4020
Qy	4037	ACAAACACTTCCAATGGACAGCCCTCGACCTTAACATATTTTCGAGACAGCACTGTGAATC	4096
Db	4021	ACAAACACTTCCAATGGACAGCCCTCGACCTTAACATATTTTCGAGACAGCACTGTGAATC	4080
Qy	4097	CAACCAAAATGTCAAGTCCGTTCCGAGGGCAATTTTCCACTAGTTTTTTCGACTATCTAATC	4156
Db	4081	CAACCAAAATGTCAAGTCCGTTCCGAGGGCAATTTTCCACTAGTTTTTTCGACTATCTAATC	4140
Qy	4157	CACATGTACTTTTTTTTTTACTTTTGGCAACAATAATTTATACATACAAGATGCTAGTTTCAAT	4216
Db	4141	CACATGTACTTTTTTTTTTACTTTTGGCAACAATAATTTATACATACAAGATGCTAGTTTCAAT	4200
Qy	4217	TTGAATATTTCTCCC	4231
Db	4201	TTGAATATTTCTCCC	4215

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Db 121 TGAAGCCCAACCGCTGAGAGCGCGAACCTCTGCTACACCGGTGTTCTTCTGGTGGCTCA 180
QY 198 ATCCCTGTTTAAATTTGGCCATAAACGGAGATTAGAGGAAGATGATATGATTTCACTGTC 257
Db 181 ATCCCTGTTTAAATTTGGCCATAAACGGAGATTAGAGGAAGATGATATGATTTCACTGTC 240
QY 258 TGCAGAACACCGCTCACAGACCTTGGAGAGGAGTTGCNAGGGTTCTTGGGATAAAGAA 317
Db 241 TGCAGAACACCGCTCACAGACCTTGGAGAGGAGTTGCAAGGGTTCTTGGGATAAAGAA 300
QY 318 TTTTAAAGACTGAGAAATGACGACACGAACCTTCTTTTAAACAGACCAATCAATAAAGTGT 377
Db 301 TTTTAAAGACTGAGAAATGACGACACGAACCTTCTTTTAAACAGACCAATCAATAAAGTGT 360
QY 378 ACTGGAATCTTATTTAGTTTGGGAATTTTACGTTAAATGAGGAAAGTGCCAAAGTAA 437
Db 361 ACTGGAATCTTATTTAGTTTGGGAATTTTACGTTAAATGAGGAAAGTGCCAAAGTAA 420
QY 438 TCCAGCCCATATTTTGGGAAAATTAATTAATTTTGAATAATATGATPCCCATGAT 497
Db 421 TCCAGCCCATATTTTGGGAAAATTAATTAATTTTGAATAATATGATPCCCATGAT 480
QY 498 CTGTGGCTTTGAACACAGGTACGCTATGCCACGCTGCTGACTTTTGCACGCTCATTT 557
Db 481 CTGTGGCTTTGAACACAGGTACGCTATGCCACGCTGCTGACTTTTGCACGCTCATTT 540
QY 558 TGGCTATATGTCATCACTTATATTTTATCAGCTTCAGTGTGCTGGGATGAGGTTACGAG 617
Db 541 TGGCTATATGTCATCACTTATATTTTATCAGCTTCAGTGTGCTGGGATGAGGTTACGAG 600
QY 618 TAGCCATGTCCATATGATTTATCGGAAGGCACCTTGTCTTATAGTAACATGGCCATGGGA 677
Db 601 TAGCCATGTCCATATGATTTATCGGAAGGCACCTTGTCTTATAGTAACATGGCCATGGGA 660
QY 678 AGACAAACACAGCCAGATAGTCACTCTGCTCCAAATGATGACAAAGTTGATCAGG 737
Db 661 AGACAAACACAGCCAGATAGTCACTCTGCTCCAAATGATGACAAAGTTGATCAGG 720
QY 738 TGACAGTGTCTTACACTTCTGTGGGAGGACCACTGCAGGCGATCGCAGTGCCTGCC 797
Db 721 TGACAGTGTCTTACACTTCTGTGGGAGGACCACTGCAGGCGATCGCAGTGCCTGCC 780
QY 798 TACTCTGATGAGATAGAAATATCGTCTGTGGGATGCGATGTCFAATCACTTCTCC 857
Db 781 TACTCTGATGAGATAGAAATATCGTCTGTGGGATGCGATGTCFAATCACTTCTCC 840
QY 858 TGCCCTTCAAGCTGTTTGGGAAGTTGTTCTCATCACTGAGGATGAACTGCAACTT 917
Db 841 TGCCCTTCAAGCTGTTTGGGAAGTTGTTCTCATCACTGAGGATGAACTGCAACTT 900
QY 918 TCAGGATGCCAGGATCAGGACCATGAATGAAGTTTAACTGGTATAGGATAAATAAAA 977
Db 901 TCAGGATGCCAGGATCAGGACCATGAATGAAGTTTAACTGGTATAGGATAAATAAAA 960
QY 978 TGTACGCTGGAAAGTCATTTTCAATCTTATTTACCAATTTGAGAAAGAGGAGATT 1037
Db 961 TGTACGCTGGAAAGTCATTTTCAATCTTATTTACCAATTTGAGAAAGAGGAGATT 1020
QY 1038 CCAAGATTTGAGAGTTTCTGCTCAGGGGATCAATTTGGCTTCGTTTTCAGTGCAA 1097
Db 1021 CCAAGATTTGAGAGTTTCTGCTCAGGGGATCAATTTGGCTTCGTTTTCAGTGCAA 1080
QY 1098 GCAAAATCATGTTGTGACCTTACCACCTACGCTCTCTCGGAGTGTGATCAGAC 1157
Db 1081 GCAAAATCATGTTGTGACCTTACCACCTACGCTCTCTCGGAGTGTGATCAGAC 1140
QY 1158 CCAGCGGCTGTTGTGCGAGTACGCTGTATGGGGCTGTGCGGCTGACGGTTACCCCT 1217
Db 1141 CCAGCGGCTGTTGTGCGAGTACGCTGTATGGGGCTGTGCGGCTGACGGTTACCCCT 1200
QY 1218 TCTTCCCTTCAGCAATTCAGAGGCTGTCAGAGGCAATCGTCAGCAATCCAGAAATCCAGA 1277
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Db 1201 TCTTCCCTCAGCCATTGAGAGGTTGTGAGAGCAATCTCAGCATCCGAAGAAATCCAGA 1260
QY 1278 CCTTTTGTCTACTTGTATGAGATATACAGCGCAACCCGTCAGCTCCGTCAGATGGTAAAA 1337
Db 1261 CCTTTTGTCTACTTGTATGAGATATACAGCGCAACCCGTCAGCTCCGTCAGATGGTAAAA 1320
QY 1338 AGATGGTCATGTGTCAGGATTTTACTGCTTTTGGGATAAAGCATACAGAGACCCCAACTC 1397
Db 1321 AGATGGTCATGTGTCAGGATTTTACTGCTTTTGGGATAAAGCATACAGAGACCCCAACTC 1380
QY 1398 TACAAGCCCTTCTTACTGTCTAGACCTGCGCAATTTGTTAGCTGTGTGCGCCCCGTTG 1457
Db 1381 TACAAGCCCTTCTTACTGTCTAGACCTGCGCAATTTGTTAGCTGTGTGCGCCCCGTTG 1440
QY 1458 GAGCAGGGAAGTCACTACTGTTAAAGTCCGTCGCGGGAATTTGCCCAAGTCACGGGC 1517
Db 1441 GAGCAGGGAAGTCACTACTGTTAAAGTCCGTCGCGGGAATTTGCCCAAGTCACGGGC 1500
QY 1518 TGGTCAGCGTCATGGAAGAAATTCCTATGTCTCAGCAGCCCTGGGTGTTCTCGGGAA 1577
Db 1501 TGGTCAGCGTCATGGAAGAAATTCCTATGTCTCAGCAGCCCTGGGTGTTCTCGGGAA 1560
QY 1578 CTCTGAGGAGTAATATTTTATTTGGGAGAAATATGAAAGGAACGATATGAAAAGTCA 1637
Db 1561 CTCTGAGGAGTAATATTTTATTTGGGAGAAATATGAAAGGAACGATATGAAAAGTCA 1620
QY 1638 TAAAGGCTTCTGCTCTGAAAAGGATTTACAGCTGTTGGAGGATGGTGTGACTGTGA 1697
Db 1621 TAAAGGCTTCTGCTCTGAAAAGGATTTACAGCTGTTGGAGGATGGTGTGACTGTGA 1680
QY 1698 TAGGAGATCGGGAAACACGCTGAGTGGAGGCAAGAACGACGCGTAAACCTTCCAAAG 1757
Db 1681 TAGGAGATCGGGAAACACGCTGAGTGGAGGCAAGAACGACGCGTAAACCTTCCAAAG 1740
QY 1758 CAGTGTATCAAGATGCTGTGACATCTATCTCTGGACGATCTCTCAGTGCAGTAGATCGG 1817
Db 1741 CAGTGTATCAAGATGCTGTGACATCTATCTCTGGACGATCTCTCAGTGCAGTAGATCGG 1800
QY 1818 AAGTTAGCAGACACTTGTTCGAACCTGTATTTGTCAAAATTTTGCATGAGAAGATCAAA 1877
Db 1801 AAGTTAGCAGACACTTGTTCGAACCTGTATTTGTCAAAATTTTGCATGAGAAGATCAAA 1860
QY 1878 TTTTACTGACTCATCAGTTGCTGACCTCAAGCTCAAGCTCAAGTCTCATATTTGAAAG 1937
Db 1861 TTTTACTGACTCATCAGTTGCTGACCTCAAGCTCAAGCTCAAGTCTCATATTTGAAAG 1920
QY 1938 ATGGTAAAATGGTGCAGAGGAGCTTACACTGAGTTCCTTAAATCTGGTATAGATTTG 1997
Db 1921 ATGGTAAAATGGTGCAGAGGAGCTTACACTGAGTTCCTTAAATCTGGTATAGATTTG 1980
QY 1998 GCTCCCTTTTAAAGAGGATAATGAGGAAAGTGAACAACTCCAGTTCAGGAACTCCCA 2057
Db 1981 GCTCCCTTTTAAAGAGGATAATGAGGAAAGTGAACAACTCCAGTTCAGGAACTCCCA 2040
QY 2058 CACTAAGGAATCGTACCTTCTCAGAGTCTTGGTTCCTCAACAACTTCTTAGACCT 2117
Db 2041 CACTAAGGAATCGTACCTTCTCAGAGTCTTGGTTCCTCAACAACTTCTTAGACCT 2100
QY 2118 CTTTGAAGATGGTGTCTGAGAGGCAAGATACAGAGAATGTCCTAGTTCACACTAC 2177
Db 2101 CTTTGAAGATGGTGTCTGAGAGGCAAGATACAGAGAATGTCCTAGTTCACACTAC 2160
QY 2178 AGGAAACCTTCTGAGGAAAGTGGTTCAGGCCCTATAAGAATTTACTTCAGAGCTG 2237
Db 2161 AGGAAACCTTCTGAGGAAAGTGGTTCAGGCCCTATAAGAATTTACTTCAGAGCTG 2220
QY 2238 GTGCTCACTGGATGTCTTCAATTTCTTATTTCTCTTAAACACTGCAGCTCAGGTTGCCT 2297
Db 2221 GTGCTCACTGGATGTCTTCAATTTCTTATTTCTCTTAAACACTGCAGCTCAGGTTGCCT 2280
QY 2298 ATGCTCTCAAGATGGTGTGCTTATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2357
Db 2281 ATGCTCTCAAGATGGTGTGCTTCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340

QY 2358 CTGTAARTGGAGGAGAAATGTAACCGAGAGCTAGATCTTAACCTGGTACTTAGAAATTT 2417
Db 2341 CTGTAARTGGAGGAGAAATGTAACCGAGAGCTAGATCTTAACCTGGTACTTAGAAATTT 2400
QY 2418 ATTCAAGTTTAACTGTAGCTACCGTCTCTTTTGGCATAGCAAGATCTCTATTGTGATTTCT 2477
Db 2401 ATTCAAGTTTAACTGTAGCTACCGTCTCTTTTGGCATAGCAAGATCTCTATTGTGATTTCT 2460
QY 2478 ACGTCCCTGTTAACTCTTCACAACTTTGACAAACAAATGTTTTCAGTCAATTTCTGAAAG 2537
Db 2461 ACGTCCCTGTTAACTCTTCACAACTTTGACAAACAAATGTTTTCAGTCAATTTCTGAAAG 2520
QY 2538 CTCGGTATTAATCTTTGATAGAAATCCAATAGGAAGAAATTTTAAATCGTTTCTCCAAAG 2597
Db 2521 CTCGGTATTAATCTTTGATAGAAATCCAATAGGAAGAAATTTTAAATCGTTTCTCCAAAG 2580
QY 2598 ACATTGGACACTTTGGATGATTGCTGCGCTGAGCTTTTGTAGATTTTCATCCAGACATTCG 2657
Db 2581 ACATTGGACACTTTGGATGATTGCTGCGCTGAGCTTTTGTAGATTTTCATCCAGACATTCG 2640
QY 2658 TACAAGTGGTGTGGTGTCTCTGTGCTGTGGCCGTGATTCCTTGGATCGCAATACCCCT 2717
Db 2641 TACAAGTGGTGTGGTGTCTCTGTGCTGTGGCCGTGATTCCTTGGATCGCAATACCCCT 2700
QY 2718 TGGTTCCTCTGGAACTCATTTTCTCTGGCGCATATTTTGGAAACGTCAAGAG 2777
Db 2701 TGGTTCCTCTGGAACTCATTTTCTCTGGCGCATATTTTGGAAACGTCAAGAG 2760
QY 2778 ATGTGAAGCCCTGGAACTTACAACTCGGAGTCCAGTGTTCCTCCACTTGTTCATCTTCTC 2837
Db 2761 ATGTGAAGCCCTGGAACTTACAACTCGGAGTCCAGTGTTCCTCCACTTGTTCATCTTCTC 2820
QY 2838 TCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAGAGAGGTGTGAGAACTGTTG 2897
Db 2821 TCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAGAGAGGTGTGAGAACTGTTG 2880
QY 2898 ATGCACAC - CAGGATTTACATTCAGAGGCTTGGTCTCTGTTTGGAAAGCTCCGCTGG 2956
Db 2881 ATGCACACGAGGATTTACATTCAGAGGCTTGGTCTCTGTTTGGAAAGCTCCGCTGG 2940
QY 2957 TTCGCCCTCCGCTCGGATGCATCTGTGCCATGTTTGTCTCATCTGCTTGGGTC 3016
Db 2941 TTCGCCCTCCGCTCGGATGCATCTGTGCCATGTTTGTCTCATCTGCTTGGGTC 3000
QY 3017 CTGATCTGGCAAAACTCTGGATGCCGGCAGGTTGGTTTGGCACTGTCTATGCCCCC 3076
Db 3001 CTGATCTGGCAAAACTCTGGATGCCGGCAGGTTGGTTTGGCACTGTCTATGCCCCC 3060
QY 3077 ACGCTATGGGGATGTTTCACTGGTGTGTTTCGACAAAGTCTGAAGTTGAGATATGATG 3136
Db 3061 ACGCTATGGGGATGTTTCACTGGTGTGTTTCGACAAAGTCTGAAGTTGAGATATGATG 3120
QY 3137 ATCTCAGTAGAAAGGTCATTTGAATACACAGCTTGAAAGAAAGACCTTGGGAATAT 3196
Db 3121 ATCTCAGTAGAAAGGTCATTTGAATACACAGCTTGAAAGAAAGACCTTGGGAATAT 3180
QY 3197 CAGAAAGCCCAACACAGCTGGCCCCCATGAAGAGTGTATCTTTTGAATATGTTGAAC 3256
Db 3181 CAGAAAGCCCAACACAGCTGGCCCCCATGAAGAGTGTATCTTTTGAATATGTTGAAC 3240
QY 3257 TTCATGTACAGTCCAGTGGGCTCTGGTACTGAGCATCTGACAGCACTCATTAATCA 3316
Db 3241 TTCATGTACAGTCCAGTGGGCTCTGGTACTGAGCATCTGACAGCACTCATTAATCA 3300
QY 3317 CAAGAAAGGTTGGCATTTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTCATCTCAGCC 3376
Db 3301 CAAGAAAGGTTGGCATTTGGGAAGAACCGGAGCTGGAAAAAGTTCCCTCATCTCAGCC 3360
QY 3377 CTTTTTAGATTGTGACAAACCCGAGGTAAATTTTGGATTGATAGATCTTTGACAACTGAA 3436
Db 3361 CTTTTTAGATTGTGACAAACCCGAGGTAAATTTTGGATTGATAGATCTTTGACAACTGAA 3420

QY 3437 ATTGACCTTCAGGATTTTAAAGAAAGAAATGTCAATCATACCTCAGAAACCTGTTTGTTC 3496
Db 3421 ATTGACCTTCAGGATTTTAAAGAAAGAAATGTCAATCATACCTCAGAAACCTGTTTGTTC 3480
QY 3497 ACTGAAACAATCAGCAAAACCTGGATCCCTTTTAAAGGAGCACACGGATGAGGAACCTGTGG 3556
Db 3481 ACTGAAACAATCAGCAAAACCTGGATCCCTTTTAAAGGAGCACACGGATGAGGAACCTGTGG 3540
QY 3557 AATGCTTTACAGAGGTACAACTTAAAGAAACCAATTTTAAAGATCTTCCCTGTTAAATGGAT 3616
Db 3541 AATGCTTTACAGAGGTACAACTTAAAGAAACCAATTTTAAAGATCTTCCCTGTTAAATGGAT 3600
QY 3617 ACTGAATTTAGCAGAAATCAGGATCCAAATTTTGTGTTGGACAAAGACAATGTTGTGCTCTT 3676
Db 3601 ACTGAATTTAGCAGAAATCAGGATCCAAATTTTGTGTTGGACAAAGACAATGTTGTGCTCTT 3660
QY 3677 GCCAGGCAATTTCTCAGCAAAACCTGATATTTGATTTATGATGAGGCGACGCAATGTG 3736
Db 3661 GCCAGGCAATTTCTCAGCAAAACCTGATATTTGATTTATGATGAGGCGACGCAATGTG 3720
QY 3737 GATCCAAAGACTGATGAGTTAATACAAAATAATCCGGAGAAATTTGCCCACTGCACC 3796
Db 3721 GATCCAAAGACTGATGAGTTAATACAAAATAATCCGGAGAAATTTGCCCACTGCACC 3780
QY 3797 GTGCTAACCTTTGCACACAGATTTGAACACCATTTATTTGACGCGCAAGATAATGTTTGA 3856
Db 3781 GTGCTAACCTTTGCACACAGATTTGAACACCATTTATTTGACGCGCAAGATAATGTTTGA 3840
QY 3857 GATTCAGAAAGACTGAAAGAAATATGATGAGCGGTATGTTTGTCTGCAAAATTAAGAGAC 3916
Db 3841 GATTCAGAAAGACTGAAAGAAATATGATGAGCGGTATGTTTGTCTGCAAAATTAAGAGAC 3900
QY 3917 CTATTTTACAAGATGTTGCAACAACTGGCGAAGGAGGCGCTGCCCTCACTGAAACA 3976
Db 3901 CTATTTTACAAGATGTTGCAACAACTGGCGAAGGAGGCGCTGCCCTCACTGAAACA 3960
QY 3977 GCATAACAGGTATCTTCAAAAGAAATTTATCCACATTTTGTTCACACTGACCAATGGTT 4036
Db 3961 GCATAACAGGTATCTTCAAAAGAAATTTATCCACATTTTGTTCACACTGACCAATGGTT 4020
QY 4037 ACAACACTTCCCAATGGACGCGCTCGACCTTAACTATTTTTCGACAGCACTGTGAATC 4096
Db 4021 ACAACACTTCCCAATGGACGCGCTCGACCTTAACTATTTTTCGACAGCACTGTGAATC 4080
QY 4097 CAACAAATGTCAGTCCGTTCCGAAAGGCAATTTTCCACTAGTTTGGACTATGTAAC 4156
Db 4081 CAACAAATGTCAGTCCGTTCCGAAAGGCAATTTTCCACTAGTTTGGACTATGTAAC 4140
QY 4157 CACATTGTACTTTTTTTTACTTTTGGCAACAATATTTATATACATAAGATGCTAGTTCA 4216
Db 4141 CACATTGTACTTTTTTTTACTTTTGGCAACAATATTTATATACATAAGATGCTAGTTCA 4200
QY 4217 TTGAATTTTCTCCC 4231
Db 4201 TTGAATTTTCTCCC 4215

RESULT 9

ABV24188

ID ABV24188 standard; cdna; 4515 BP.

XX ABV24188;

XX

XX 16-SEP-2002 (first entry)

XX

XX Human prostate expression marker cdna 24179.

DE

XX

KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

KW pharmacogenomic marker; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200160860-A2.

XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US05171.
XX PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX DR Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX Claim 1; Page 4506-4507; 11750pp; English.
PS The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX SQ Sequence 4515 BP; 1253 A; 942 C; 1059 G; 1261 T; 0 other;
Query Match 99.2%; Score 4196.6; DB 23; Length 4515;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4210; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
Qy 18 GGAGCCCGCAGCATCCCTGCTTGAGTCCAGGAGCGGAGCCGCGCCAGATGCTGCTGAT 77
Db 1 GGAGCCCGCAGCATCCCTGCTTGAGTCCAGGAGCGGAGCCGCGCCAGATGCTGCTGAT 60
Qy 78 CAGCGCGACCCCGCGCCCGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 137
Db 61 CAGCGCGACCCCGCGCCCGCGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Qy 138 TGAAGCCCAACCCGTCGAGCAGCGGACATCTGCTCAGCGGTGCTCTGCTGCTGCTCA 197
Db 121 TGAAGCCCAACCCGTCGAGCAGCGGACATCTGCTCAGCGGTGCTCTGCTGCTGCTCA 180
Qy 198 ATCCCTTGTTTAAATTTGGCCATAACCGAGATTAGAGGAAGATGATGATTTTCAAGTGC 257
Db 181 ATCCCTTGTTTAAATTTGGCCATAACCGAGATTAGAGGAAGATGATGATTTTCAAGTGC 240
Qy 258 TGCAGAGACCGCTCAGACACCTTGGAGAGGAGTTCGAAGGTTCTGGGATAAAGAG 317
Db 241 TGCAGAGACCGCTCAGACACCTTGGAGAGGAGTTCGAAGGTTCTGGGATAAAGAG 300
Qy 318 TTTTAAAGAGCTGAGAAATGACCCAGAGACCTTCTTTAAAGAGCAATATCAAGTGT 377
Db 301 TTTTAAAGAGCTGAGAAATGACCCAGAGACCTTCTTTAAAGAGCAATATCAAGTGT 360
Qy 378 ACTGGAATCTTATTAGTTTGGGAATTTTACGTTAAATGAGGAAGTCCCAAGTAA 437
Db 361 ACTGGAATCTTATTAGTTTGGGAATTTTACGTTAAATGAGGAAGTCCCAAGTAA 420

Qy 438 TCCAGCCCATATTTTGGGAAAAATTTATTTATTTTGAATAATATATCATCCCATGGATT 497
Db 421 TCCAGCCCATATTTTGGGAAAAATTTATTTATTTTGAATAATATATCATCCCATGGATT 480
Qy 498 CTGTGGCTTTTGAACACACAGCGTACGCCTATGCCACAGGCTGCTGACTTTTTCAGCGCTCATTT 557
Db 481 CTGTGGCTTTTGAACACACAGCGTACGCCTATGCCACAGGCTGCTGACTTTTTCAGCGCTCATTT 540
Qy 558 TGGCTATACCTGATCAGTCACTTATTTTATCAGCTTCACTGTGCTGGGATGAGGTTACGAG 617
Db 541 TGGCTATACCTGATCAGTCACTTATTTTATCAGCTTCACTGTGCTGGGATGAGGTTACGAG 600
Qy 618 TAGCCATGTGCCATATGATTTTATCGAAGGACCTTCGCTTTAGTAACATGCGCCATGGGGA 677
Db 601 TAGCCATGTGCCATATGATTTTATCGAAGGACCTTCGCTTTAGTAACATGCGCCATGGGGA 660
Qy 678 AGACAACACACAGGCCAGATAGTCAATCTGCTGTCCAAATGATGTGAACAAGTTTGTATCAGG 737
Db 661 AGACAACACACAGGCCAGATAGTCAATCTGCTGTCCAAATGATGTGAACAAGTTTGTATCAGG 720
Qy 738 TGACAGTGTCTTACACTTCTGCTGGGAGGACCACTGCAGGCGATCGACTGACTGCC 797
Db 721 TGACAGTGTCTTACACTTCTGCTGGGAGGACCACTGCAGGCGATCGACTGACTGCC 780
Qy 798 TACTCTGGATGGAGATAGGAATATCGCCCTTGTGGGATGGGAGTCTATATCTCTCC 857
Db 781 TACTCTGGATGGAGATAGGAATATCGCCCTTGTGGGATGGGAGTCTATATCTCTCC 840
Qy 858 TGCCCTTGCAGGCTGTTTGGGAAAGTGTCTCATCTGAGGAGTAAAACTGCAACTT 917
Db 841 TGCCCTTGCAGGCTGTTTGGGAAAGTGTCTCATCTGAGGAGTAAAACTGCAACTT 900
Qy 918 TCAGGATGCCAGATCAGGACCAATGAAGTTAATCTGTTAAGGATAATAAAA 977
Db 901 TCAGGATGCCAGATCAGGACCAATGAAGTTAATCTGTTAAGGATAATAAAA 960
Qy 978 TGTACGCTGGGAAAGTCAATTTTCAATCTTATTTCAATTTTGAAGAAAGAGATTT 1037
Db 961 TGTACGCTGGGAAAGTCAATTTTCAATCTTATTTCAATTTTGAAGAAAGAGATTT 1020
Qy 1038 CCAAGATTTGAGAAGTTCTGCTCAGGGGATGAATTTGGCTTCGTTTTTTCAGTGCAA 1097
Db 1021 CCAAGATTTGAGAAGTTCTGCTCAGGGGATGAATTTGGCTTCGTTTTTTCAGTGCAA 1080
Qy 1098 GCAAAATCATCTGTTTGTGACCTTCAACACTACCTGCTGCGGAGTGTGATCACAG 1157
Db 1081 GCAAAATCATCTGTTTGTGACCTTCAACACTACCTGCTGCGGAGTGTGATCACAG 1140
Qy 1158 CCAGCGCGCTGTTCTGCTGAGTCACTGCTGATGGGCTGTCGCTGACCGTTACCTCT 1217
Db 1141 CCAGCGCGCTGTTCTGCTGAGTCACTGCTGATGGGCTGTCGCTGACCGTTACCTCT 1200
Qy 1218 TCTTCCCTCAGCCATTGAGAGGTTGTAGAGGCAATTCGTACGATCCGAAGAAATCCAGA 1277
Db 1201 TCTTCCCTCAGCCATTGAGAGGTTGTAGAGGCAATTCGTACGATCCGAAGAAATCCAGA 1260
Qy 1278 CTTTTTGTCTACTTGTATGATATACAGGCAACCGTCACTGCTGCTGATGTTGTTAAAA 1337
Db 1261 CTTTTTGTCTACTTGTATGATATACAGGCAACCGTCACTGCTGCTGATGTTGTTAAAA 1320
Qy 1338 AGATGTGATGTGCAAGGATTTTACTGCTTTTGGGATAGGATCAGAGACCCCACTC 1397
Db 1321 AGATGTGATGTGCAAGGATTTTACTGCTTTTGGGATAGGATCAGAGACCCCACTC 1380
Qy 1398 TACAAGGCTTTTCTTTTACTGTGACACCTGGCGAATTTTAGTGTGGTGGCGCGTGG 1457
Db 1381 TACAAGGCTTTTCTTTTACTGTGACACCTGGCGAATTTTAGTGTGGTGGCGCGTGG 1440
Qy 1458 GAGCAGGAGTCACTGTTTAAAGTGGCGTGTCTGGGAAATTTGGCCCCCAAGTACGGGC 1517
Db 1441 GAGCAGGAGTCACTGTTTAAAGTGGCGTGTCTGGGAAATTTGGCCCCCAAGTACGGGC 1500

Db 3661 GCAGGGCAATTCACAGAAATCAGATATTCATTATTGATGAACGACGCGCAATGTG 3720
Qy 3737 GATCCAGAACTGATGAGTAAATACAAAAAAATCCGGGAGAAATTTGCCCACTGCACC 3796
Db 3721 GATCCAGAACTGATGAGTAAATACAAAAAAATCCGGGAGAAATTTGCCCACTGCACC 3780
Qy 3797 GTGCTAACCATTCACACAGATTCACACCATATTTAGACAGGACAGATATGTTTAA 3856
Db 3781 GTGCTAACCATTCACACAGATTCACACCATATTTAGACAGGACAGATATGTTTAA 3840
Qy 3857 GATTCAGGAAGACTGAAAGAAATATGATGAGCGGTATGTTTGTGCAAAATAAAGAGAG 3916
Db 3841 GATTCAGGAAGACTGAAAGAAATATGATGAGCGGTATGTTTGTGCAAAATAAAGAGAG 3900
Qy 3917 CTATTTTACAAGATGGTGAACAACATGCGACCTTAACTATTTTCGAGACAGCACTGTGAATC 3976
Db 3901 CTATTTTACAAGATGGTGAACAACATGCGACCTTAACTATTTTCGAGACAGCACTGTGAATC 3960
Qy 3977 GCAAAACAGGTATCTTCAAAAGAAATATCCACATATTTGTCACACTGACCACTGTT 4036
Db 3961 GCAAAACAGGTATCTTCAAAAGAAATATCCACATATTTGTCACACTGACCACTGTT 4020
Qy 4037 ACAAACTTCCATGAGACAGCCCTCGACCTTAACTATTTTCGAGACAGCACTGTGAATC 4096
Db 4021 ACAAACTTCCATGAGACAGCCCTCGACCTTAACTATTTTCGAGACAGCACTGTGAATC 4080
Qy 4097 CAACCAAAATGTCAGTCCGTTCCGAAGGCAATTTTCCACTAGTATTTTGGACTATGTAAC 4156
Db 4091 CAACCAAAATGTCAGTCCGTTCCGAAGGCAATTTTCCACTAGTATTTTGGACTATGTAAC 4140
Qy 4157 CACATTGTACTTTTTTTTACTTTGGCAACAATATTTATACATAAAGATGCTAGTTCAT 4216
Db 4141 CACATTGTACTTTTTTTTACTTTGGCAACAATATTTATACATAAAGATGCTAGTTCAT 4200
Qy 4217 TTGAATATTTCTCC 4231
Db 4201 TTGAATATTTCTCC 4215

RESULT 10
ABV24580
ID ABV24580 standard; cDNA; 4515 BP.
XX
AC ABV24580;
XX
16-SEP-2002 (first entry)
XX
Human prostate expression marker CDNA 24571.
XX
Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
Homo sapiens.
XX
WO200160860-A2.
XX
23-AUG-2001.
XX
20-FEB-2001; 2001WO-US05171.
XX
17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
Schlegel R, Endege WO, Monahan JE;
PI
XX
WPI; 2001-662795/76.
DR
XX

PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 4662-4663; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX

SQ Sequence 4515 BP; 1253 A; 942 C; 1059 G; 1261 T; 0 other;

Query Match 99.2%; Score 4196.6; DB 23; Length 4515;

Best Local Similarity 99.9%; Pred. No 0;

Matches 4210; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 18 GGAGCCCCAGCATCCCTGCTTGTAGGTCAGAGCGGAGCCCGGCGCCAGCCGCTGAT 77

Db 1 GGAGCCCCAGCATCCCTGCTTGTAGGTCAGAGCGGAGCCCGGCGCCAGCCGCTGAT 60

Qy 78 CAGCGGACCCCGGCGCCCGCCCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 137

Db 61 CAGCGGACCCCGGCGCCCGCCCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120

Qy 138 TGAAGCCCAACCGCTGCAGAGCGCGCAACATCTGCTCACGCGTGTCTTCTGTGCTCA 197

Db 121 TGAAGCCCAACCGCTGCAGAGCGCGCAACATCTGCTCACGCGTGTCTTCTGTGCTCA 180

Qy 198 ATCCCTGTTTAAATTTGGCCATAAAGCGAGATTAGAGGAAGATATATTCAGTGC 257

Db 181 ATCCCTGTTTAAATTTGGCCATAAAGCGAGATTAGAGGAAGATATATTCAGTGC 240

Qy 258 TGCCAGAACCGCTCACAGCACTTTGGAGAGAGTTGCAAGGTTCTGGGATAAAGAG 317

Db 241 TGCCAGAACCGCTCACAGCACTTTGGAGAGAGTTGCAAGGTTCTGGGATAAAGAG 300

Qy 318 TTTTAAGAGCTGAGATGACGACAGAGCGCTTCTTTTAAACAGCAATCATATAAGTGT 377

Db 301 TTTTAAGAGCTGAGATGACGACAGAGCGCTTCTTTTAAACAGCAATCATATAAGTGT 360

Qy 378 ACTGGAATCTTATTTAGTTTGGGAAATTTTACGTTTAAATTTGAGGAAAGTCCAAAGTAA 437

Db 361 ACTGGAATCTTATTTAGTTTGGGAAATTTTACGTTTAAATTTGAGGAAAGTCCAAAGTAA 420

Qy 438 TCCAGCCCATATTTTGGGAAAAATTTAAATTTTGAATAATATGATCCCATGATT 497

Db 421 TCCAGCCCATATTTTGGGAAAAATTTAAATTTTGAATAATATGATCCCATGATT 480

Qy 498 CTGTGGCTTTGAACACAGCGTACGCTATGCGACGCTGCTGACTTTTTCACGCTCATTT 557

Db 481 CTGTGGCTTTGAACACAGCGTACGCTATGCGACGCTGCTGACTTTTTCACGCTCATTT 540

Qy 558 TGGCTATACATGACATTTATTTTATCAGTTTCAGTGTGCTGGATGAGGTACGAG 617

Db 541 TGGCTATACATGACATTTATTTTATCAGTTTCAGTGTGCTGGATGAGGTACGAG 600

Qy 618 TAGCCATGTCATATGATTATTCGAGGCACTTCGCTTATAGTAACATGCGCATGGGA 677

Db 601 TAGCCATGTCATATGATTATTCGAGGCACTTCGCTTATAGTAACATGCGCATGGGA 660

Qy 678 AGACAACCACAGGCCAGATAGTCAATCTCTCTCCATCATGTGACACAGTTTGATCAGG 737

QY 2898 ATGCACAC -CAGGATTACATTCAGAGGCTTGGTTCTGTTTTCAGACAGTCCCGCTGG 2956
 Db 2881 ATGCACACGAGATTACATTCAGAGGCTTGGTTCTGTTTTCAGACAGTCCCGCTGG 2940
 QY 2957 TTCGCCGTCCTGATGCCATCTGTGCCATGTTTGTTCATCATCTGTTGCCCTTTGGGTCC 3016
 Db 2941 TTCGCCGTCCTGATGCCATCTGTGCCATGTTTGTTCATCATCTGTTGCCCTTTGGGTCC 3000
 QY 3017 CTGATCTGCGCAAACTCTGATGCCGGCAGGTTGGTTGGCAGTCTGCTTATGCCCTTC 3076
 Db 3001 CTGATCTGCGCAAACTCTGATGCCGGCAGGTTGGTTGGCAGTCTGCTTATGCCCTTC 3060
 QY 3077 AGCCTCATGGGATCTTTCAGTGGTGTGTTCCACAAAGTGTGCTTGGCAATATGATG 3136
 Db 3061 AGCCTCATGGGATCTTTCAGTGGTGTGTTCCACAAAGTGTGCTTGGCAATATGATG 3120
 QY 3137 ATCTCAGTAGAAGGTCATTGAATACACAGACCTTTGAAAAGAACGACCTTTGGGAATAT 3196
 Db 3121 ATCTCAGTAGAAGGTCATTGAATACACAGACCTTTGAAAAGAACGACCTTTGGGAATAT 3180
 QY 3197 CAGAAACCCACACAGCCTGGCCCATGAGGAGTGATAATCTTTGACAATCTGAAC 3256
 Db 3181 CAGAAACCCACACAGCCTGGCCCATGAGGAGTGATAATCTTTGACAATCTGAAC 3240
 QY 3257 TTCATGTACAGTCCAGTGGGCTCTGTGCTACTGAAGCATCTGACAGCACTATTAAATCA 3316
 Db 3241 TTCATGTACAGTCCAGTGGGCTCTGTGCTACTGAAGCATCTGACAGCACTATTAAATCA 3300
 QY 3317 CAAGAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGAAAAGTTCCTCATCTCAGCC 3376
 Db 3301 CAAGAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGAAAAGTTCCTCATCTCAGCC 3360
 QY 3377 CTTTTAGATTGTGAGAACCCGAGGTAAATTTGGATTGATAAGATCTTGACAACTGAA 3436
 Db 3361 CTTTTAGATTGTGAGAACCCGAGGTAAATTTGGATTGATAAGATCTTGACAACTGAA 3420
 QY 3437 ATTGACTTACAGATTAAAGAAAGAAATGTCATCATCTCAGGAACCTGTTTGTTC 3496
 Db 3421 ATTGACTTACAGATTAAAGAAAGAAATGTCATCATCTCAGGAACCTGTTTGTTC 3480
 QY 3497 ACTGGAACAACTGAGGAAAACCTGGATCCCTTTAAGGAGCACGCGATGAGGAAGTGG 3556
 Db 3481 ACTGGAACAACTGAGGAAAACCTGGATCCCTTTAAGGAGCACGCGATGAGGAAGTGG 3540
 QY 3557 ATGCTCTTACAGAGGTACAACTTAAAGAAACCAATGGAAGATCTTCCTGGTAAATGGAT 3616
 Db 3541 ATGCTCTTACAGAGGTACAACTTAAAGAAACCAATGGAAGATCTTCCTGGTAAATGGAT 3600
 QY 3617 ACTGAATTACAGAACTCAGGATCCAAATTTAGTGTGGACAAACACTGGTGTGCTT 3676
 Db 3601 ACTGAATTACAGAACTCAGGATCCAAATTTAGTGTGGACAAACACTGGTGTGCTT 3660
 QY 3677 GCCAGGCAATCTTCAGGAAAATTCAGATATTGATTATGATGAAGCGACGCAAAATGTG 3736
 Db 3661 GCCAGGCAATCTTCAGGAAAATTCAGATATTGATTATGATGAAGCGACGCAAAATGTG 3720
 QY 3737 GATCCAGAACTGATGAGTTAATACAAAAAATTCGGGAGAAATTTGCCACTGCACC 3796
 Db 3721 GATCCAGAACTGATGAGTTAATACAAAAAATTCGGGAGAAATTTGCCACTGCACC 3780
 QY 3797 GTGCTAACCATTCACACAGATTGAACACCAATTTATTCAGACGCAAGATAATGGTTTAA 3856
 Db 3781 GTGCTAACCATTCACACAGATTGAACACCAATTTATTCAGACGCAAGATAATGGTTTAA 3840
 QY 3857 GATTCAGGAAGTGAAGAAATGATGAGCGGTATGTTTGTGCGCAAAATAAGAGAGC 3916
 Db 3841 GATTCAGGAAGTGAAGAAATGATGAGCGGTATGTTTGTGCGCAAAATAAGAGAGC 3900
 QY 3917 CTATTTTACAGATGTTGCAACAACTGGGCAAGGAGGAGCGGCTGCCCTCACTGAAACA 3976
 Db 3901 CTATTTTACAGATGTTGCAACAACTGGGCAAGGAGGAGCGGCTGCCCTCACTGAAACA 3960

QY 3977 GCAAAACAGGTATACATTCCTCAAAAGAAATATCCACATATTTGTCACACTGACCATGTT 4036
 Db 3961 GCAAAACAGGTATACATTCCTCAAAAGAAATATCCACATATTTGTCACACTGACCATGTT 4020
 QY 4037 ACAAACACATTCCTCAATGAGACAGCCCTCGACCTTAACCTTAACTATTTTCGAGACAGCAGTGAATC 4096
 Db 4021 ACAAACACATTCCTCAATGAGACAGCCCTCGACCTTAACCTTAACTATTTTCGAGACAGCAGTGAATC 4080
 QY 4097 CAACCAAAATGTCAAGTCCCTTCGGAAGGCAATTTCCACTAGTATTTTGGACTATGTAAC 4156
 Db 4081 CAACCAAAATGTCAAGTCCCTTCGGAAGGCAATTTCCACTAGTATTTTGGACTATGTAAC 4140
 QY 4157 CACATTTGTTACTTTTTTTTACTTTTGGCAACAAATATTTATACATACAAAGATGCTAGTTTCAT 4216
 Db 4141 CACATTTGTTACTTTTTTTTACTTTTGGCAACAAATATTTATACATACAAAGATGCTAGTTTCAT 4200
 QY 4217 TTGAATATTTCTCCC 4231
 Db 4201 TTGAATATTTCTCCC 4215

RESULT 11
 ABV26511
 ID ABV26511 standard; cdNA; 4515 BP.
 AC ABV26511;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cdNA 26502.
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX Homo sapiens.
 XX WO200160860-A2.
 PN 23-AUG-2001.
 PD
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1; Page 5356-5357; 11750pp; English.
 CC
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;

QY 2058 CACTAAGGAATCGTACCTCTCAGAGTCCTTCGGTTGGTCTCACAAATCTTCTAGACCCCT 2117
 Db 2041 CACTAAGGAATCGTACCTCTCAGAGTCCTTCGGTTGGTCTCACAAATCTTCTAGACCCCT 2100
 QY 2118 CTTGAAAGATGGTGTCTGGAGAGCCAGATACAGAGAATGTCGCCAGTTTACACTATFCAG 2177
 Db 2101 CTTGAAAGATGGTGTCTGGAGAGCCAGATACAGAGAATGTCGCCAGTTTACACTATFCAG 2160
 QY 2178 AGGAGAACCGTCTGAAGGAAAGTTGGTTTTTCAGGCCATATAAGAAATTAATCTCAGAGCTG 2237
 Db 2161 AGGAGAACCGTCTGAAGGAAAGTTGGTTTTTCAGGCCATATAAGAAATTAATCTCAGAGCTG 2220
 QY 2238 GTGCTCAGTGGATGTCCTTCAATTTCTTATCTCTAATCTTAACTGCTCAGCTCAGCTGGCT 2297
 Db 2221 GTGCTCAGTGGATGTCCTTCAATTTCTTATCTCTAATCTTAACTGCTCAGCTCAGCTGGCT 2280
 QY 2298 ATGTGCTTCAAGATTTGGTGGCTTTTCATCTGGGCAACAAACAAATATGCTAAATGTCA 2357
 Db 2281 ATGTGCTTCAAGATTTGGTGGCTTTTCATCTGGGCAACAAACAAATATGCTAAATGTCA 2340
 QY 2358 CTGTAATGGAGGAGAAATGAACCGAGAAGCTAGATCTTAATCTGCTACTTAGGAATTT 2417
 Db 2341 CTGTAATGGAGGAGAAATGAACCGAGAAGCTAGATCTTAATCTGCTACTTAGGAATTT 2400
 QY 2418 ATTCAGGTTTAACTGTAGTACCGTTCTTTTGGGATAGCAAGATCTATTTGGTATTCCT 2477
 Db 2401 ATTCAGGTTTAACTGTAGTACCGTTCTTTTGGGATAGCAAGATCTATTTGGTATTCCT 2460
 QY 2478 AGCTCCTTGTAACTCTTCAACAACTTTCGCAACAAATATGTTGAGTCAATTCGAAG 2537
 Db 2461 AGCTCCTTGTAACTCTTCAACAACTTTCGCAACAAATATGTTGAGTCAATTCGAAG 2520
 QY 2538 CTCGGTATTAATCTTTGATAGAAATCCAAATAGGAGAAATTTTAAATCGTTTCTCCAAAG 2597
 Db 2521 CTCGGTATTAATCTTTGATAGAAATCCAAATAGGAGAAATTTTAAATCGTTTCTCCAAAG 2580
 QY 2598 ACATTGGACACTTGATGATTTGCTGGCGCTCAGCTTTTATGATTTTATCCAGACATTCG 2657
 Db 2581 ACATTGGACACTTGATGATTTGCTGGCGCTCAGCTTTTATGATTTTATCCAGACATTCG 2640
 QY 2658 TACAAAGTGGTGGTGTGCTGTGGCTGTGGCGTGTATCTTGGATTCGCAATACCT 2717
 Db 2641 TACAAAGTGGTGGTGTGCTGTGGCTGTGGCGTGTATCTTGGATTCGCAATACCT 2700
 QY 2718 TGGTTCCTTGGAAATCAATTTTCTTCGCGATATTTTGGAAAGCTCAAGAG 2777
 Db 2701 TGGTTCCTTGGAAATCAATTTTCTTCGCGATATTTTGGAAAGCTCAAGAG 2760
 QY 2778 ATGTGAAGCGCTGGAATCTACAACTCGGAGTCCAGTGTTCCTCAGTTCATCTCTC 2837
 Db 2761 ATGTGAAGCGCTGGAATCTACAACTCGGAGTCCAGTGTTCCTCAGTTCATCTCTC 2820
 QY 2838 TCCAGGGCTCTGGACCATCCGGGCATACAAAGCAGAGAGAGTGTGAGGAATCTTTG 2897
 Db 2821 TCCAGGGCTCTGGACCATCCGGGCATACAAAGCAGAGAGAGTGTGAGGAATCTTTG 2880
 QY 2898 ATGCACAC - CAGGATTTACATTCAGAGCTGGTTCCTTTTGGAAAGCTCCCGCTGG 2956
 Db 2881 ATGCACACGAGGATTTACATTCAGAGCTGGTTCCTTTTGGAAAGCTCCCGCTGG 2940
 QY 2957 TTCGCGCTCTGGAGTCCATCTGTGCGATGTTTGTTCATCATCTGTTGGCTTTGGGTC 3016
 Db 2941 TTCGCGCTCTGGAGTCCATCTGTGCGATGTTTGTTCATCATCTGTTGGCTTTGGGTC 3000
 QY 3017 CTGATTTGGCAAAATCTCTGATGCGGCGAGTGTGTTGGCACTCTCTATGCCCTC 3076
 Db 3001 CTGATTTGGCAAAATCTCTGATGCGGCGAGTGTGTTGGCACTCTCTATGCCCTC 3060
 QY 3077 ACGCTCATGGGATGTTTCACTGGTGTGTTCCGACAAAGTGTGAAGTTGAGAATATGATG 3136
 Db 3061 ACGCTCATGGGATGTTTCACTGGTGTGTTCCGACAAAGTGTGAAGTTGAGAATATGATG 3120
 QY 3137 ATCTCAGTAGAAGGGTCATTGAATACACAGACCTTGGAAAGAACCTTGGGAATAT 3196

Db 3121 ATCTCAGTAGAAGGGTCATTGAATACACAGACCTTGGAAAGAGACCTTGGGAATAT 3180
 QY 3197 CAGAAAGCCACACACAGACCTGGCCCATGAAGAGTGAATACTTTGACAATGTGAAC 3256
 Db 3181 CAGAAAGCCACACACAGACCTGGCCCATGAAGAGTGAATACTTTGACAATGTGAAC 3240
 QY 3257 TTCAATGTACAGTTCAGGTGGCCCTCTGTACTGAAGCATCTTGACAGCACTCATTAATCA 3316
 Db 3241 TTCAATGTACAGTTCAGGTGGCCCTCTGTACTGAAGCATCTTGACAGCACTCATTAATCA 3300
 QY 3317 CAAGAAAAGGTGGCATTTGGGAAAGACCGAGCTGGAAAAGTTCCTCATCTCAGCC 3376
 Db 3301 CAAGAAAAGGTGGCATTTGGGAAAGACCGAGCTGGAAAAGTTCCTCATCTCAGCC 3360
 QY 3377 CTTTTAGATTTGTCAGAACCGGAGGTAATAATTTGGATTTGATAAGATCTTGACAACGTAA 3436
 Db 3361 CTTTTAGATTTGTCAGAACCGGAGGTAATAATTTGGATTTGATAAGATCTTGACAACGTAA 3420
 QY 3437 ATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATACCTCAGGAACCTGTTTGTTC 3496
 Db 3421 ATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATACCTCAGGAACCTGTTTGTTC 3480
 QY 3497 ACTGGAAATAGAGGAAAAACCTGGATCCCTTTAAGGAGCACACGATGAGGAACCTGTGG 3556
 Db 3481 ACTGGAAATAGAGGAAAAACCTGGATCCCTTTAAGGAGCACACGATGAGGAACCTGTGG 3540
 QY 3557 AATGCCCTTACAGAGGTACAACTTAAAGAAACCAATTTAGTCTGGCAAAAGCAACTGTTGCTT 3616
 Db 3541 AATGCCCTTACAGAGGTACAACTTAAAGAAACCAATTTAGTCTGGCAAAAGCAACTGTTGCTT 3600
 QY 3617 ACTGAATTTAGCAGAAATCAGATCCAAATTTAGTCTGGCAAAAGCAACTGTTGCTT 3676
 Db 3601 ACTGAATTTAGCAGAAATCAGATCCAAATTTAGTCTGGCAAAAGCAACTGTTGCTT 3660
 QY 3677 GCCAGGCAATTTCTCAGGAAAAATCAGATATTTGATTTGATGAAGCGACGCAAAATGTG 3736
 Db 3661 GCCAGGCAATTTCTCAGGAAAAATCAGATATTTGATTTGATGAAGCGACGCAAAATGTG 3720
 QY 3737 GATCCAGAACTGATGAGTTAATAAATAAATCCGGGAGAAATTTGCCACTGCACC 3796
 Db 3721 GATCCAGAACTGATGAGTTAATAAATAAATCCGGGAGAAATTTGCCACTGCACC 3780
 QY 3797 GTGCTAACCATTCACACAGATTTGAACCCATTTATGACAGCGACAGATAAATGGTTTTA 3856
 Db 3781 GTGCTAACCATTCACACAGATTTGAACCCATTTATGACAGCGACAGATAAATGGTTTTA 3840
 QY 3857 GATTCAGGAAGACTGAAAGAAATATGATGAGCCGTATGTTTGTGCAAAATAAAGAGAGC 3916
 Db 3841 GATTCAGGAAGACTGAAAGAAATATGATGAGCCGTATGTTTGTGCAAAATAAAGAGAGC 3900
 QY 3917 CTATTTTACAAGTGTGCAACAACTGGGCAAGGAGAGCCGCTGCCCTCTACTGAAACA 3976
 Db 3901 CTATTTTACAAGTGTGCAACAACTGGGCAAGGAGAGCCGCTGCCCTCTACTGAAACA 3960
 QY 3977 GCAAAACAGGTATACCTTCAAAAGAAATTTATCCACATATTTGGTCCACACTGACCATGGTT 4036
 Db 3961 GCAAAACAGGTATACCTTCAAAAGAAATTTATCCACATATTTGGTCCACACTGACCATGGTT 4020
 QY 4037 ACAACACTTCCAATGGACAGCCCTCGACCTTAACATTTTTCGAGACAGCACTGTGAATC 4096
 Db 4021 ACAACACTTCCAATGGACAGCCCTCGACCTTAACATTTTTCGAGACAGCACTGTGAATC 4080
 QY 4097 CAACCAAAATGTCAAGTCCGTTCCGAGGAGATTTTCCACTAGTTTTGGAGATGTAAAC 4156
 Db 4081 CAACCAAAATGTCAAGTCCGTTCCGAGGAGATTTTCCACTAGTTTTGGAGATGTAAAC 4140
 QY 4157 CACATGTACTTTTTTTTACTTTTGGCAAAATATTTATACATACAGATGCTAGTTCAT 4216
 Db 4141 CACATGTACTTTTTTTTACTTTTGGCAAAATATTTATACATACAGATGCTAGTTCAT 4200
 QY 4217 TTGAATATTTCTCC 4231

Db 4201 TTGAAATATTTCTCCC 4215

RESULT 12
ABV28224
ID ABV28224 standard; cDNA; 4515 BP.
XX
AC ABV28224;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 28215.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW Pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer
XX
PS Claim 1; Page 5861-5862; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 4515 BP; 1253 A; 942 C; 1059 G; 1261 T; 0 other;

Query Match 99.2%; Score 4196.6; DB 23; Length 4515;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4210; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 18 GGAGCCCCAGCATCCTGCTTGGGTCCAGAGCGGAGCGCGGCCCGCGGCGCTGAT 77
DB 1 GGAGCCCCAGCATCCTGCTTGGGTCCAGAGCGGAGCGCGGCCCGCGGCGCTGAT 60
QY 78 CAGCGGACCCCGGCG 137
DB 61 CAGCGGACCCCGGCG 120

QY 138 TGAAGCCCAACCCGCTGCAGGACCGCAACATCTGCTCAGCGGTGTTCTTCTGGTGGCTCA 197
DB 121 TGAAGCCCAACCCGCTGCAGGACCGCAACCTCTGCTCAGCGGTGTTCTTCTGGTGGCTCA 180
QY 198 ATCCCTTGTGTTAAATTTGGCCCATAAACGGAGATTAGAGGAAGATGATGATTTCAGTGC 257
DB 181 ATCCCTTGTGTTAAATTTGGCCCATAAACGGAGATTAGAGGAAGATGATGATTTCAGTGC 240
QY 258 TGCCAGAGACCGCTCACAGCACCTTGGAGAGAGTTTCAAGGGTTCTGGGATAAAGAG 317
DB 241 TGCCAGAGACCGCTCACAGCACCTTGGAGAGAGTTTCAAGGGTTCTGGGATAAAGAG 300
QY 318 TTTTAAGAGCTGAGAATGACGACAGAGCCTTCTTTAAACAGAGCAATCATATAAGTGT 377
DB 301 TTTTAAGAGCTGAGAATGACGACAGAGCCTTCTTTAAACAGAGCAATCATATAAGTGT 360
QY 378 ACTGGAATCTTATTTAGTTTGGGAATTTTACGTTAATTTGAGAAAGTCCCAAGTAA 437
DB 361 ACTGGAATCTTATTTAGTTTGGGAATTTTACGTTAATTTGAGAAAGTCCCAAGTAA 420
QY 438 TCCAGCCCATATTTTGGGAAAAATTTAATTTTGAATAATTTATGATCCCATGGATT 497
DB 421 TCCAGCCCATATTTTGGGAAAAATTTAATTTTGAATAATTTATGATCCCATGGATT 480
QY 498 CTGTGGCTTTGAACACAGCGGTACGCCCTATGCCAGGTGCTGACTTTTTCACGCTCATTT 557
DB 481 CTGTGGCTTTGAACACAGCGGTACGCCCTATGCCAGGTGCTGACTTTTTCACGCTCATTT 540
QY 558 TGGCTATACCTGACATCATATATTTTATCAGTTTCTAGTGTGCTGGGATGAGTTACAG 617
DB 541 TGGCTATACCTGACATCATATATTTTATCAGTTTCTAGTGTGCTGGGATGAGTTACAG 600
QY 618 TAGCCATGTCCATATGATTTATCGGAAGGCACCTTCGCTTAGTAACATGCCATGGGGA 677
DB 601 TAGCCATGTCCATATGATTTATCGGAAGGCACCTTCGCTTAGTAACATGCCATGGGGA 660
QY 678 AGACAACACAGGCGCAGATAGTCAATCTGCTGTCCAATGATGTGAACAAGTTTGTATCAGG 737
DB 661 AGACAACACAGGCGCAGATAGTCAATCTGCTGTCCAATGATGTGAACAAGTTTGTATCAGG 720
QY 738 TGACAGTGTCTTACACTTCTCTGTGGGAGGACACCTGCAGGCGATGCAGTGACTGCC 797
DB 721 TGACAGTGTCTTACACTTCTCTGTGGGAGGACACCTGCAGGCGATGCAGTGACTGCC 780
QY 798 TACTCTGGATGGAGATAGGAATATCGTGCCTTGTGGGATGGCAGTCTAATCATTTCTCC 857
DB 781 TACTCTGGATGGAGATAGGAATATCGTGCCTTGTGGGATGGCAGTCTAATCATTTCTCC 840
QY 858 TGCCCTTGAACAGCTGTTTGGGAAAGTTTCTCATCACTGAGGAGTAAAACTGCAACTT 917
DB 841 TGCCCTTGAACAGCTGTTTGGGAAAGTTTCTCATCACTGAGGAGTAAAACTGCAACTT 900
QY 918 TCACGGATGCCAGGATCAGGACCATGATGAATGAAGTTAATGATTAAGGATAATAAAA 977
DB 901 TCACGGATGCCAGGATCAGGACCATGATGAATGAAGTTAATGATTAAGGATAATAAAA 960
QY 978 TGTACGCTCGGAAAAAGTCAATTTTCAATCTTATTACCAATTTTGAAGAAAGAGATT 1037
DB 961 TGTACGCTCGGAAAAAGTCAATTTTCAATCTTATTACCAATTTTGAAGAAAGAGATT 1020
QY 1038 CCAAGATTTCTGAGAAGTTCTGCTCAGGGGGATGAATTTGGCTTCGTTTTTCAGTGCAA 1097
DB 1021 CCAAGATTTCTGAGAAGTTCTGCTCAGGGGGATGAATTTGGCTTCGTTTTTCAGTGCAA 1080
QY 1098 GCAAAATCATCTGTTGTTGACCTTACACACTACGCTGCTCCTCGGAGTGTATACAG 1157
DB 1081 GCAAAATCATCTGTTGTTGACCTTACACACTACGCTGCTCCTCGGAGTGTATACAG 1140
QY 1158 CAGGCGCGTGTTCGTTGGGAGTACGCTGTATGGGCTGTCCGCTCAGGTTACCTCT 1217
DB 1141 CAGGCGCGTGTTCGTTGGGAGTACGCTGTATGGGCTGTCCGCTCAGGTTACCTCT 1200
QY 1218 TCTTCCCCTCAGCCATTTAGAGGGTGTGTAGAGGCAATCGTCAGCATCCGAAGATCCAGA 1277

QY 3437 ATTGGACTTCACGATTTAAGGAGAAAATGTCATCATACCTCAGGACCTGTTTGTTC 3496
 Db |||||||
 QY 3421 ATTGGACTTCACGATTTAAGGAGAAAATGTCATCATACCTCAGGACCTGTTTGTTC 3480
 Db |||||||
 QY 3497 ACTGGAAATAGAGAAAACCTGGATCCCTTTAAGGAGCACACGGATGAGGAACCTGG 3556
 Db |||||||
 QY 3481 ACTGGAAATAGAGAAAACCTGGATCCCTTTAAGGAGCACACGGATGAGGAACCTGG 3540
 Db |||||||
 QY 3557 AATGCCCTTACAAGAGGTACAACTTAAGAAACCAATTAAGAACTTCTCTGTTAAATGGAT 3616
 Db |||||||
 QY 3541 AATGCCCTTACAAGAGGTACAACTTAAGAAACCAATTAAGAACTTCTCTGTTAAATGGAT 3600
 Db |||||||
 QY 3617 ACTCAATTTACAGATCAGATCCATTTTAGTGTGGCAAGACAACTGGTGCTT 3676
 Db |||||||
 QY 3601 ACTGAATTTAGCAATCAGATCCATTTTAGTGTGGCAAGACAACTGGTGCTT 3660
 Db |||||||
 QY 3677 GCCAGGCAATTCAGGAAAATCAGATATTGATATTGATGAAGCGACGCAAAATGTG 3736
 Db |||||||
 QY 3661 GCCAGGCAATTCAGGAAAATCAGATATTGATATTGATGAAGCGACGCAAAATGTG 3720
 Db |||||||
 QY 3737 GATCCAAAGACTGATGAGTTAATACAAAAAATCCGGGAGAAATTTGCCCACTGCACC 3796
 Db |||||||
 QY 3721 GATCCAAAGACTGATGAGTTAATACAAAAAATCCGGGAGAAATTTGCCCACTGCACC 3780
 Db |||||||
 QY 3797 GTCTTAACATTCGACACAGATTGACACCAATTTATGACAGGACAAAGATTAATGGTTTA 3856
 Db |||||||
 QY 3781 GTCTTAACATTCGACACAGATTGACACCAATTTATGACAGGACAAAGATTAATGGTTTA 3840
 Db |||||||
 QY 3857 GATTAGGAAGACTGAAAGAAATATGATAGCCGCTATGTTTGTGCAAAATAAGAGAGC 3916
 Db |||||||
 QY 3841 GATTAGGAAGACTGAAAGAAATATGATAGCCGCTATGTTTGTGCAAAATAAGAGAGC 3900
 Db |||||||
 QY 3917 CTATTTTACAAGATGTTGCAACAACTGGGCAAGGCGAGAACCCGCTGCTCACTGAAACA 3976
 Db |||||||
 QY 3901 CTATTTTACAAGATGTTGCAACAACTGGGCAAGGCGAGAACCCGCTGCTCACTGAAACA 3960
 Db |||||||
 QY 3977 GCAAAACAGGTATACCTCAAAAGAAATTTATCCACATATGGTCACACTGACCAATGGTT 4036
 Db |||||||
 QY 3961 GCAAAACAGGTATACCTCAAAAGAAATTTATCCACATATGGTCACACTGACCAATGGTT 4020
 Db |||||||
 QY 4037 ACAACACTTCCAAATGGACAGCCCTCGACCTTAACCTATTTTCGAGACAGCACTGTAATC 4096
 Db |||||||
 QY 4021 ACAACACTTCCAAATGGACAGCCCTCGACCTTAACCTATTTTCGAGACAGCACTGTAATC 4080
 Db |||||||
 QY 4097 CAACCAAAATGTCAGTCCGTTCCGAAAGCAATTTCCACTAGTTTTTGGACTATGTAAC 4156
 Db |||||||
 QY 4081 CAACCAAAATGTCAGTCCGTTCCGAAAGCAATTTCCACTAGTTTTTGGACTATGTAAC 4140
 Db |||||||
 QY 4157 CACATTTGACTTTTTTTTACTTTGGCAACAAATATTATACATACAGATGCTAGTTTAT 4216
 Db |||||||
 QY 4141 CACATTTGACTTTTTTTTACTTTGGCAACAAATATTATACATACAGATGCTAGTTTAT 4200
 Db |||||||
 QY 4217 TTGAATATTCTCCC 4231
 Db |||||||
 QY 4201 TTGAATATTCTCCC 4215
 Db |||||||

RESULT 13

ABK92135

ID ABK92135 standard; DNA; 3978 BP.

XX

AC ABK92135;

XX

DT 15-AUG-2002 (first entry)

XX

DE Prostate cancer-associated DNA sequence #21.

XX

KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
 gene therapy; gene; ds.

XX

OS Mammalia.

XX

PN WO200230268-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 12-OCT-2001; 2001WO-US32045.
 XX
 PR 13-OCT-2000; 2000US-0687576.
 PR 08-DEC-2000; 2000US-0733288.
 PR 24-JAN-2001; 2001US-263957P.
 PR 16-MAR-2001; 2001US-276791P.
 PR 16-MAR-2001; 2001US-276888P.
 PR 06-APR-2001; 2001US-281922P.
 PR 24-APR-2001; 2001US-286214P.
 PR 30-APR-2001; 2001US-0847046.
 PR 04-MAY-2001; 2001US-288589P.
 XX
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezl P.
 XX
 DR WPI; 2002-471335/50.
 XX
 DR P-PSDB; ABG61820.
 XX
 PT Detecting a prostate cancer-associated transcript in a cell in a
 patient, useful for diagnosing prostate cancer (PC) or screening
 PT modulators of PC, by determining if prostate cancer-associated genes
 PT are expressed in a prostate tissue
 XX
 PS Claim 22; Page 316; 436pp; English.
 XX
 CC The present invention relates to methods of detecting a prostate
 CC cancer-associated transcript in a cell from a patient. The method
 CC comprises contacting a biological sample from the patient with
 CC prostate cancer-associated polynucleotides (designated PC genes) that
 CC selectively hybridise to a sequence that is at least 80% identical
 CC to them. The prostate cancer-associated polynucleotide sequences
 CC are differentially expressed in prostate tumour tissue or in
 CC prostate cancer and are derived from the tissues of various
 CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
 CC The methods of the invention are useful for diagnosing and treating
 CC prostate cancer in mammals. The prostate cancer-associated genes are
 CC useful for diagnosing or treating prostate cancer, as well as for
 CC identifying modulators of prostate cancer or agents that inhibit
 CC prostate cancer. The nucleic acid sequences are particularly useful
 CC in gene therapy, as a vaccine or in antisense applications.
 CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
 CC sequences.
 XX

Sequence 3978 BP; 1113 A; 817 C; 956 G; 1092 T; 0 other;

Query Match 93.9%; Score 3973.2; DB 24; Length 3978;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 3975; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 116 ATGCTGCCCTGTACCGAGAGGTGAAGCCCAACCCGCTGCAGGACGCGAATCTGCTCA 175

Db 1 ATGCTGCCCTGTACCGAGAGGTGAAGCCCAACCCGCTGCAGGACGCGAATCTGCTCA 60

QY 176 CGCGTGTCTTCTGGTGGCTCAATCCCTTTTAAATTTGGCCATAACGAGATTAGAG 235

Db 61 CGCGTGTCTTCTGGTGGCTCAATCCCTTTTAAATTTGGCCATAACGAGATTAGAG 120

QY 236 GAAGATGATATGATATTCAAGTCTGCCAGAGACCGCTTCACAGACACCTTGGAGAGAGTTG 295

Db 121 GAAGATGATATGATATTCAAGTCTGCCAGAGACCGCTTCACAGACACCTTGGAGAGAGTTG 180

QY 296 CAAGGTTCTGGGATAAAGAAAGTTTAAAGAGCTCAGAATGACGACAGACCTTCTTTTA 355

Db 181 CAAGGTTCTGGGATAAAGAAAGTTTAAAGAGCTCAGAATGACGACAGACCTTCTTTTA 240

QY 356 ACAAGAGCAATCATAAAGTGTACTGGAATCTTATTAGTTTGGGAATTTTACGTTA 415

Db |||||||

Db	241	ACAAGACGAATCATAAAGTGTCTACTGGAATCTTATTTAGTCTTTGGGAATTTTACGTTA	300
QY	416	ATTGAGAAAGTGCCAAAGTAATACAGCCCATATTTTGGGAAAAATTAATTAATATTTT	475
Db	301	ATTGAGAAAGTGCCAAAGTAATCAGCCCATATTTTGGGAAAAATTAATTAATATTTT	360
QY	476	GAATAATTATGATCCCATGGAATCTGTGGCTTTGAACACAGCGTACGCCATGACCAGGTG	535
Db	361	GAATAATTATGATCCCATGGAATCTGTGGCTTTGAACACAGCGTACGCCATGACCAGGTG	420
QY	536	CTGACCTTTTGCACGCTCATTTTGGCTATACGTGCATCAGTTATATTTTATCAGGTTCA	595
Db	421	CTGACCTTTTGCACGCTCATTTTGGCTATACGTGCATCAGTTATATTTTATCAGGTTCA	480
QY	596	TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGCACCTTGGT	655
Db	481	TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGCACCTTGGT	540
QY	656	CTTAGTACATGGCCATGGGGAAGACAACACAGGCCAGATAGTCAATCTGCTGCCAAT	715
Db	541	CTTAGTACATGGCCATGGGGAAGACAACACAGGCCAGATAGTCAATCTGCTGCCAAT	600
QY	716	GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCCTGTGGCAGGACCACTG	775
Db	601	GATGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCCTGTGGCAGGACCACTG	660
QY	776	CAGGCGATCGCAGTGCCTACTCTGGATGGAGATAGGAATATCGTCCCTGCTGGG	835
Db	661	CAGGCGATCGCAGTGCCTACTCTGGATGGAGATAGGAATATCGTCCCTGCTGGG	720
QY	836	ATGGCAGTTCTAATCATTTCTCCTGCCCTTGCAAGCTGTTTGGGAAGTGTGTTCTCATCA	895
Db	721	ATGGCAGTTCTAATCATTTCTCCTGCCCTTGCAAGCTGTTTGGGAAGTGTGTTCTCATCA	780
QY	896	CTGAGGAGTAAACTGCAACTTTACAGGATGCCAGGATCAGACCATGAATGAAGTTATA	955
Db	781	CTGAGGAGTAAACTGCAACTTTACAGGATGCCAGGATCAGACCATGAATGAAGTTATA	840
QY	956	ACTGTTAAGGATAATAAAAATGTACGCCCTGGGAAAAAGTCATTTCAAATCTTATTACC	1015
Db	841	ACTGTTAAGGATAATAAAAATGTACGCCCTGGGAAAAAGTCATTTCAAATCTTATTACC	900
QY	1016	AATTTGAGAAAGAGGAGATTTCGAAGATCTGAGAAGTTCTGCCCTCAGGGGGATGAAT	1075
Db	901	AATTTGAGAAAGAGGAGATTTCGAAGATCTGAGAAGTTCTGCCCTCAGGGGGATGAAT	960
QY	1076	TGCGCTTCGTTTTTCAGTGCAGCAAAAATCATCGTTGTTGTGACCTTCACCACCTACGTG	1135
Db	961	TGCGCTTCGTTTTTCAGTGCAGCAAAAATCATCGTTGTTGTGACCTTCACCACCTACGTG	1020
QY	1136	CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTCTGGCAGTGACGCTGTATGGGGCT	1195
Db	1021	CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTCTGGCAGTGACGCTGTATGGGGCT	1080
QY	1196	GTGGCGCTGACGGTTACCTCTTCTCCCTCAGCCATGTAGAGGGGTCTCAGAGGCAATC	1255
Db	1081	GTGGCGCTGACGGTTACCTCTTCTCCCTCAGCCATGTAGAGGGGTCTCAGAGGCAATC	1140
QY	1256	GTCAGCATCCGAAGATCCAGACCTTTTGGCTACTTGTATGATGAGATATCACACGCCAACC	1315
Db	1141	GTCAGCATCCGAAGATCCAGACCTTTTGGCTACTTGTATGATGAGATATCACACGCCAACC	1200
QY	1316	CAGCTGCCGTGATGTTGTTAAGATGGTGCATGTGAGGAGTTTACTGCTTTTGGGAT	1375
Db	1201	CAGCTGCCGTGATGTTGTTAAGATGGTGCATGTGAGGAGTTTACTGCTTTTGGGAT	1260
QY	1376	AAGCATACAGAGCCCCAACTCTACAAGGCTTTTCCCTTTACTGTGCAGACCTTGGCGAATG	1435
Db	1261	AAGCATACAGAGCCCCAACTCTACAAGGCTTTTCCCTTTACTGTGCAGACCTTGGCGAATG	1320
QY	1436	TAGCTGTGTCGCCCGGTGGGAGCAGGGAAGTCATCATCTGTTAAGTGCCGCTGCTCGGG	1495
Db	1321	TAGCTGTGTCGCCCGGTGGGAGCAGGGAAGTCATCATCTGTTAAGTGCCGCTGCTCGGG	1380

the diagnosis and treatment of cancer, especially prostate cancer -
Claim 1; Page 412-414; 579pp; English.
The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polynucleotide of the invention.

Query Match 92.4%; Score 3910.2; DB 22; Length 6140;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 4040; Conservative 0; Mismatches 3; Indels 118; Gaps 1;

PT	the diagnosis and treatment of cancer, especially prostate cancer -	
XX	Claim 1; Page 412-414; 579pp; English.	
XX	The invention relates to isolated prostate-specific	
CC	polynucleotides, polypeptides, fusion proteins of the polypeptides,	
CC	antibodies raised against the polypeptides (or antigenic epitopes	
CC	derived from them) and antigen-presenting cells expressing the	
CC	polypeptides. The antibodies are useful for detecting the presence of	
CC	cancer, especially prostate cancer. The polypeptides, polynucleotides and	
CC	the antigen-presenting cells are useful for stimulating and/or expanding	
CC	T cells specific for a tumour protein, and for inhibiting the development	
CC	of cancer especially prostate cancer. Compositions comprising the	
CC	polynucleotide and/or polypeptide are useful for stimulating an immune	
CC	response, and for treating cancer. The oligonucleotide is useful for	
CC	detecting cancer. The present sequence is a prostate specific	
XX	polynucleotide of the invention.	
XX		
SQ	Sequence 6140 BP; 1737 A; 1260 C; 1353 G; 1780 T; 10 other;	
	Query Match 92.4%; Score 3910.2; DB 22; Length 6140;	
	Best Local Similarity 97.1%; Pred. No. 0;	
	Matches 4040; Conservative 0; Mismatches 3; Indels 118; Gaps 1;	
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DB	233 GGTGGCTCAATCCCTGTTTAAATGGCCATAAACGAGGATTAGAGGAAGATGATATGT 292	QY 969 TAATAAAATGTACGGCTGGGAAAAGTCATTTTCAATCTTATTAACCAATTTGAGAAGA 1028
QY	249 ATTCAGTCTCCAGAGACCGCTCACAGCACCCTGGAGAGAGTGGAAAGGTTCTGGG 308	DB 1013 TAATAAAATGTACGGCTGGGAAAAGTCATTTTCAATCTTATTAACCAATTTGAGAAGA 1072
DB	293 ATTCAGTCTCCAGAGACCGCTCACAGCACCCTGGAGAGAGTGGAAAGGTTCTGGG 352	QY 1029 AGCAGATTTCAGAGATTCTCAGAGATTCCGCTCAGGGGGATGAATTTGGCTTCGTTTT 1088
QY	309 ATAAGAAGTTTAAAGAGTGAAGATGACGACAGACGCTTCTTTAAACAGAGCAATCA 368	DB 1073 AGCAGATTTCAGAGATTCTCAGAGATTCCGCTCAGGGGGATGAATTTGGCTTCGTTTT 1132
DB	353 ATAAGAAGTTTAAAGAGTGAAGATGACGACAGACGCTTCTTTAAACAGAGCAATCA 412	QY 1089 TCAGTCAAGCAAAATCATCGTGTGTGACCTTCACCACTACCTGCTCCTCGGCAGTG 1148
QY	369 TAAAGTGTACTGGAAATCTTATTAGTTTGGGAAATTTTACGTTAATTTGAAAATATGATC 428	DB 1133 TCAGTCAAGCAAAATCATCGTGTGTGACCTTCACCACTACCTGCTCCTCGGCAGTG 1192
DB	413 TAAAGTGTACTGGAAATCTTATTAGTTTGGGAAATTTTACGTTAATTTGAAAATATGATC 472	QY 1149 TGNACACAGCCAGCCGCTGCTGTCGAGTGACGCTGATATGGGCTGTGCGGCTGACGG 1208
QY	429 CCAAGTAATCCAGCCCATATTTTGGGAAATTTTACGTTAATTTGAAAATATGATC 488	DB 1193 TGNACACAGCCAGCCGCTGCTGTCGAGTGACGCTGATATGGGCTGTGCGGCTGACGG 1252
DB	473 CCAAGTAATCCAGCCCATATTTTGGGAAATTTTACGTTAATTTGAAAATATGATC 532	QY 1209 TTACCCCTCTTCTCCCTCAGCCATTGAGAGGGTGTGAGAGGCAATCGTCAGCATCCGAA 1268
QY	489 CCATGGATTCTGTGGCTTTGAACACAGCGTACGCGTATGCCACGCTGCTGACTTTTGCA 548	DB 1253 TTACCCCTCTTCTCCCTCAGCCATTGAGAGGGTGTGAGAGGCAATCGTCAGCATCCGAA 1312
DB	533 CCATGGATTCTGTGGCTTTGAACACAGCGTACGCGTATGCCACGCTGCTGACTTTTGCA 592	QY 1269 GAATCCAGACCTTTTGTGCTACTTGATGAGATATCACAGCGCAACCGTCAGCTCCGCTCAG 1328
QY	549 CGCTCATTTTGGCTATACGTCATCACTATATTTTATFCAGTTTCAGTGTCTGGGATGA 608	DB 1313 GAATCCAGACCTTTTGTGCTACTTGATGAGATATCACAGCGCAACCGTCAGCTCCGCTCAG 1372
DB	593 CGCTCATTTTGGCTATACGTCATCACTATATTTTATFCAGTTTCAGTGTCTGGGATGA 652	QY 1329 ATGGTAAAAGATGGTGCATGTCAGGATTTTACTGCTTTTGGGATAAGGCATCAGAGA 1388
QY	609 GGTTCAGATAGCCATGCGCATATGATTTATCGAAGGCACTTCGCTTAGTACATAGG 668	DB 1373 ATGGTAAAAGATGGTGCATGTCAGGATTTTACTGCTTTTGGGATAAGGCATCAGAGA 1432
DB	653 GGTTCAGATAGCCATGCGCATATGATTTATCGAAGGCACTTCGCTTAGTACATAGG 712	QY 1389 CCCCACTCTACAAGCCCTTCTTCTTACTGTCAGACCTGGCGAATTTGTAGCTGTGGTGC 1448
QY	669 CCATGGGGAAGACAAACACAGGCGAGATAGTCAATCTGCTCAATGATGATGAACAGT 728	DB 1433 CCCCACTCTACAAGCCCTTCTTCTTACTGTCAGACCTGGCGAATTTGTAGCTGTGGTGC 1492
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DB	833 TGACTGCCCTACTCTGATGAGATAGGAATATCGTCTGCTGGGATGCGCACTTCTAA 892	QY 1569 TCTCGGAACTCTGAGGAGTAAATTTTATTTGGGAAAGAAATACGAAAAGGAACGATATG 1628
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QY 2109 CTAGACCTCTCTTGAAGATGGTCTCTGGAGAGCCAAAGATACAGAGAATGTCCAGTTA 2168
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Db 2333 AGGTTCCCTATGTCTCAAGATTGCTTTCATAGTGTGCTTTCATAGTGGGCAACAACAAGTATGC 2392
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QY 2409 TAGGAATTTATCAGGTTTAACTGTAGTACCGTTCTTTTGGCATAGCAAGATCTCTAT 2468
Db 2453 TAGGAATTTATCAGGTTTAACTGTAGTACCGTTCTTTTGGCATAGCAAGATCTCTAT 2512
QY 2469 TGGTATTTCTACGTCCTTGTAACTCTTCAAACTTTGCACACAAATGTTTGGTCAAA 2528
Db 2513 TGGTATTTCTACGTCCTTGTAACTCTTCAAACTTTGCACACAAATGTTTGGTCAAA 2572
QY 2529 TTCTGAAAGCTCGGTATTAATTTCTTATGATAGAAATCCAATAGGAAGAAATTTAAATCGTT 2588
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Db 2693 AGACATTTGCTACAAAGTGTGTGTGCTCTGCTGCTGCTGCGCGTGAATTCCTTGGATCG 2752
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QY 2769 CGTCAAGAGATGTGAAGCCCTGGAAATCTACAACTCGGAGTCCAGTGTTCCTCCACTTGT 2828
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Db 4013 CTGAAACAGCAAAACAGAGATGGGTTTCAACATGTTGGCCAGGCTGGTCTCAAACTCCT 4072
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Search completed: December 18, 2002, 07:46:31
Job time : 554.063 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:04:10 ; Search time 6968.22 Seconds
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Title: US-09-647-140a-1

Perfect score: 4231

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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5: gb_ov:*

6: gb_pat:*

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11: gb_sts:*

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13: gb_un:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	4231	100.0	4231	9	AF071202	AF071202 Homo sapi
3	4211	99.5	6082	6	AX141045	Sequence
4	4211	99.5	6082	6	AX200905	Sequence
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6	4125.8	97.5	5759	9	AX267561	Sequence
7	3910.2	92.4	6140	6	AX081219	Homo sapi
8	3910.2	92.4	6140	6	AX141046	Sequence
9	3910.2	92.4	6140	6	AX200906	Sequence
10	2875	68.0	2940	9	AX267562	Sequence
11	1045.4	24.7	1074	6	AF071203	Homo sapi
12	1045.4	24.7	1074	6	AX201051	Sequence
13	651.8	15.4	2275	6	AX267850	Sequence
14	611.8	14.5	176082	3	AX046474	Sequence
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27	469.4	11.1	227848	3	AC009740	Drosophila
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					AR099619	Sequence

ALIGNMENTS

RESULT 1

AX210645

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

AX210645
Sequence 287 from Patent WO0157058.
AX210645
AX210645.1 GI:15424905
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4231)
Rosenthal,A., Hinzmann,B., Schaefer,R., Zuber,J., Tchernitsa,O.,
Grips,M., Hellriegel,M., Schmitz,A.C. and Sers,C.
Detection of differential gene expression

AX210645
Sequence 287 from Patent WO0157058.
AX210645
AX210645.1 GI:15424905
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4231)
Rosenthal,A., Hinzmann,B., Schaefer,R., Zuber,J., Tchernitsa,O.,
Grips,M., Hellriegel,M., Schmitz,A.C. and Sers,C.
Detection of differential gene expression

AX210645
Sequence 287 from Patent WO0157058.
AX210645
AX210645.1 GI:15424905
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4231)
Rosenthal,A., Hinzmann,B., Schaefer,R., Zuber,J., Tchernitsa,O.,
Grips,M., Hellriegel,M., Schmitz,A.C. and Sers,C.
Detection of differential gene expression

JOURNAL Patent: WO 0157058-A 287 09-AUG-2001:
Metagen Gesellschaft fuer Genomforschung mbH (DE)
FEATURES Location/Qualifiers
source 1. 4231

BASE COUNT 1170 a 895 c 1015 g 1151 t
ORIGIN /organism="Homo sapiens"
/db_xref="taxon:9606"

Query Match 100.0%; Score 4231; DB 6; Length 4231;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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 VERSION AF071202.1 GI:3335172
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 SOURCE Homo sapiens.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 Lee, K., Belinsky, M.G., Bell, D.W., Testa, J.R. and Kruh, G.D.
 Isolation of MOAT-B, a widely expressed multidrug
 resistance-associated protein/canicular multispecific organic
 anion transporter-related transporter
 Cancer Res. 58 (13), 2741-2747 (1998)
 98324262
 PUBMED 9661885
 REFERENCE 2 (bases 1 to 4231)
 AUTHORS Lee, K., Belinsky, M.G., Bell, D.W., Testa, J.R. and Kruh, G.D.
 TITLE Direct Submission
 JOURNAL Submitted (09-JUN-1998) Medical Oncology, Fox Chase Cancer Center,
 7701 Burholme Ave., Philadelphia, PA 19111, USA
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 Query Match

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Db 1621 ACGATATGAAAAGTCAATAAAGCTTGTGCTCTGAAAAGGATTTACAGCTGTTGGAGGA 1680
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Db 1741 GSTAAACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGACGATCTCT 1800
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AX141045			
LOCUS			
DEFINITION Sequence 535 from Patent WO0134802.			
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Accession	AX141045
Version	AX141045.1
Keywords	GI:14281100
Source	human.
Organism	Homo sapiens
Reference	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Authors	Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Reed, S.G., Kalos, M.D., Retter, M.W., Stolk, J.A., Day, C.H., Skeiky, Y.A. and Wang, A.
Title	Compositions and methods for the therapy and diagnosis of prostate cancer
Journal	Patent: WO 0134802-A 535 17-MAY-2001;
Features	CORIXA CORPORATION (US)
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	/db_xref="taxon:9606"
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Query Match	99.5%; Score 4211; DB 6; Length 6082;
Best Local Similarity	99.9%; Pred. No. 0;
Matches 4225; Conservative	0; Mismatches 5; Indels 1; Gaps 1;

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QY	121	GCCGCTGACAGGAGTCAAGCCCAACCGCTGACGAGCGCGCGCGCGCGCGCGCGCT	180
Db	191	GCCGCTGACAGGAGTCAAGCCCAACCGCTGACGAGCGCGCGCGCGCGCGCGCT	250
QY	181	GTTCTTCTGGTGGCTCAATCCCTTGTAAATTTGGCCATAAACGGAGATTTAGAGGA	240
Db	251	GTTCTTCTGGTGGCTCAATCCCTTGTAAATTTGGCCATAAACGGAGATTTAGAGGA	310
QY	241	TGATATGATTTACAGTGTCCGAGAGACCGCTCAGACACCTTTGGAGAGAGTTGCAAG	300
Db	311	TGATATGATTTACAGTGTCCGAGAGACCGCTCAGACACCTTTGGAGAGAGTTGCAAG	370
QY	301	GTTCTGGGATAAAGAGTTTAAAGAGCTGAGATGACGACAGAGCCCTTCTTTAACAAG	360
Db	371	GTTCTGGGATAAAGAGTTTAAAGAGCTGAGATGACGACAGAGCCCTTCTTTAACAAG	430
QY	361	AGCAATCAATAGTGTACTTGGAAATCTTTATTTAGTTTGGAAATTTTACGTTAATGA	420
Db	431	AGCAATCAATAGTGTACTTGGAAATCTTTATTTAGTTTGGAAATTTTACGTTAATGA	490
QY	421	GGAAAGTCCCAAGTAATCCACCCCATATTTTGGGAAAAATTTAATTTTGA	480
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RESULT 4
AX200905
LOCUS AX200905 6082 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 535 from Patent WO0151633.
ACCESSION AX200905
VERSION AX200905.1 GI:15390771
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6082)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 535 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
Location/Qualifiers
source 1..6082
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 1721 a 1249 c 1357 g 1755 t
ORIGIN
Query Match 99.5%; Score 4211; DB 6; Length 6082;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4225; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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RESULT 5
AX267561
LOCUS AX267561 6082 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 535 from Patent WO0173032.
ACCESSION AX267561
VERSION AX267561.1 GI:16516283
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Xu, J., Dillon, D. C., Mitcham, J. L., Harlocker, S. L., Jiang, Y.,
Kalos, M. D., Fanger, G. R., Retter, M. W., Stolk, J. A., Day, C. H.,
Vedvick, T. S., Carter, D., Li, S. X., Wang, A., Skeiky, Y. A., Hepler, W. T.
and Henderson, R. A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0173032-A 535 04-OCT-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1. 6082
/organism="Homo sapiens"
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BASE COUNT 1721 a 1249 c 1357 g 1755 t
ORIGIN

Query Match 99.5%; Score 4211; DB 6; Length 6082;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4225; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 GGACAGCGTGGCGCGGAGCCAGCATCCCTGCTTGGAGTCCAGGAGCGAGCCGCG 60
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KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
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AUTHORS     Adachi,M., Sampath,J., Sun,D. and Schuetz,J.D.
TITLE       Isolation of human ATP-binding cassette, sub-family C (CFTR/MRP),
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JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 5759)
AUTHORS     Adachi,M., Sampath,J., Sun,D. and Schuetz,J.D.
TITLE       Direct Submission
JOURNAL     Submitted (22-FEB-2002) Pharmaceutical Sciences, St. Jude
            Children's Research Hospital, 332 North Lauderdale St., Memphis, TN
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DEFINITION Sequence 536 from Patent WO0151633.
ACCESSION AX200906
VERSION AX200906.1 GI:15390773
KEYWORDS

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 6140)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 536 19-JUL-2001;
CORIXA CORPORATION (US)
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REFERENCE
AUTHORS
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Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kalus, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hepler, W.T.
and Henderson, R.A.
TITLE
Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL
Patent: WO 0173032-A 536 04-OCT-2001;
CORIXA CORPORATION (US)
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REFERENCE 1 (bases 1 to 2940)
AUTHORS Lee K., Belinsky, M.G., Bell, D.W., Testa, J.R. and Kruh, G.D.
TITLE Isolation of MOAT-B, a widely expressed multidrug
resistance-associated protein/canalicular multispecific organic
anion transporter-related transporter
Cancer Res. 58 (13), 2741-2747 (1998)
JOURNAL 98324262
MEDLINE 9661885
PUBMED
REFERENCE 2 (bases 1 to 2940)
AUTHORS Lee, K. and Kruh, G.D.
TITLE Isolation of another form of MOAT-B
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 2940)
AUTHORS Lee, K., Belinsky, M.G., Bell, D.W., Testa, J.R. and Kruh, G.D.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-1998) Medical Oncology, Fox Chase Cancer Center,
7701 Burholme Ave., Philadelphia, PA 19111, USA
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QY	4105	ATGCTCAAGTCCGTTCCGAGGAGATTTTCCACTAGTTTTTGGACTATGTTAAACACATTGT	4164
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RESULT 11			
LOCUS	AX201051		
DEFINITION	Sequence 681 from Patent WO0151633.		
ACCESSION	AX201051		
VERSION	AX201051.1	GI:15390859	
KEYWORDS	human.		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1074)		
AUTHORS	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,X., Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skelky,Y.A., Wang,A. and Meagher,M.J.		
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer		
JOURNAL	Patent: WO 0151633-A 681 19-JUL-2001;		
FEATURES	CORIXA CORPORATION (US)		
source	1..1074		
BASE COUNT	298 a 223 c 275 g 278 t		
ORIGIN			
Query Match	24.7%; Score 1045.4; DB 6; Length 1074;		
Best Local Similarity	99.9%; Pred. NO. 5.1e-257;		
Matches 1046;	Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
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Db	544	CAAGATGCTGACATCTATCTCTGGACGATCCCTCTCAGTGCAGTAGATGCGGAAGTTAGC	603
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LOCUS AX267850			
DEFINITION Sequence 824 from Patent WO0173032.			
ACCESSION AX267850			
VERSION AX267850.1 GI:16516496			
KEYWORDS human.			
SOURCE Homo sapiens			
ORGANISM Homo sapiens			
REFERENCE 1			
AUTHORS Xu, J., Dillon, D. C., Mitcham, J. L., Harlocker, S. L., Jiang, Y., Kalos, M. D., Fanger, G. R., Retter, M. W., Stolk, J. A., Day, C. H., Vedwick, T. S., Carter, D., Li, S. X., Wang, A., Skeiky, Y. A., Hepler, W. T. and Henderson, R. A.			
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer			
JOURNAL Patent: WO 0173032-A 824 04-OCT-2001;			
CORIXA CORPORATION (US)			
FEATURES Location/Qualifiers			
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RESULT 13
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LOCUS

AX046474

2275 bp

DNA

linear

PAT 24-NOV-2000

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DEFINITION      Sequence 10 from Patent WO0058471.
ACCESSION       AX046474
VERSION         AX046474.1 GI:11344431
KEYWORDS        human.
SOURCE          Homo sapiens
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE       1 (bases 1 to 2275)
AUTHORS        Schuetz, J. and Fridland, A.
TITLE          Multidrug resistance associated proteins and uses thereof
JOURNAL        Patent: WO 0058471-A 10 05-OCT-2000;
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FEATURES        Location/Qualifiers
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Best Local Similarity 99.7%; Pred. No. 7.6e-156;
Matches 653; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 181 AATACAAAAAATTCGGGAGAAATTTGCCACTGCACGCTGCTACCACTTGCACACAG 240
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DEFINITION      Drosophila melanogaster, chromosome 2L, region 38F-39A, BAC clone
                 BACR06G10, complete sequence.
ACCESSION       AC007144
VERSION         AC007144.13 GI:13702789
KEYWORDS        HTG.
SOURCE          Drosophila melanogaster.
ORGANISM        Drosophila melanogaster
REFERENCE       1 (bases 1 to 176082)
AUTHORS        Celnik, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
                 Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
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                 Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.
                 Sequencing of Drosophila chromosome 2L, region 38F-39A
                 Unpublished
                 2 (bases 1 to 176082)
                 Celnik, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazef, R.G.,
                 Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
                 Doyle, C.N., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,
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                 Rubin, G.M.
                 Direct Submission
                 Submitted (24-MAR-1999) Drosophila Genome Center, Lawrence Berkeley
                 Laboratory, MS 64-121, Berkeley, CA 94720, USA
                 On Apr 21, 2001 this sequence version replaced gi:7264767.
                 Sequence submitted by:
                 Lawrence Drosophila Genome Project
                 Berkeley National Laboratory
                 Berkeley, CA 94720
                 This sequence was assembled using end sequences from a whole genome
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                 For further information about this sequence, including its location
                 and relationship to other sequences, please visit our sequence
                 archive web site (http://www.fruitfly.org/sequence/) or send email
                 to bdg@fruitfly.berkeley.edu.
FEATURES        Location/Qualifiers
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Best Local Similarity 50.8%; Pred. No. 4.2e-145;
Matches 1751; Conservative 0; Mismatches 1587; Indels 107; Gaps 8;
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SUMMARIES

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38	274.6	6.5	4560	4	US-09-256-703-1	Sequence 1, Appli
39	274.6	6.5	5635	1	US-08-136-742A-3	Sequence 3, Appli
40	274.6	6.5	5635	3	US-09-248-026-3	Sequence 3, Appli
41	274.6	6.5	5635	5	PCT-US93-11667-3	Sequence 3, Appli
42	274.6	6.5	6126	2	US-08-951-912-3	Sequence 3, Appli
43	274.6	6.5	6126	4	US-09-174-077-3	Sequence 3, Appli
44	274.6	6.5	6129	1	US-07-637-621-1	Sequence 1, Appli
45	274.6	6.5	6129	1	US-08-136-742A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-605-785-535
; Sequence 535, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-605-785-535

Query Match 99.5%; Score 4211; DB 4; Length 6082;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4225; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy	1	GGACAGGGGTGGCGCGGAGCCCGGAGCCCGCCGCGCCGCGCCGCGCGGCAAGATGCT	60
Db	71	GGACAGGGGTGGCGCGGAGCCCGGAGCCCGCCGCGCCGCGCCGCGGAGGAGCCCGC	130
Qy	61	GGCCACCGCGCGCTGATCAGCGCGAGCCCGCGCCGCGCCGCGCGGCAAGATGCT	120
Db	131	GGCCACTGGCGCTGATCAGCGCGAGCCCGCGCCGCGCCGCGCGGCAAGATGCT	190
Qy	121	GGCCGTGTACCGAGGAGTGAAGCCCAACCCGCTGCAGGACGCGCAACATCTGCTACGCGT	180
Db	191	GGCCGTGTACCGAGGAGTGAAGCCCAACCCGCTGCAGGACGCGCAACCTCTGCTACGCGT	250

Qy	181	GTCTCTCTCGTGGCTCAATCCCTTGTTTAAATTTGCCATTAACGGAGATTTAGACGAAGA	241
Db	251		
Qy	241	TGATATGATTATTCAGTGTGCTCCAGAAGACCGCTCAGACACCTTTGGAGAGGAGTTTCCAAGG	300
Db	311		
Qy	301	GTCTCGGGATAAAGAAGTTTAAAGAGCTGAGAAATGACGCACAGAAGCCCTCTCTTAACAAAG	360
Db	371		
Qy	361	AGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTGGGAATTTTACGTTAAATTGA	420
Db	431		
Qy	421	GGAAAGTGCCAAAGTAATCAGCCCATATTTTGGGAAAAAATTTAATAATTTTGGAAAA	480
Db	491		
Qy	481	TTATGATPCCATGGAATTCGTGGCTTTGAACACAGCGTACGCCCTATGCCACGGTCTGAC	540
Db	551		
Qy	541	TTTTTTCGAGCTCATTTTGGCTTACTGCATCACHATATTTTATCAGTTTCAGTGTGC	600
Db	611		
Qy	601	TGGGATGAGGTTACGAGTAGCCCATGTGCCATATGATTTATCGGAAGGCACTTCTGCTTTAG	660
Db	671		
Qy	661	TACATGCGCATGGGGAAGAACACACAGGCGCAGATAGTCAATCTGCTGCTCCAAATGATGT	720
Db	731		
Qy	721	GAACAAGTTTGATCAGGTGCACAGTGTCTTACACHTTCTGTGGCGAGGACACACGTGAGGC	780
Db	791		
Qy	781	GATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCCTGCTGGGATGGC	840
Db	851		
Qy	841	AGTTCTAATCATCTCCGCCCTTCGAAAGCTGTTTTGGGAAGTTGTCTCATCACTGAG	900
Db	911		
Qy	901	GAGTAAACTGCAACTTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATAACTGG	960
Db	971		
Qy	961	TATAAGGATAATAAAATGTAGCCCTGGGAAAAGTCATTTTCAAATCTTATTTACCAATTT	1020
Db	1031		
Qy	1021	GAGAAAGAGGAGATTTCCAAGATTCTGAGAAAGTTCTGCGCTCAGGGGGATGAATTTGGC	1080
Db	1091		
Qy	1081	TTTCGTTTTTCAGTGAACGAAAATCATCGTGTGTGACCTTCACCACTACGTCGTCCT	1140
Db	1151		
Qy	1141	CGGAGTGTGATCACAGCCAGCCGGCTGTCTGCGCAGTACGCTGTATGGGGCTGTGGC	1200
Db	1211		
Qy	1201	GCTGACGGTTACCTCTTCTTCCCTTCAGCAATTCAGAGGCTGTTCAGAGGCAATTCGTGAC	1260
Db	1271		

QY	1261	CATCCGAAGAAATCCAGACCTTTTGTCTACTTGTATGAGATATCACAGCGCAACCGTCAGCT	1320
DB	1331	CATCCGAAGAAATCCAGACCTTTTGTCTACTTGTATGAGATATCACAGCGCAACCGTCAGCT	1390
QY	1321	GC CGT CAG ATG GTG TAA AAG ATG TGC ATG TGC AGG ATTTT TACT TGC TTTT TGG ATG AAG C	1380
DB	1391	GC CGT CAG ATG GTG TAA AAG ATG TGC ATG TGC AGG ATTTT TACT TGC TTTT TGG ATG AAG C	1450
QY	1381	ATCAGAGACCCCAACTCTACAAGCCCTTTCCTTTACTGTCTCAGACCTGGCGAAATGTTTGGC	1440
DB	1451	ATCAGAGACCCCAACTCTACAAGCCCTTTCCTTTACTGTCTCAGACCTGGCGAAATGTTTGGC	1510
QY	1441	TGTGTTGGCCCGTGGGAGCAGGGAAGTCAATCACTGTTAAGTCCCGTGTCTCGGGAAATTT	1500
DB	1511	TGTGTTGGCCCGTGGGAGCAGGGAAGTCAATCACTGTTAAGTCCCGTGTCTCGGGAAATTT	1570
QY	1501	GGCCCCAAGTCAAGGCGCTGGTCAAGCGTGCATGGAAGAAATTCCTATGTCTCAGCAGCC	1560
DB	1571	GGCCCCAAGTCAAGGCGCTGGTCAAGCGTGCATGGAAGAAATTCCTATGTCTCAGCAGCC	1630
QY	1561	CTGGGTGTTCTCGGGAACCTCTGAGGAGTAAATATTTTATTTTGGGAAGAAATATCAAAAGGA	1620
DB	1631	CTGGGTGTTCTCGGGAACCTCTGAGGAGTAAATATTTTATTTTGGGAAGAAATATCAAAAGGA	1690
QY	1621	ACGATATGAAAAAGTCAATAAAGCCTTGTCTCTGAAAAAGATTTACAGCTGTTGGAGGA	1680
DB	1691	ACGATATGAAAAAGTCAATAAAGCCTTGTCTCTGAAAAAGATTTACAGCTGTTGGAGGA	1750
QY	1681	TGGTGATCTGACTGTGATAGGAGATCGGGGAACCCAGCTGAGTGGAGGGCAGAAAGCAGC	1740
DB	1751	TGGTGATCTGACTGTGATAGGAGATCGGGGAACCCAGCTGAGTGGAGGGCAGAAAGCAGC	1810
QY	1741	GGTAAACCTTGC AAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGACGATCCTCT	1800
DB	1811	GGTAAACCTTGC AAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGACGATCCTCT	1870
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DB	1871	CAGTGCAGTATGATGCGGAAGTTAGCAGACACTTGTTCGAACCTGTGTATTGTCAAAATTTT	1930
QY	1861	GCATGAGAAGATCACAAATTTTACTGTACTCATCAGTTTGCAGTACCTCAAAGCTGCAAGTCA	1920
DB	1931	GCATGAGAAGATCACAAATTTTACTGTACTCATCAGTTTGCAGTACCTCAAAGCTGCAAGTCA	1990
QY	1921	GATTCCTGATTTGAAAGATGGTAAATATGCTGCAGAAGGGGACTTACACTGAGTTCCTAAA	1980
DB	1991	GATTCCTGATTTGAAAGATGGTAAATATGCTGCAGAAGGGGACTTACACTGAGTTCCTAAA	2050
QY	1981	ATCTCGGTATGATTTTGGCTCCCTTTTAAAGAAAGGATAATGAGGAAAGTGAACAACCTCC	2040
DB	2051	ATCTCGGTATGATTTTGGCTCCCTTTTAAAGAAAGGATAATGAGGAAAGTGAACAACCTCC	2110
QY	2041	AGTTCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCA	2100
DB	2111	AGTTCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCA	2170
QY	2101	ACAATCTTCTACACCTCCTCTCAAAGATGGTCTCTGGAGAGCCCAAGATACAGAGAATCT	2160
DB	2171	ACAATCTTCTACACCTCCTCTCAAAGATGGTCTCTGGAGAGCCCAAGATACAGAGAATCT	2230
QY	2161	CCAGTTACTACTATCAGAGGAACCGTTTCTGAAGAAAGTTGGTTTTCAGCGCCTATAA	2220
DB	2231	CCAGTTACTACTATCAGAGGAACCGTTTCTGAAGAAAGTTGGTTTTCAGCGCCTATAA	2290
QY	2221	GAAATTACTTCAGAGCTGGTGTCTACTGGATGCTTTCATTTTCTCTTATTTCTCCTAAACAC	2280
DB	2291	GAAATTACTTCAGAGCTGGTGTCTACTGGATGCTTTCATTTTCTCTTATTTCTCCTAAACAC	2350
QY	2281	TGCAGCTCAGGTTGGCTATGTCTTCAAGATTTGGTGGCTTTTCATACTGGGCAACAACA	2340
DB	2351	TGCAGCTCAGGTTGGCTATGTCTTCAAGATTTGGTGGCTTTTCATACTGGGCAACAACA	2410
QY	2341	AAGTATGCTAAATGTCATCTGTAATGGGAGGAGAAATGTAACCGGAGAAGCTAGATCTTAA	2400


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; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-535

Query Match          99.5%; Score 4211; DB 4; Length 6082;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4225; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 GGACAGCGTGGCGCGGAGCCAGCAGCCCTGCTGTTGAGTCCAGAGCGGAGCCCGC 60
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Db 71 GGACAGCGTGGCGCGGAGCCAGCAGCCCTGCTGTTGAGTCCAGAGCGGAGCCCGC 130

QY 61 GGCCACCGCGCTGATCAGCGGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGT 120
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QY 121 GCCCGTGTACCAGGAGGTGAAGCCCAACCGCTGCAGGAGCGCAACATCTGCTACGCGT 180
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Db 191 GCCCGTGTACCAGGAGGTGAAGCCCAACCGCTGCAGGAGCGCAACCTCTGCTACGCGT 250

QY 181 GTTCTCTGCTGCTCAATCCCTTGTAAATTTGGCCATAAACGGAGATTAGAGGAAGA 240
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QY 241 TGATATGATATCAGTCTGCCAGAGACCGCTCACAGCACCTTGGAGAGAGTTCGAAG 300
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Db 311 TGATATGATATCAGTCTGCCAGAGACCGCTCACAGCACCTTGGAGAGAGTTCGAAG 370

QY 301 GTTCTGGGATAAAGAGTTTAAAGAGCTGAGAAATGACGACAGAGCCCTCTTTAAACAG 360
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Db 371 GTTCTGGGATAAAGAGTTTAAAGAGCTGAGAAATGACGACAGAGCCCTCTTTAAACAG 430

QY 361 AGCAATCAATAAGTGTACTGGAAATCTTATTTAGTTTGGGAAATTTTACGTTAATGA 420
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Db 431 AGCAATCAATAAGTGTACTGGAAATCTTATTTAGTTTGGGAAATTTTACGTTAATGA 490

QY 421 GGAAAGTGCAGAGTAATCCAGCCATATTTTGGGAAATTTATTAATTTTGAAGA 480
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Db 491 GGAAAGTGCAGAGTAATCCAGCCATATTTTGGGAAATTTATTAATTTTGAAGA 550

QY 481 TTATGATCCATGGATCTGTGGCTTTGAACACAGCGTACGCCATATGCCAGCGTGTGAC 540
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Db 551 TTATGATCCATGGATCTGTGGCTTTGAACACAGCGTACGCCATATGCCAGCGTGTGAC 610

QY 541 TTTTTCACGCTCATTTTGGCTATCTGCTATCTGCTATATTTTATATCATGCTGCTG 600
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Db 611 TTTTTCACGCTCATTTTGGCTATCTGCTATCTGCTATATTTTATATCATGCTGCTG 670

QY 601 TGGGATGAGGTACGAGTACCATGTCATATGATTTATCGAAGCGACCTTGGCTTAG 660
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Db 671 TGGGATGAGGTACGAGTACCATGTCATATGATTTATCGAAGCGACCTTGGCTTAG 730

QY 661 TAACATGGCCATGGGGAAGACACACAGCGGAGATAGTCAATCTGCTGCTCAATCATGT 720
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Db 731 TAACATGGCCATGGGGAAGACACACAGCGGAGATAGTCAATCTGCTGCTCAATCATGT 790

QY 721 GAACAGTTTGTATCAGGTGACAGTGTCTTACATCTCTGCTGGGAGGACCACTGCAGGC 780
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Db 791 GAACAGTTTGTATCAGGTGACAGTGTCTTACATCTCTGCTGGGAGGACCACTGCAGGC 850

QY 781 GATCGAGTGAATGCTGCTGATGAGATAGGAATATCGTGCCTTGTGGGATGCG 840
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Db 851 GATCGAGTGAATGCTGCTGATGAGATAGGAATATCGTGCCTTGTGGGATGCG 910

QY 841 AGTTCTTAATCATCTCCCTTGCAGAGCTGTTTGGGAAAGTGTCTTCATCACTGAG 900
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Db 1991 GATTCTGATTTGAAAGATGGTAAATGGTGCAGAGGGGACTTACACTGAGTCTCTTAA 2050
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Db 971 GAGTAAAGCTCAACTTTTACGGATGCGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1030
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QY 1741 GGTAAACCTTGCAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGAGCAGGATCTCT 1800
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Db 1931 GCATGAGAGATCACAAATTTTGTGACTCATCATGTTGTCAGTACCTCAAAAGCTCAAGTCA 1990
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Db 1991 GATTCTGATATTGAAAGATGGTAAATGGTGCAGAGGGGACTTACACTGAGTCTCTTAA 2050
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QY 1981 ATCTGCTATAGATTTTGGCTCCCTTTTAAAGAGGATTAATGAGGAAAGTGAACAACCTCC 2040
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QY 2041 AGTTCCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCA 2100
DB AGTTCCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCA 2170
QY 2101 ACAATCTTCTAGACCCCTCCCTTGAAGAGTGTCTCTGGAGAGCCCAAGATACAGAGAATGT 2160
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QY 2221 GAATTAATCTCAGAGCTGGTGTCTCACTGGATTCTCTTCAATTTTCCCTTATCTCTTAACAC 2280
DB GAATTAATCTCAGAGCTGGTGTCTCACTGGATTCTCTTCAATTTTCCCTTATCTCTTAACAC 2350
QY 2281 TGCAGCTCAGGTTGCTATGTCTTCAAGATTGGTGGCTTTTCATCTAGTGGCAAAACAACA 2340
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QY 2341 AAGTATGCTAAATGCTACTGTAAATGGAGGAGGAAATGTAAACCGAGAGCTAGATCTTAA 2400
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QY 2401 CTGGTACTTAGGAATTTATCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATAGCAAG 2460
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QY 2461 ATCTCTATTGGTATTTCTACGCTCTTGTAACTCTTCAACAACCTTGGCAACAACAAATGTT 2520
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QY 2521 TGAGTCAATCTGAAAGCTCCGGTATTAATCTTTGATAGAAATCCAATAGGAAGAAATTT 2580
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QY 2641 TTTCAATCCAGACATTTGCTACAAGTGGTGGTGGTCTCTGTGGCTGTGGCGGTGATTC 2700
DB TTTCAATCCAGACATTTGCTACAAGTGGTGGTGGTCTCTGTGGCTGTGGCGGTGATTC 2770
QY 2701 TTGGATCGCAATACCTTTGGTTCCTTGGAAATCAATTTTCATTTTCTTGGCGGATATTT 2760
DB TTGGATCGCAATACCTTTGGTTCCTTGGAAATCAATTTTTCATTTTCTTGGCGGATATTT 2830
QY 2761 TTTGGAACGCTCAAGAGATGTGAAGCGCTCGAATCTACAACCTCGGAGTCCAGTGTTC 2820
DB TTTGGAACGCTCAAGAGATGTGAAGCGCTCGAATCTACAACCTCGGAGTCCAGTGTTC 2890
QY 2821 CCACCTGTCAATCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAGAGAG 2880
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QY 3181 AGCACCTTGGGAATATCAGAAAACGCCACCACAGCTGGCCCATCAAGAGGTGATAAT 3240
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QY 3301 AGCACCTCATTAATCACAAGAAAGTTGGCATTTGGGGAAGAACCGGAGCTGGAAAAG 3360
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QY 3361 TTCCTCTCATCTCAGCCCTTTTATAGATTGTCAGAACCCGAGGTAAATTTGGATTGATA 3420
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QY 3481 GGAACCTGTTTGGTTCACCTGGAAACATAGGAAAAACCTGGATCCCTTTAAGGAGCACAC 3540
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DB TCCTGGTAAATGGGATGATCTGAATTTAGCAGAACTCAGGATCCAATTTTGTGTTGACAAAG 3730
QY 3661 ACAACTGGTGTGCTTCCAGGCGCAATCTCAGGAAAAATCAGATATTGATTATGATGA 3720
DB ACAACTGGTGTGCTTCCAGGCGCAATCTCAGGAAAAATCAGATATTGATTATGATGA 3790
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QY 3781 APTTCCCACTGCACCCGTGCTAACCATTTGCACAGATTGAACACCATTTATTGACACGA 3840
DB APTTCCCACTGCACCCGTGCTAACCATTTGCACAGATTGAACACCATTTATTGACACGA 3909
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QY 3901 GCAAAATAAGAGAGCCCTATTTTACAAGATGTCGAACAACTGGGCAAGGCGAGAGCCGC 3960
DB GCAAAATAAGAGAGCCCTATTTTACAAGATGTCGAACAACTGGGCAAGGCGAGAGCCGC 4029
QY 3961 TGCCCTCACTGAACAGCAAAAACAGGTATCTTCAAAAGAAAATTTCCACATATTTGGTCA 4020
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QY 4081 GACAGCACTGTGAATCCCAACCAAAATGTCAAGTCCGTTCCGAGGCAATTTTCCACTAGTT 4140
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QY 4201 CAAGATGCTAGTTCATTTGAATATTTCTCC 4231
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Db 4270 CAAGATGCTAGTTCATTTGAATATTTCTCC 4300

RESULT 3
US-09-605-785-536
; Sequence 536, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows version 3.0
; SEQ ID NO 536
; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (4535)
; OTHER INFORMATION: n=A,T,C or G
US-09-605-785-536

Query Match 92.4%; Score 3910.2; DB 4; Length 6140;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 4040; Conservative 0; Mismatches 3; Indels 118; Gaps 1;

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QY 3729 CAAATGTGGATCCAGAACTGATGATTAATACAAAAAATAATCCGGGAGAAATTTGCC 3788
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RESULT 4
 US-09-439-313-536
 ; Sequence 536, Application US/09439313
 ; Patent No. 6329505

; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan Louise
 ; APPLICANT: Jiang Yuqul
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Kalos, Michael
 ; APPLICANT: Fanger, Gary
 ; APPLICANT: Retter, Mark
 ; APPLICANT: Solk, John
 ; APPLICANT: Day, Craig

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
 ; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.427C9
 ; CURRENT APPLICATION NUMBER: US/09/439,313
 ; CURRENT FILING DATE: 1999-11-12
 ; NUMBER OF SEQ ID NOS: 575
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 536

; LENGTH: 6140
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (4535)
 ; OTHER INFORMATION: n=A,T,C or G

US-09-439-313-536

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Query Match          92.4%; Score 3910.2; DB 4; Length 6140;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 4040; Conservative 0; Mismatches 3; Indels 118; Gaps 1;

QY 189 GGTGGCTCAATCCCTCTGTTTAAATTTGCCCATAAACGGAGATTAGAGAAAGATGATATGT 248
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QY	1809	TGATGCGGAAGTTAGCAGACACTTTGTCGAAGTGTGTTATTTGTCAAATTTTGCATGAGA	1868
Db	1853	TGATGCGGAAGTTAGCAGACACTTTGTCGAAGTGTGTTATTTGTCAAATTTTGCATGAGA	1912
QY	1869	AGATCACAATTTTGTGACTCATCAGTTGTCAGTACCTCAAAGTGCAGATCAGATCTGA	1928
Db	1913	AGATCACAATTTTGTGACTCATCAGTTGTCAGTACCTCAAAGTGCAGATCAGATCTGA	1972
QY	1929	TATTCAAAGATGGTAAATGGTGCAGAGGGGACCTTACACTCAGTTTCTTAAATCTGTTA	1988
Db	1973	TATTCAAAGATGGTAAATGGTGCAGAGGGGACCTTACACTCAGTTTCTTAAATCTGTTA	2032
QY	1989	TAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGAAAGTGAACAACCTCCAGTTCCAG	2048
Db	2033	TAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGAAAGTGAACAACCTCCAGTTCCAG	2092
QY	2049	GAATCCACACTAGGAATCGTACTTCTCAGAGCTTTCGGTTTGGTCTCAACAATCTT	2108
Db	2093	GAATCCACACTAGGAATCGTACTTCTCAGAGCTTTCGGTTTGGTCTCAACAATCTT	2152
QY	2109	CTAGACCTCTCTTGAAGATGGTCTCTGGAGAGCCAGATACAGAAATGTCACAGTTA	2168
Db	2153	CTAGACCTCTCTTGAAGATGGTCTCTGGAGAGCCAGATACAGAAATGTCACAGTTA	2212
QY	2169	CACATACAGAGAGAACCGTTCTGAAGAAAGTTGGTTTTTCAGGCCCTATAGAATTA	2228
Db	2213	CACATACAGAGAGAACCGTTCTGAAGAAAGTTGGTTTTTCAGGCCCTATAGAATTA	2272
QY	2229	TCAGAGCTGGTCTCACGTGGATGTCCTTATTTTCCTTATTTCTTAAACACTGCAGCTC	2288
Db	2273	TCAGAGCTGGTCTCACGTGGATGTCCTTATTTTCCTTATTTCTTAAACACTGCAGCTC	2332
QY	2289	AGGTGCTCTGCTTCAAGATTTGGTGGCTTTCATACTGGGCAACAAACAAAGTATGC	2348

Qy	3429	CAACTGAAATTTGGACTTTCAGATTTTAAGGAAGAAATGTCAATCATACTCTCAGGAACCTG	3488
Db	3473	CAACTGAAATTTGGACTTTCAGATTTTAAGGAAGAAATGTCAATCATACTCTCAGGAACCTG	3532
Qy	3489	TTTTGTTCACCTGGAACAATGAGGAAAAAACCCTGGATCCCTTTAAGGAGACACCGATGAGG	3548
Db	3533	TTTTGTTCACCTGGAACAATGAGGAAAAAACCCTGGATCCCTTTAAGGAGACACCGATGAGG	3592
Qy	3549	AACTGTGGAAATGCTTTACAAGAGGTACAACTTAAAGAAACCATTTGAAGATCTTCCCTGGTA	3608
Db	3593	AACTGTGGAAATGCTTTACAAGAGGTACAACTTAAAGAAACCATTTGAAGATCTTCCCTGGTA	3652
Qy	3609	AAATGGATACTGAATTTAGCAGAATCAGGATCCAAATTTTGTGTGGACAAGACAACTGG	3668
Db	3653	AAATGGATACTGAATTTAGCAGAATCAGGATCCAAATTTTGTGTGGACAAGACAACTGG	3712
Qy	3669	TGTGCCCTTGGCAGGGCAATTCACAGAAAAATTCAGATATTTGATTTGATGAAGCGACGG	3728
Db	3713	TGTGCCCTTGGCAGGGCAATTCACAGAAAAATTCAGATATTTGATTTGATGAAGCGACGG	3772
Qy	3729	CAAAATGTGATCCAAAGCACTGATGAGTTTAATACAAAAAATAATCCGGGAGAAATTTGCC	3788
Db	3773	CAAAATGTGATCCAAAGCACTGATGAGTTTAATACAAAAAATAATCCGGGAGAAATTTGCC	3832
Qy	3789	ACTGCACCGTGTCAACATTGACACACAGATTTGAACACCAATTTATGACAGCGGACAAGATAA	3848
Db	3833	ACTGCACCGTGTCAACATTGACACACAGATTTGAACACCAATTTATGACAGCGGACAAGATAA	3892
Qy	3849	TGTTTTAGATTCAGGAAGACTGAAAGAAATATGATGAGCCGTATGTTTTGCTGCAAAATA	3908
Db	3893	TGTTTTAGATTCAGGAAGACTGAAAGAAATATGATGAGCCGTATGTTTTGCTGCAAAATA	3952
Qy	3909	AAGAGAGCCCTATTTTACAAGATGGTGCAACAACCTGGGCAAGGACAGACCGCTGCCCTCA	3968
Db	3953	AAGAGAGCCCTATTTTACAAGATGGTGCAACAACCTGGGCAAGGACAGACCGCTGCCCTCA	4012
Qy	3969	CTGAACACGCAAAACAG-----	3985
Db	4013	CTGAACACGCAAAACAGATGGGTTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCT	4072
Qy	3986	-----	3985
Db	4073	GACCTCAAGTGAATCAACCTGGCTTGGCCCTCCAAACTGCTGAGATTACAGGTGTGAGCCA	4132
Qy	3986	-----GTACTTCAAAAAGAAATATCCACATATTTGGTCCACACTGACCAC	4030
Db	4133	CCAGGCCACCGCTGAGTATACTTCAAAAGAAATTTATCCACATATTTGCTCACACTGACCAC	4192
Qy	4031	ATGGTTTACAAACATTTCCAAATGGACAGCCCTCGACCTTAACTATTTTCGAGACAGCACTG	4090
Db	4193	ATGGTTTACAAACATTTCCAAATGGACAGCCCTCGACCTTAACTATTTTCGAGACAGCACTG	4252
Qy	4091	TGAATCCAAACAAATGTCAAAGTCCGTTCCGAGGCAATTTTCCACTAGTTTTTTGGACTAT	4150
Db	4253	TGAATCCAAACAAATGTCAAAGTCCGTTCCGAGGCAATTTTCCACTAGTTTTTTGGACTAT	4312
Qy	4151	GTAACCAACATTTGACTTTTTTTTACTTTTGGCAACAATATTTATACATAACAAGATGCTTA	4210
Db	4313	GTAACCAACATTTGACTTTTTTTTACTTTTGGCAACAATATTTATACATAACAAGATGCTTA	4372
Qy	4211	GTTTCATTTGAATATTTTCCCT	4231
Db	4373	GTTTCATTTGAATATTTTCCCT	4393

RESULT 5
US-09-605-785-824
; Sequence 824, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.

```

; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 824
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-605-785-824

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Query Match	24.7%; Score 1045.4; DB 4; Length 1074;	
Best Local Similarity	99.9%; Pred. No. 7e-292;	
Matches 1046; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
QY 1226	TCAGCCATTGAGAGGGTCTCAGAGCAATCGTCAGCATCCGAAGATCCAGACCTTTTG 1285	
Db 4	TCAGCCATTGAGAGGGTCTCAGAGCAATCGTCAGCATCCGAAGATCCAGACCTTTTG 63	
QY 1286	CTACTTGATGAGATATCATACGCGCAACCGTCAGTGCCTCAGATGTTAAAAAGATGCTG 1345	
Db 64	CTACTTGATGAGATATCATACGCGCAACCGTCAGTGCCTCAGATGTTAAAAAGATGCTG 123	
QY 1346	CATGTGCAGGATTTTACTGCTTTTGGGTAAGGCATCAGAGACCCCAACCTCTACAAGCC 1405	
Db 124	CATGTGCAGGATTTTACTGCTTTTGGGTAAGGCATCAGAGACCCCAACCTCTACAAGCC 183	
QY 1406	CTTTCCCTTTACTGTCAGACCTGGCGAAATTGTAGTGTGGCGCCCGTGGGAGCAGGG 1465	
Db 184	CTTTCCCTTTACTGTCAGACCTGGCGAAATTGTAGTGTGGCGCCCGTGGGAGCAGGG 243	
QY 1466	AAGTCATCACTGTTAAGTGGCGTCTGGGGAATTGGCCCCAAGTCAGCGGCTGTCAGC 1525	
Db 244	AAGTCATCACTGTTAAGTGGCGTCTGGGGAATTGGCCCCAAGTCAGCGGCTGTCAGC 303	
QY 1526	GTGCATGGAAGAAATTGCCATGTGCTCAGCAGGCCCTGGGTCTCGGGAACTCTTGAGG 1585	
Db 304	GTGCATGGAAGAAATTGCCATGTGCTCAGCAGGCCCTGGGTCTCGGGAACTCTTGAGG 363	
QY 1586	AGTAATATTTTATTGGGAGAGAAATATGAAAGGAACGATATGAAAAAGTCATAAGGCT 1645	
Db 364	AGTAATATTTTATTGGGAGAGAAATATGAAAGGAACGATATGAAAAAGTCATAAGGCT 423	
QY 1646	TGTGCTCTGAAAAAGGATTTACAGCTGTTGGAGATGCTGATCTGACTGTGATAGGAGAT 1705	
Db 424	TGTGCTCTGAAAAAGGATTTACAGCTGTTGGAGATGCTGATCTGACTGTGATAGGAGAT 483	
QY 1706	CGGGGAACACCGCTGAGTGGAGGCGAGAAAGCACGGGTAAACCTTGCAGAGCAGTGTAT 1765	
Db 484	CGGGGAACACCGCTGAGTGGAGGCGAGAAAGCACGGGTAAACCTTGCAGAGCAGTGTAT 543	
QY 1766	CAGATGCTCAGATCTATCTCCTGGAGCATCCTCTCAGTCGAGTAGATGCGGAAGTTAGC 1825	
Db 544	CAGATGCTCAGATCTATCTCCTGGAGCATCCTCTCAGTCGAGTAGATGCGGAAGTTAGC 603	
QY 1826	AGACACTGTGTTCCGAACCTGTGTATTGTGTCAAATTTTGCATGAGAAGATTCACAAATTTTAGTG 1885	

Db 604 AGACACTGTTCCGACCTGATGTTGTTGCAAAATTTGTCATGAGAAGATCAAAATTTTAGTG 663
QY 1886 ACTCATCAGTTGTCAGTACCTCAAGCTGCAAGTCAAGTCTGATATTTGAAAGATGTTAA 1945
Db 664 ACTCATCAGTTGTCAGTACCTCAAGCTGCAAGTCAAGTCTGATATTTGAAAGATGTTAA 723
QY 1946 ATGGTCCAGAAAGGGACTTACACTGAGTTCCTAAATCTGGGTATAGATTTGGCTCCCTT 2005
Db 724 ATGGTCCAGAAAGGGACTTACACTGAGTTCCTAAATCTGGGTATAGATTTGGCTCCCTT 783
QY 2006 TTAAGAAAGGATAATCAGGAAAGTGAACACCTCCAGTTCAGGAACTCCACACTAAGG 2065
Db 784 TTAAGAAAGGATAATCAGGAAAGTGAACACCTCCAGTTCAGGAACTCCACACTAAGG 843
QY 2066 AATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTTCTAGACCTCCTTGAA 2125
Db 844 AATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAATCTTCTAGACCTCCTTGAA 903
QY 2126 GATGGTGCTCGAGAGCCCAAGATACAGAGAATGTCCTCCAGTTACACTATCAGAGGAGAAC 2185
Db 904 GATGGTGCTCGAGAGCCCAAGATACAGAGAATGTCCTCCAGTTACACTATCAGAGGAGAAC 963
QY 2186 CTTCTGAGGAAAGTTGGTTTTCAGGCTTATAGAAATTTACTTCAGAGCTGGTGCTCAC 2245
Db 964 CTTCTGAGGAAAGTTGGTTTTCAGGCTTATAGAAATTTACTTCAGAGCTGGTGCTCAC 1023
QY 2246 TGGATTGCTCTCATTTTCTCTTATTC 2272
Db 1024 TGGATTGCTCTCATTTTCTCTTATTC 1050

RESULT 6

US-09-001-273-1
; Sequence 1, Application US/09001273
; Patent No. 5994130
; GENERAL INFORMATION:
; APPLICANT: SHYJAN, Andrew
; TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/001,273
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON, Gillian M
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: MIL-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4781 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..4360

US-09-001-273-1

Query Match 10.3% Score 437.4; DB 2; Length 4781;
Best Local Similarity 48.8%; Pred. No. 9.4e-116;
Matches 124; Conservative 0; Mismatches 1296; Indels 9; Gaps 2;
QY 1394 ACTCTACAAGSCCTTCTCTTACTGTCTCAGACCTGGCGAAATTTGTTAGCTGTGGTGGGCC 1453
Db 1778 AACTGCACAGCATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTCGGGCAGT 1837
QY 1454 GTGGGACAGGAAGTCACTCACTGTTAAGTGCCCTGCTCGGGGAATTTGGCCCCAAGTCAC 1513
Db 1838 GTGGGAAGTGGAAAACTCTCTCATTTAGCCCAATTTTAGGCCAGATGACGCTCTTAGAG 1897
QY 1514 GGGCTGCTCAGCGTGCATGGAAGAAATTCCTATGTCTCTCAGCAGCCCTGGGTGTTCTCG 1573
Db 1898 GGAGCAATTCGATTCAGTGGAACTCTGCTTATGTGCCCGCAGGCTGGATCTCTCAAT 1957
QY 1574 GGAACCTCTGAGGAGTAAATATTTTATTTGGGAAGAAATATGAAAAAGGAACGATATGAAAA 1633
Db 1958 GCTACTCTGAGAGACACATCTCTTTTGGGAAGGAATATGATGAAGAAAGATACAATCT 2017
QY 1634 GTCATAAGCGTTGTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 1693
Db 2018 GTGCTGAACAGCTGCTGCTGAGGCTGACCTGSCCATTTCTTCCACAGCAGGCTGACG 2077
QY 1694 GTGATAGGAGATCGGGGAACCACTGCTGAGTGGAGGGCAGAAAGCAGCGGTAAACCTTGCA 1753
Db 2078 GAGATTGGAGAGCGAGGAGCAACCTGAGCGGTGGCGAGGCCAGAGAGTACAGCTTGCC 2137
QY 1754 AGACAGTGTATCAAGATGCTGACATCTATCTCTGACGATCTCTCTCAGTGCAGTATAGT 1813
Db 2138 CGGCGCTTGTATAGTGACAGGAGCATCTACATCTCTGACGACCCCTCTGCTCTTATAGT 2197
QY 1814 GCGGAAGTTAGACAGACACTTGTTCGAACTGTGATTTGTCATAATTTTTCATGAGAAGATC 1873
Db 2198 GCGCATGTGGCAACCACTCTTCAATAGTCTATCGGAACATCTCAAGTCCCAAGACA 2257
QY 1874 ACAATTTTAGTACTCATCATGTTGCACTGCTCAAGCTCAAGTCCAGTCACTGATATTG 1933
Db 2258 GTTCTGTTTACCACCACTGTTACAGTCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTT 2317
QY 1934 AAAGATGTTAAATGGTGCAGAGGGGACTTACACTGAGTTCCTAAATCTGGTATAGAT 1993
Db 2318 AAAGAGGCTGTATTACGGAAGAGCCACCCATGAGGAATGATGATTTAAATGGTGAC 2377
QY 1994 TTTGGCTCCCTTTTAAAGAAAGGATAATAGGAAAGTGAACAACTCCAGTTCAGGAACT 2053
Db 2378 TATGCTTACCCTTTTAAATACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCA 2437
QY 2054 CCCACACTAAGGAATCGTACCTTCTCAGAGTCTTGGTGGTCTCAACAACTCTTCTAGA 2113
Db 2438 AAAAGGAACCACTGTTTACAGAAAGTTCACAGAAAGTTCACAGAAAGGTTCTTAAACAGGATCA 2497
QY 2114 CCCTCTCTGAAAGATGGTCTCTGAGAGCCAAAGATACAGAGATGTCCTGCTGCTGCTGCT 2173
Db 2498 ATAAGAAAGGAAAGCAGTAAAGCCAGAGGAAGGCGAGCTTGTGAGCTGGGAAGAGAA 2557
QY 2174 TCAGAGGAGAACCGTTCTGAAGGAAAGTTGGTTTTCAGGCCCTTATAGAAATTTACTTCAGA 2233
Db 2558 GGGCAGGGTTCAGTGGCCCTGGTCAATATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2617
QY 2234 GCTGGTCTCACTGGATTTGCTCTTCAATTTTCTTATTTCTCTTAACTGAGCTGAGGTT 2293
Db 2618 TTGGCAATCTCTGTTTATTTATGGCCCTTTTCTATGCTGAATGTAGGAGCACCGCTTTCAGC 2677
QY 2294 GCCTATGTGCTTCAAGATTGGTGGCTTTTCATCTGCGCAACAAACAAAGTATGCTTAAAT 2353
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QY 2354 GTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAAGTATGATCTTAACTGCTTACTTAGGA 2413
Db 2738 AACGAGACCTCGTGTGATGACACGATGAGGAGCAATCTCTCATATGCTGCTGCTGCTGCTGCTGCT 2797

QY 2414 ATTTATTCAGGTTTAACTGTAGCTACCGTCTTTTGGCATAGCAAGATCTCTATTGGTA 2473
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 QY 2474 TTCTACGTCCTTTGTTAACTCTTCAAACTTTGACAAACAAATGTTTGGAGTCAATCTCG 2533
 Db GTCAAGGCGCCTGCGAGCTTCTCCCGGCTGATGACGAGCTTTTCCGAGGATCTCTT 2917
 QY 2534 AAAGTCGGTATTATTCTTTGATAGAAATCCAAATAGGAAGAAATTTTAAATCGTTTCTCC 2593
 Db CGAAGCCCTATGAAGTTTGTGACACGACCCACAGGAGGATTTCTCAACAGGTTTTC 2977
 QY 2594 AAAGCATTTGACACTTGGATGATTTGCTGCCCTGAGCTTTTATAGATTTTATCCAGACA 2653
 Db AAAGCATGGAATGAAGTGTGAGCTGCGGCTGCCGTTCCAGGCCGAGATGTTTATCCAGAAC 3037
 QY 2654 TTGCTACAAGTGGTTGGTGTCTGTGTGCTGTGCGCTGATTCCTTTGGATCGCAATA 2713
 Db GTTATCTGTGTCTTCTGTGTGGATGATCCAGAGTCTTCCCGTGGTCTCTGTG 3097
 QY 2714 CCCTTGGTCCCTTGGAACTATTTTCTTTTCTCGGAGATATTTTGGAAACGTCA 2773
 Db GCACTGGGGCCCTTGTCTATCTCTTTTCACTGCTGACATTTGTCTCTCCACATCACGTC 3157
 QY 2774 AGAGATGGAAGCCCTGGATCTACAACTCGGAGTCCAGTGTTCCTCCACTTGTCTAT 2833
 Db CGGAGCTGAAGCGCTGGAACATATCACGAGTCTTCTCTCCACATCACGTC 3217
 QY 2834 TCTCTCAGGGGCTCTGGACATCCGGCATACAAACGAGAGAGTGTGAGCAACTG 2893
 Db AGCATACAGGGCTTGGCCATCCAGCCCTACAAATGAAGGCGAGGATTTCTGCACAGA 3277
 QY 2894 TTGATGCACACAGGATTTACATTCAGAGCTTGTCTTTGTTTTCACAACTCCCGC 2953
 Db TACAGGAGCTGTGGATGACAAAGCTCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3337
 QY 2954 TGGTTCGCCCTGCTGAGTGCATCTGTGCAATGTTTGTGATCATCTGTTGCTTGGG 3013
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 QY 3014 TCCTGTATCTGCAAACTCTGATGCGGCGGCTGTTGGCAGTGTGCTGCTATGCT 3073
 Db ATCGTCTTATGACGCGGAGATTCCTCCAGCTATCGGGTCTCGCATCTCTATGCT 3457
 QY 3074 CTCAGCTATGAGGATTTTCACTGTGTGTGCAAGAGTGTGAGTGTGAGATATG 3133
 Db GTCCAGTTAACGGGCTGTTCAGTTTACGCTGAGCTGCTGAGACAGAGCTCGA 3517
 QY 3134 ATGATCTCAGTAAAGGTCATTGATACACAGACCTT-----GAAAAGAGACCT 3187
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 QY 3188 TGGGAATATCAGAAACCCACACAGCTGCGCCCTCAAGAGAGTGAATCTTTGAC 3247
 Db AGAATTAAGAACAGGCTCCTCCCTGACTGCGCCACAGGAGGAGTGTGACCTTTGAG 3637
 QY 3248 AATGTAACCTTATGATACAGTCCAGGTGGGCTCTGTGTAAGCATCTGACAGCACTC 3307
 Db AACGCAGATGAGTACCGAGAAACCTCCCTCTGCTCTAAAGAAAGTATCTTCAAG 3697
 QY 3308 ATTAATCAGAAAGGTTGCTATGTTGGAGAGACCGGAGCTGGAAGTTCCCTC 3367
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 QY 3368 ATCTAGCCCTTTTATGATGTCAGA---ACCGAAGGTAAATTTGGATTGATAAGATC 3424
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 QY 3425 TTGACAACCTGAAATTTGACTTCAAGATTTAAGGAAGAAATGTCAATCATACCTCAGAA 3484
 Db AGAATCAGTATATTGCGCTTGGCGAGCTCCGAGCAACTCTCTATCATCTCAGAG 3877

QY 3485 CCTGTTTGTTCACCTGGAAACAAATAGGAAAAACCTGGATCCCTTTAAGGAGACACAGAT 3544
 Db CCGTGTCTGTTTCACTGGGACCTGTCAGTCAAAATTTGGACCCCTTCAACACGATACAGTAA 3937
 QY 3545 GAGGAACCTGGAATGCGCTTCAAGAGGTTCACTTAAAGAAACCAATGGAAGATCTTCT 3604
 Db GACCAAGATTTGGGATGCGCTGGAGAGACACATGAAGAATGATTCTCAGCTACCT 3997
 QY 3605 GGTAATGGAATGTAATAGCAGAACTAGGATCCAAATTTTAGTGTGGCAAGACAA 3664
 Db CTGAACCTTGAATCTGAAGTGTGAGATGGGATTAATCTCAGTGGGGAACGGCAG 4057
 QY 3665 CTGTTGCTGCTGCGGCAATCTCAGGAAAAATCAGATTTGATTTAGTGAAGCG 3724
 Db CTCTTGTGATAGCTAGAGCCCTGCTCGCCACTGTAAGATTTCTGATTTAGATGAAGCC 4117
 QY 3725 ACGGCAAAATGGAATGGAAGAACTGATGATTAATACAAAAAATCCGGGAGAAATTT 3784
 Db ACAGTGCATGGACACAGACAGACTTATTGATTCAGAGACCATCCGAGAAGCATTT 4177
 QY 3785 GCCACTGCACCGTGTAACTTGCACACAGATTTGAACACCATTTATTGACAGCAGCAAG 3844
 Db GCAGACTGTACCATGCTGACCATTCGCCATCGCTGACACAGCTTCTAGGCTCCGATAGG 4237
 QY 3845 ATATGTTTGTAGATTCAGGAAGACTGAAAGAAATATGATGAGCCGCTATGTTTGTGCA 3904
 Db ATTATGTTGCTGGCCAGGACAGTGTGAGTTTGACCCCATCGTCTTCTGCTGCTC 4297
 QY 3905 AATAAGAGAGCTTATTACAGATGTT 3933
 Db AACGACATTCCTGATCTATGCTGCTGCT 4326

RESULT 7
 US-08-843-459A-1
 : Sequence 1, Application US/08843459A
 : Patent No. 6162616
 : GENERAL INFORMATION:
 : APPLICANT: SHYAN, Andrew
 : TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
 : TITLE OF INVENTION: POLYPEPTIDE
 : NUMBER OF SEQUENCES: 8
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: LAHIVE & COCKFIELD, LLP
 : STREET: 28 State Street
 : CITY: Boston
 : STATE: Massachusetts
 : COUNTRY: USA
 : ZIP: 02109
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/843,459A
 : FILING DATE: 16-APR-1997
 : CLASSIFICATION: 536
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Hanley, Elizabeth A.
 : REGISTRATION NUMBER: 33,505
 : REFERENCE/DOCKET NUMBER: MNI-056 (formerly MIL-001)
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (617)227-7400
 : TELEFAX: (617)742-4214
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 4781 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : FEATURE:
 : NAME/KEY: CDS

LOCATION: 2..4360
US-08-843-459A-1

Query Match 10.3%; Score 437.4; DB 4; Length 4781;
Best Local Similarity 48.8%; Pred. No. 9.4e-116;
Matches 1244; Conservative 0; Mismatches 1296; Indels 9; Gaps 2;

QY 1394 ACTCTACAGGCTTTCCTTACTGTCACTGTCAGACCTGGCGAATTTGTTAGCTGTGGTCGGCCCC 1453
DB 1778 ACACGTGCACAGCATCGATCTGGAGATCCAAAGAGGGTAAACTGGTTGGAATCTGCGGCAGT 1837
QY 1454 GTGGGAGCAGGAAGTCATCACTGTTAAAGTGCCTCGCGGAATTTGGCCCAAGTCAC 1513
DB 1838 GTGGGAAGTGGAAACCTCTCTCAITTCAGCCATTTTGGCCAGATGACGCTTCTAGAG 1897
QY 1514 GGGCTGGTCAGCGTGCATGGAGAATTTGCTATGTCTCAGCAGCCCTGGGTTCGTCG 1573
DB 1898 GGCAGCATTTGCAATCAGTGGAACTTCGCTTATGTGGCCAGCAGGCCCTGGATCCTCAAT 1957
QY 1574 GGAACCTCGAGAGTAATATTTTNTTGGGAAGAATATGAAAGAACGATATGAAAAA 1633
DB 1958 GCTACTCTGAGAGACAACATCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCT 2017
QY 1634 GTCATAAAGGCTTGCTCTGAAAAAGGATTTACAGCTCTTGGAGGATGGTCTGACT 1693
DB 2018 GTGCTGAACAGCTGCTGCTGAGGCTGACCTGGCCATTCCTCCAGCAGCAGCTGAGG 2077
QY 1694 GTGATPAGGAGATCGGGGAACCAACGCTGAGTGGAGGCGAGAAAGCACGGGTAAACCTTGCA 1753
DB 2078 GAGATTGGAGCGAGGAGGCCAACCTGAGCGTGGCGAGCGCCAGAGGATCAGCCTTGCC 2137
QY 1754 AGAGCAGTGTATCAGATGCTGACATCTATCTCTGGAGGATCTCTCAGTGCAGTAGAT 1813
DB 2138 CGGGCCCTTGTATGATGACAGGAGCATCTACATCTCTGGACGACCCCTCAGTGCCTTAGAT 2197
QY 1814 GCGGAAGTTAGCAGACATCTGTTGCAACTGTCTATTTGTCAATTTTGCATGAGAGATC 1873
DB 2198 GCCATGTGGGCAACCATCTTCAATAGTGTATCCGGAAACATCTCAAGTCCAGACA 2257
QY 1874 ACAATTTTGTAGTCACTCAGTGTGCACTACCTCAAGCTGCAAGTCAGATTCGTATATG 1933
DB 2258 GTTCTGTTTGTATCCACCACAGTTACAGTACCTGTTGACTGTGATGAAGTATCTCATG 2317
QY 1934 AAGATGTAAATGGTCCAGAGGGGACTTACACTGAGTTCCTTAAATCTGGTATAGAT 1993
DB 2318 AAGAGGCTGTATTTACGGGAAGAGGCCACCATGATGAGGAACATGATGAATTTAAATGGTGAC 2377
QY 1994 TTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAGTGAACACCTCCAGTTCAGGAAC 2053
DB 2378 TATGCTACCATTTTAAATACCTGTTGCTGGAGAGACCCCGCAGTTGAGATCAATTCA 2437
QY 2054 CCCACACTAAGGAATCGTACCTCTCAGAGTCTTCGGTTCCTCAACAATCTTCTAGA 2113
DB 2438 AAAAGGAACACAGTGTTCAGAGAAGAGTCACAAGACAAGGGTCTTAAACAGGATCA 2497
QY 2114 CCCTCCTTGAAGATGGTCTCTGGAGAGCCCAAGATACAGAGATGTCCAGTATACACTA 2173
DB 2498 ATAAGAAGGAAGAAAGCAGTAAAGCCAGGAGGAGGCCAGCTTGTGCAGCTGGAAGAGAA 2557
QY 2174 TCAGAGAGAACCGCTTCTGAAGGAAAAGTGTGTTTTCAGGCTTATAAGAAATTAATTCAGA 2233
DB 2558 GGGCAGGGTTCAGTCCCTGTGCTAGTATATGGTGTCTACATCCAGGCTGTGGGGCCCC 2617
QY 2234 GCTGGTCTCACTGGATTTGCTTCAATTTTCTTATTTCTCTTAAACACTGCACTCAGGTT 2293
DB 2618 TTGGCAATTCCTGGTTATTTATGGCCCTTTTCATGCTGATGTAGCAGCAGCCGCTTCAGC 2677
QY 2294 GCCTATGTGCTTCAAGATTTGGTGGCTTTCATCTGAGGCAACAAACAAAGTATGCTAAAT 2353
DB 2678 ACCTGGTGGTGTAGTTACTGTGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGG 2737
QY 2354 GTCATGTAAATGAGGAGGAATATGTACCCGAGAGCTAGATCTTAATCTGCTACTTAGGA 2413

DB 2738 AACGAGACCTCGGTGAGTGACAGCATGAAGGACAAATCCTCATATSCAGTACTATSCCAGC 2797
QY 2414 ATTATTCAGGTTTAACTGTAGCTACCGTTCTTTTGGCATAGCAAGATCTCTATTGGTA 2473
DB 2798 ATCTACCCCTCTCCATGGCAGTATCTGATCTCTGAAGCCATTCGAGGAGTGTCTTT 2857
QY 2474 TTCTACGCTCTGTGTAATCTTTCACAAACTTTGCACAAACAAATGTTTGAGTCAATCTG 2533
DB 2858 GTCAAGGCGACGCTGCGAGCTTCTCCCGCTGCATCAGAGCTTTTCCGAGAGATCCTT 2917
QY 2534 AAAGCTCCGCTATATTTCTTTGATAGAAATCCAAATAGGAAGATTTTAAATCGTTTCTCC 2593
DB 2918 CGAAGCCCTATGAAGTTTGTGACAGCACCCACAGAGGAGTATCTCAACAGGTTTTCC 2977
QY 2594 AAAGACATTCGACACTTTGGATGATTTGCTGCGCTGACGTTTITAGATTTTCATCCACACA 2653
DB 2978 AAAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3037
QY 2654 TTGCTACAAAGTGTGGTGTGCTCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCTGTGGCT 2713
DB 3038 GTTATCTGCTGTTCTTCTGTGTGGGAATGATCGCAGGAGTCTTCCGCTGCTGCTTGTG 3097
QY 2714 CCCTTGGTCCCTTGGAAATCTTCAATTTTCTTGGCGATATTTTGGAAACGTCA 2773
DB 3098 GCASTGGGCCCCCTTGTCTATCTCTTTCAGTCTGACATTTGTCTCCAGGGTCTGATT 3157
QY 2774 AGAGATGTGAAGCGCTGGAAATCTACAACTCGGAGTCCAGTGTTCCTCCACTTGTCTATCT 2833
DB 3158 CGGAGCTGAGGCGCTGGACAATTCACGAGTCACTTCTCTCCACATCACGCTCC 3217
QY 2834 TCTCTCAGGGCTCTGGACCATTCGGGATCCGGGATCAAAAGCAGAGAGTGTCAAGAACTG 2893
DB 3218 AGCATACAGGCGCTTCCACCATCCAGCTACAAATAAAGGCGAGGATTTCTTGACAGA 3277
QY 2894 TTTGATGCACACCAAGATTTACATTCAGAGGCTTGGTCTTGTGTTTGAACAAGTCCCGC 2953
DB 3278 TACCAGGAGCTGCTGGATGACAAACAGTCTCTTTTGTGTTTACGTGCGGATGCGG 3337
QY 2954 TGTCTCGGCTGCTGCTGATGCCATCTGTGCCATCTTGTGCATCATCTTGTGCTTTGGG 3013
DB 3338 TGGTGGCTGTGGGCTGGACCTATCAGATCGCCCTCATCACCACGAGGGGCTGATG 3397
QY 3014 TCCCTGATTTCTGGCAAAAATCTTGGATCGGGCAGTGTGGTGTGGCACTGTCTATGCC 3073
DB 3398 ATCGTCTTATGCACGGCAGATTTCCCGAGCTATGCGGGTCTCCGCTCTCTTATGCT 3457
QY 3074 CTCACGCTCATGGGATGTTTCACTGCTGTGTTGCAAAAGTCTGAAAGTGTGAAGATATG 3133
DB 3458 GTCCAGTTAACGGGCTGTTCCAGTTTACGGTCAGACTGTGAGACAGAAAGCTCGA 3517
QY 3134 ATGATCTCAGTAGAAGGCTCATTTGAATACACAGACCTT-----GAAAAGAACACCT 3187
DB 3518 TTCACCTCGGTGAGGAGTCAATCACTACATTAAGACTCTGTCTTGAAGACCTGCC 3577
QY 3188 TGGGAATATCAGAAAGCCACACAGCCTGGCCCATGAAGAGTGTAACTTTTGTGAC 3247
DB 3578 AGAATTAAGAAACAGGCTCCCTCCCTGACTGGCCCGCAGGAGGAGTGTGACCTTTGAG 3637
QY 3248 AATGTGAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3307
DB 3638 AACGAGAGATGAGTACCGAGAAACCTTCCCTCTGCTCTAAAGAAAGTATCTTCAAG 3697
QY 3308 ATTAATACAAAGAAAGGTTGGCATTTGGGAAGAACCGGAGCTGGAAGAGTTCCTC 3367
DB 3698 ATCAACCTTAAGAGAGAGATTTGGCATTTGGGGCGAGAGGATCAGGGAAGTCTCGCTG 3757
QY 3368 ATCTCAGCCCTTTTATGATTTGTCAGA---ACCCGAAGGTAAAAATTTGGATTTGATAAGATC 3424
DB 3758 GGGATGGCCCTCTTCCGCTGTGGGAGTATCTGGAGGCTGATCAGATCAGATGAGGATG 3817
QY 3425 TTGACAACCTGAATTTGAGTTCACGATTTAAGGAAGAAATGTCAATCATCATCAGGAA 3484
DB 3818 AGAATCAGTGATATTTGGCTTCCCGACCTCCCGAACCAACTCTCTATCATCTCTCAAGAG 3877

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QY 2414 ATTTATTCAGGTTTAACTAGTACCTACCGTCTCTTTTGGCATAGCAAGATCTCTATTGGTA 2473
Db 2864 ATCTAGCCCTCTCCATGCGAGTCACTGATCTCTGAAAGCCATTGCGAGGAGTGTCTTT 2923
QY 2474 TTCTAGGCTCTTGTAACTCTTCACAACTTTGCACAACTTTGAGTCAATTCG 2533
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QY 2534 AAAGTCTCGGTATTTCTTTCATAGAAATCCAATAGGAAGATTTAAATCGTTTCTCC 2593
Db 2984 CGAAGCCCTATGAAGTTTTCACAGCAGCCACAGGAGGATCTCAACAGGTTTCC 3043
QY 2594 AAAGACATTTGACACTTGGATGATTTGTCGCGCTGACGCTTTTATGATTTTCATCCAGACA 2653
Db 3044 AAAGACATGGATGAAGTTGACGTGCGGCTGCGGTTCCAGGCGGAGATGTTCCATCCAGAAC 3103
QY 2654 TTGCTACAAGTGGTGGTGTCTGTGTGGCTGTGGCGGTGATTCCTTGGATCGCAATA 2713
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QY 2714 CCCTTGGTTCCTTGGATCATTTTTCATTTCTTTCGCGGATATTTTGGAAAGCTCA 2773
Db 3164 GCAGTGGGCGCCCTGTCTATCTCTTTTCAGTCTGACATGCTCCAGGCTCCTGAT 3223
QY 2774 AGAGATGTAAGCGGCTCGAATCTACAACTCGGAGTCCAGTGTCTTCCCACTGTGTCATCT 2833
Db 3224 CGGAGCTGAAGCGTCTGGAAATATCACCGAGTCACTTCTCTCCACATCACGTC 3283
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QY 2894 TTTGATGCACACCATGATTTACATTCAGAGCTGTGGTCTTCTTGTTCACACAGTCCCGC 2953
Db 3344 TACCAGGAGCTGTGGATGACAAACCACTCTCTTTTGTTCAGTGTGCGATGCGG 3403
QY 2954 TGGTTCGCGCTGCTGAGTGCATCTGTCATCTGTCATCTGTCATCTGTCATCTGTCG 3013
Db 3404 TGGTTCGCTGTCGCTGAGCTCATCAGCATCGCCCTCATCACACACCGGCTGATG 3463
QY 3014 TCCCTGATTCGCAAACTCTGATGCGCGGAGGTGTTGGCACTGCTCTATGCC 3073
Db 3464 ATCTGTTTATGACGGGAGATTTCCCCACGCTATGCGGCTCGCCATCTCTTATGCT 3523
QY 3074 CTCACGCTCATGGGATGTTTCACTGTGTGTCGACAAAGTGTGAAGTTGAGATATG 3133
Db 3524 GTCCAGTTAAGGGGCTGTTCCAGTTTACGTCAGCTGGCATCTGACACAGAAGCTCGA 3583
QY 3134 ATGATCTAGTAGAAGGGTCAATTAATACACAGACCTT-----GAAAGAGACACCT 3187
Db 3584 TTCACCTCGGTGAGAGGATCAATCACTACATTAAGACTCTGCTTGGAGACACCTGCC 3643
QY 3188 TGGAATATCAGAAACCCACACACAGCTGCGCCCATGAGAGTGAATCTTTGAC 3247
Db 3644 AGAATTAAGAACAGGCTCTCCCTGACTGGGCGGAGGAGGAGTGAACCTTTGAG 3703
QY 3248 AATGTGAATCTCATGATCCAGTTCAGGTGGGCTCTGCTACTGAAGCATCTGACAGCACTC 3307
Db 3704 AACGCAGAGATGAGTACCGAGAAACCTCCCTCTGCTCTAAAGAAGTATCTCTCAAG 3763
QY 3308 ATTAATCACAAGAAAGTTGGCATTTGGGAAGAACCGAGCTGGAAAGTTCCCTC 3367
Db 3764 ATCAAACTTAAGAGAAGATTTGGCATTTGGGCGGAGAGGATCAGGAAGTCTCGCTG 3823
QY 3368 ATCTCAGCCCTTTTAGATTGTCAGA---ACCGAAGGTAAATTTGGATTGATAAGATC 3424
Db 3824 GGGATGCCCTCTTCCGCTGCTGGAGTATCTCGAGGCTGTCATCAAGATTGATGGAGTG 3883
QY 3425 TTGACAACTGAATTTGACATTCACGATTTTAAGGAAGAAATGTCATCATACCTCAGGAA 3484

Db 3884 AGAATCAGTGATATTGGCCTTGGCGACCTCGAAGCAAACTCTCTATCATTCCTCAAGAG 3943
QY 3485 CCTGTTTTGTTCACTGCAACAANTCAGAAACCTTGATCCCTTTAGAGGACACACGAT 3544
Db 3944 CCGTGTCTTTAGTGGCAGCTGTCAGATCAAAATTTGACCCCTTCAACCACTACACTGAA 4003
QY 3545 GAGGAACGTGGATGCTTTACAGAGAGGTACAACTTAAAGAAACCATTTGAAGATCTTCT 3604
Db 4004 GACCAGATTTGGGATGCCCTGGAGAGGACACACATGAAGAATGATTTGCTCAGCTACCT 4063
QY 3605 GGTAAATGATGATGCTAATTTAGCAGAAATCAGGATCCAAATTTTAGTGTGGCAAAAGCAA 3664
Db 4064 CTGAACCTTGAATCTGAAGTGAATGGGATTAATCTCAGTGGGGAACGCGAG 4123
QY 3665 CTGCTGCTCTCCAGGCAATCTCAGGAAATATCAGGAAATATGATTTATGATGAAGCG 3724
Db 4124 CTCTTGTGATAGCTAGAGCCCTGCTCCGCACTGTGAAGATTTCTGATTTTAGATGAAGCC 4183
QY 3725 ACGGCAATGTGGATCCAGAACTGATAGTTAATACAAAAAATCCGGGAGAAATTT 3784
Db 4184 ACAGCTGCCATGACACAGAGACAGACTTATTGATTCAGAGACCATCCGAGAAAGCATTT 4243
QY 3785 GCCACTGACCTGCTTAACCATTTGACACAGATTTGAACACCATTTATTTGACAGCAAG 3844
Db 4244 GCAGACTGTACCATGCTGACCATTTGCCCATCGCTGCACACGCTTCTAGCTCCGATAGG 4303
QY 3845 ATAATGTTTTAGATTTCAGAGACACTGAAAGAAATATGATGACGCGTATGTTTGTCTGCA 3904
Db 4304 ATTAGTGTCTGCGCCAGGACAGGTGGTGGAGTTTGACACCCCATCGGCTTCTTCTGTC 4363
QY 3905 AATAAGAGAGCTTATTTTACAAGATGGT 3933
Db 4364 AACGACAGTTCCGATTTCTATGCCATGTT 4392

RESULT 9
US-08-141-893-1
; Sequence 1, Application US/08141893
; Patent No. 5489519
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,893
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923; 08/029,340
; FILING DATE: 27-OCT-1992; 8-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PQI-002
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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs

QY	518	TACGCTATGCCAGCGCTGACTGTTTTTCCAGCTCATTTTTGGCTATACTGCATCACTTA	577
Db	1285	TACTTCTACACCGTGTCTGTTGTGTACTGCTGCCGTCAGACCCCTCGTCTGCCACG	1344
QY	578	TATTTTTATCACGTTTCAGTGTGCTGGGATGAGGTTTACGAGTAGCCATGTGCCATATGATT	637
Db	1345	TACTTCCACATCTGTTCTCGTAGTGGCATGAGGATCAAGACCGCTGTCAATTTGGGCGTGC	1404
QY	638	TATCGGAAGCAGCTTCGCTTTTGTAGTAACTGGCCATGGGGAAGACAACACAGGCCAGATA	697
Db	1405	TATCGGAAGCCCTGTGTGATCACCAAATTCAGCCAGAAATCCTCCACGGTCGGGAGATT	1464
QY	698	GTCAATCTGCTGCCAATCATCTGTACACAGTTTGATCAGGTGACAGTGTCTTACACTTC	757
Db	1465	GTCAACCTCATGCTGTGGACGCTCAGAGGTTTATGGACTTTGGCCACGTACATTAACATG	1524
QY	758	CTGTGGCAGGACCACTGCAGCGCATCGCAGTACTGCCCTACTCTGGATGGATAGGA	817
Db	1525	ATCTGGTCAGCCCCCTGCAAGTCATCTTGTCTCTTACCCTCTGTGCTGAATCTGGC	1584
QY	818	ATATCGTGCTTGCCTGGGATGCGAGTTCTAATCATCTCTCTGCCCTTGCCTGCAAGCTGTTTT	877
Db	1585	CCTTCGCTCCTGCTGGATGGCGGTGATGGTCCATCTGTTGCGCCGCTCAATPGCTGTGATG	1644
QY	878	GGAAAGTTGTTCTCTCATCTAGGAGTAAAACTGCAACTTTCACGGGATGCCAGATCAGG	937
Db	1645	GCATGAAGACCAAGACGTATCAGGTGGCCCCACATGAAGACAAATCGGATCAAG	1704
QY	938	ACCATGAATGAAGTTATACTGGTATAGGATAATAAAATGTACGCCCTGGGAAAAGTCA	997
Db	1705	CTGATGAACGAATTTCTCAATGGGATCAAGTGCTTAAAGCTTTTATGCTGGGAGCTGGCA	1764
QY	998	TTTTCAAATCTTATTACCAATTTGAAAGAGGAGATTTCACAGATTCTCAGAAGTTCC	1057
Db	1765	TTCAAGGCAAGGTGCTGGCCATCAGCGCAGGAGGAGCTGAAGTGCTCAAGAAGTCTGCC	1824
QY	1058	TGCTCAGGGGAGTGAATTTGGCTTCGTTTTTTCAGTGCAAGCAAAATCATCGTGTGTTGTG	1117
Db	1825	TACCTGTACGCGTGGGCACCTTTCACCTGGGTCTGTACAGCCCTTCTGTGTGCCCTTGTGC	1884
QY	1118	ACCTTCCACCACTTACGTGCTCTCTCGGCAGTGTGATCATCAGCCGCGTGTTCGTGGCA	1177
Db	1885	ACATTTCCGCTCTACGTGACCATTAACAGAGAACACATCTCTGGATGCCAGACGCTTC	1944
QY	1178	GTACGCTGTATGGGCTGTGGCGTGCAGGTTACCCCT---CTTTCTCCCTTCAGCCATT	1234
Db	1945	GTGCTTTTGGCCTTGTTCACATCTCCGGTTTCCCTTGAACATTCCTCCCATGGTCATC	2004
QY	1235	GAGAGGGTGTACAGGCATCTGCAGATCCGAGATCCAGACCTTTTTCCTACTTTGAT	1294
Db	2005	AGCAGCATCGTGACGCGAGTGTCTCCCTCAAAGCCCTTGAGGATCTTTCTCTCCCATGAG	2064
QY	1295	GAGATATCACAGCGAACCGTCAGCTGCCGTGAGATGTAATAAGATGGTGCATGTGCAG	1354
Db	2065	GACCTGGAACCTCACAGCATCAGC-GACGGCTGTCAAAGACGGCGGGGCAGACAG	2123
QY	1355	GATTTACTTACTGCTTTTGGGATA-----AGCAATCAGAGACCCCACTCTTACAAG	1404
Db	2124	CATCACCGGTGAGGAATGCCACATTCACCTGGCGCCAGGAGCACCTCCCACTGAATGG	2183

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 REGISTRATION NUMBER: 39,539
 REFERENCE/DOCKET NUMBER: Q1546
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 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5011 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 196..4788
 US-08-463-092B-1

Query Match 9.2%; Score 390.4; DB 1; Length 5011;
 Best Local Similarity 47.1%; Pred. No. 3.7e-102;
 Matches 1659; Conservative 0; Mismatches 1786; Indels 77; Gaps 12;

QY 518 TACGCCATGCCACGCTGCTGACTTTTGCACGCTCATTTTGGCTATACATCACTTA 577
 DB 1285 TACTTACACCGTGTGCTGTTTGTACCTGCTGCGACACCTCGTGGTGCACAG 1344
 QY 578 TATTTTATCACGCTTACGCTGCTGGGAGGAGTACAGGATGAGCATGATGATGAT 637
 DB 1345 TACTTCCACATCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 1404
 QY 638 TATCGAAGGACCTGCTGCTTGTAGTACATGCGCATGGGAGGAGGAGGAGGAGG 697
 DB 1405 TATCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1464
 QY 698 GTCAATCTGCTGCTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 757
 DB 1465 GTCAATCTGCTGCTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1524
 QY 758 CTGTGGGAGGACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 817
 DB 1525 ATCTGGTACGCCCCCTGCAAGTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1584
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 DB 1585 CTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1644
 QY 878 GGAAGTGTGCTCACTGAGGAGTAACTGCAACTTTCACGATGCGGAGGATCAGG 937
 DB 1645 GCGATGAAGACCAAGACGATATCAGGTGGGCCCCACATGAAGAGCAACATCGG 1704
 QY 938 ACCATGAATGAAGTATACTGGTATPAGGATATAAATAATGACGCTGGGAAAGTCA 997
 DB 1705 CTGATGAACGAAATCTCAATGGGATCAAGTCTAAAGCTTTATGCTGGGAGCTG 1764
 QY 998 TTTTCAATCTTATTAACAAATTTGAAAGAGGAGGATTTCCAGATTTCTGAGAAT 1057
 DB 1765 TTCAAGGACAAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1824
 QY 1058 TGCTCAGGGGGATGAATTTGGCTTCTGTTTTCAGTGAAGCAAAATCATGTTTGTG 1117
 DB 1825 TACCTGTACGCGTGGGACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1884
 QY 1118 ACCTTACACCACTAGTGTCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1177
 DB 1885 ACATTTGGCGTCTACGTGACCATTTGACGAGAAACAACTCTGGATGCCAGACGCT 1944
 QY 1178 GTGACCTGTATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1234
 DB 1945 GTGCTTTGGCGCTGTTTCAACATCTCTCCGCTTCCGCTTCCGCTTCCGCTTCC 2004
 QY 1235 GAGAGGCTGTCAGAGGCAATCTGACATCCGAAAGATCCAGACCTTTTGTACTTGA 1294

DB 2005 AGCAGCATCTGTGAGGCGAGTGTCTCCCTCAAACGCTTGAGGATCTTTCTCTCC 2064
 QY 1295 GAGATATCACAGCGCAACCGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1354
 DB 2065 GAGCTGGAACTGACAGCATGCTGAGC-GACGGCTCTCAAAGACGCGGGGCGCAAG 2123
 QY 1355 GATTTTACTGCTTTTGGGATA-----AGGCATCAGAGACCCCACTTACAAAG 1404
 DB 2124 CATCAGCTGAGGAATGCCATTCACCTGGGCGAGGAGGACCTCCACACATGAATGG 2183
 QY 1405 CCTTTCTCTTACTCTCAGACCTGCGGAATTTAGTGTGCTGCTGCTGCTGCTGCTGCT 1464
 DB 2184 CATCAGCTTCTCCATCCCGAAGGTGCTTTGGTGGCGGTGGTGGGCGGAGTGGCTG 2243
 QY 1465 GAAGTCATCACTGTTAAGTGCCTGGGGAATTTGGCCCAAGTCAAGGCTGGTCTAG 1524
 DB 2244 AAGTTGCTCCTGCTCTCAGCCCTCTTGGCTGAGATGGAAGTGGAGGCGACGTGGC 2303
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 DB 2304 TATCAAGGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2363
 QY 1585 GACTAATATTTATTTGGGAGAAATATGAAAAGAACGATATGAAAAGTCAATAAGGC 1644
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 QY 1645 TTGTGCTCTGAAAAGGATTTACAGCTGTTGGAGGATGCTGCTGCTGCTGCTGCTGCTG 1704
 DB 2424 CTGTGCTCCTCTCCAGACCTGGAATCTCTGCCAGTGGGATCGGACAGAGATGGCG 2483
 QY 1705 TCGGGGAACCGCTGAGTGGAGGCGAGAAAGACGCGGTAAACCTTGCAGAGCAGTGT 1764
 DB 2484 GAAGGCGTGAACCTGCTGCTGGGAGACAGACGCGGTGAGCCTGGCCCGGCGTGA 2543
 QY 1765 TCAAGATGCTGACATCTCTCTGGAGATCTCTCAGTGCAGTACGATGCGGAGTTAG 1824
 DB 2544 CTCAAGCTGACATTTACCTCTTCGATGATCTCCCTCTCAGCAGTGGATGCCATGG 2603
 QY 1825 CAGACACTTGTGCACTGTATTTGTCAA-----ATTGTGATGAGAAGTCAACAT 1878
 DB 2604 AAACACATCTTTGAAATCTGATTTGGCCCCAAGGGATGCTGAAGAACAGACGCGAT 2663
 QY 1879 TTTAGTACATCAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1938
 DB 2664 CTTGGTCAACGACAGCATGAGTACTTGGCGCAGGTGGACGCTCATCTGCTGCTGCTG 2723
 QY 1939 TGTAAATGCTGAGAGGGGACTTACACTGAGTCTCTTAAATCTGCTATAGATTTGG 1998
 DB 2724 CGCAGATCTCTGAGATGGCTCTCTACAGGAGTCTGCTGCTGCTGCTGCTGCTGCT 2783
 QY 1999 CTCCTTTTA-----AAGAAGGATAATGAGGAAATGAGGAAATGAGGAAATG 2039
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 DB 2904 GGACGTGAGGAGGAGCACTGCGACAGCAGCTCAGACGCTCTCTCTCTCTCTCTCTCT 2963
 QY 2160 TCCCAG-----TTACACTATCAGAGGAAACCTCTCTGA-----AGGAAAGTTGGTTT 2209
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 QY 2210 CAGGCTATGAAGATTTACTTCAGAGTGGTGTCTGCTGCTGCTGCTGCTGCTGCTGCT 2269
 DB 3024 GACCTGGAAGCTGATGAGGCTGACAGGCGCAGACAGGCGAGGTCAGGCTTTCCGCTGA 3083
 QY 2270 CTCCTAAACACTCAGCTCAGGTTGCCTATGTGCTTCA-----AGATTGCTGGCTTCAT 2324
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QY 2325 ACTGGGCAACAAACAAATGCTAAATGTCACTGTAATAGGAGGAGAAATGTAAACG 2384
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QY 2385 AGAAGCTAGATCTTAACGTGTAAGGAAATTAATCAGGTTTAAGTGTAGCTACCGGTC 2444
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QY 2445 TTTTGGCATAGCAAGATCTCTATTG-----GTATTCTACGCTCCTTCTTAA 2490
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QY 2491 CTCCTTCAAACTTTGCAACAAATGTTGAGTCAATTTGAAAGTCTCCGTTATTA 2550
DB 3324 GGTCTCCGCTGTCTGCAAGTGTGCTGACAGACATCTCTCCAGGAGCTGGACATGAGCTT 3383
QY 2551 CTTTGATGAATCAATAGGAAGAAATTTAATCGTTCTTCAAGACATTTGGACACTT 2610
DB 3384 CTTTGAGCGGACCCAGTGGAACTGGTGAACCGCTTCTCCAGGAGCTGGACACAGT 3443
QY 2611 GGATGATTGCTGCGGCTGACCTTTTATGATTTTCCAGACATTTGCTACAAGTGGTTGG 2670
DB 3444 GGACTCCATGATCCCGAGGTATCAAGATGTTCAAGGCTCCCTGTTCAAGCTATGG 3503
QY 2671 TGTGCTCTGTGCGTGTGGCGTGAATCTTGGATGCAATACCTTTGGTTCCCTTTGG 2730
DB 3504 TGCCTGCATCTGCTGCTGCGCACGCCATCCGCCATCATCATCCGCCCTTTGG 3563
QY 2731 AATCATTTTCAATTTTCTCGCGATATTTTGGAAAGCTCAAGAGATGTAAGCGCT 2790
DB 3564 CCTCATCTACTTCTTCTGCAAGAGTCTAGTGGCTTCTCCCGGAGCTGAAGCGCT 3623
QY 2791 GGAATCTACAACCTGGAAGTCCAGTGTCTTCCACCTTGTCTCTCCAGGGCTCTG 2850
DB 3624 CGAGTCGCTGACCGCTCCCGCTCTATCCCATTTCAACAGACCTTGTGGGGGTGAG 3683
QY 2851 GACCATCCGGCATACAAGAGAGAGAGGTGTGAGAACTGTTGATGACACACAGGA 2910
DB 3684 CGTCAATCGAGCTTCGAGGAGCAGAGCGCTTCAATCCACAGAGTGAAGTGA 3743
QY 2911 TTTACATTCAGAGCTTGGTCTTGTGTTTTCACACAGTCCCGTGTGGCTCGCTGCT 2970
DB 3744 CGAAGACAGAGGCTTATACCCAGCATCTGTGCGCAACAGGTGGCTGGCGCTGCGCT 3803
QY 2971 GGATGCCATCTGTGCATGTTGTTCATCATCTGTTGCTGCTTGGTCCCTGATTTGCAAA 3030
DB 3804 GGAGTGTGGGCAACTGCATCTGTTGTTGCTGCTGCTTGGGTGATCTCCAGGCA 3863
QY 3031 AACTCTGGATCCGGGAGGTGTTGGCACTGTCTCTATCCCTCAGCTCATGGGAT 3090
DB 3864 CAGCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3923
QY 3091 GTTTTCAGTGGTGTGTCACAAAGTGTGAAGTGTGAGATATGATGATCTCAGTAGAAG 3150
DB 3924 CTTGAATGGCTGTTGGATGTCTCATCTGAAATGAAACCAACATCTGTCGCTGGCGTGGAG 3983
QY 3151 GGTCAATTAATACAGACCTTTGAAAGAGACCTTTGGGAA--TATCAGAAACGCC 3207
DB 3984 GCTCAAGAGATTTACAGAGACTGAGAGGAGCGCCCTGGCAATTCAGGAGACACGTC 4043
QY 3208 ACCACAGCCTGGCCCCATGAAGAGTGTATTAATCTTTGACAATGTGAATTTATGATAC 3267
DB 4044 GCCCAGCAGCTGGCCCCAGTGGCGGAGTGAATTCGGAACACTGCTGCTGCTGCTGCTGCT 4103
QY 3268 TCCAGTGGGCTCTGTTACTGAGCATCTGACAGCATCTATTAAATCAACAGAAAGGT 3327
DB 4104 AGAGACCTTGGACTTCGTTCTCAGGACATCAATGTCAAGATCAATGGGGAGAAAGGT 4163
QY 3328 TGGCATTTGGGAAGACCGGAGCTGGAAAGTTCCTCTCATCTCAGCCCTTTTATGAT 3387
DB 4164 CGGCATCTGGGGGAGGAGCTGGGAAGTCTGCTCCTGACCTGGCTGCTTATTTCCGAT 4223

QY 3388 GTCAGA---ACCGAAGGTAAAAATTTGGATTGATAAGATCTTGACAACTGAAATTTGGACT 3444
DB 4224 CAACGAGTCTGCCGAGGAGAGATCATCATGATGGATCAACATCCCAAGATCGGCT 4283
QY 3445 TCAGGATTTAAGGAAGAAATGCAATCATACCTCAGGAACCTGTTTGTTCATCTGGAAC 3504
DB 4284 GCAGGACTCTCCGTTCAAGATCACCATCATCCCGAGGACCTGTTTGTTCGCGTTC 4343
QY 3505 AATGAGAAAAACCTGATCCCTTTAAGGAGACACACGATGAGGAATCTGGAATGCTT 3564
DB 4344 CTCCGAATGAACCTGGCCCATTCAGCCAGTACTCGGATGAAGAAGTCTGGACGCTCC 4403
QY 3565 ACAAGAGGTACAACTTTAAAGAAACCATTTGAAGATCTTCCCTGGTAAATGGATGTAATT 3624
DB 4404 GGAGCTGGCCCACTCAAGGACTTCGTCTCAGCCCTTCTTGACAGCTAGACCATGAATG 4463
QY 3625 AGCAGATCAGGATCAATTTTGTGTTGACAAAGACAACTGTTGCTGCTGCTGCTGCTGCTGCT 3684
DB 4464 TGCAGAGGCGCGGAGAACCTCAGTGTGGGCGAGCCAGCTTGTGTGCTAGCCCGGC 4523
QY 3685 AATCTCAGAAAAATCAGATATTTGATTTGATGAAGCAGCGCAATGTGGATCCAAG 3744
DB 4524 CTGCTGAGGAAGACGAGATCTTGTGTTGATGAGGCGACCGAGCCGTGGACCTGGA 4583
QY 3745 AACTGATGATTTAATACAAAAAATCCGGGAGAAATTTGCCACTGACCGGTGCTAAC 3804
DB 4584 AAGGAGACCTCATCCAGTCCACCATCCGACACAGATTCGAGGACTGACCGCTCTCAC 4643
QY 3805 CATTCACACAGATTTGAACACCATTTATGACAGCAGCAAGATTAATGTTTATGATTCAGG 3864
DB 4644 CATCGCCCAAGGCTCAACACCATCATGACTACACAAGGCTGATGCTTTGGACAAGG 4703
QY 3865 AAGACTGAAGATATGATGAGCCGTATGTTTGTGCTGCAAAATAAGAGAGCCCTATTTTA 3924
DB 4704 AGAATCCAGGAGTACGGCGCCCATCGGACCTCTCTGACAGAGAG---GTCTTTCTA 4760
QY 3925 CAAGATGTGCAACAACTGGCAAGGCAAGCGCGCTGCTGCT 3966
DB 4761 CAGCATGGCAAGAGCGCGCTGTTGTTGATGAGGCGACCGAGCT 4802

RESULT 11
US-08-462-109A-1
; Sequence 1, Application US/08462109A
; Patent No. 5982875
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462.109A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966.923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029.340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141.893

Qy	518	TAGCCCTATGCCACGCTGCTGACTTTTTCAGCAGCTCATTTTGGCTATACTGTCATCACTTA	577
Db	1285	TACTTCTACACCGTGTGCTGTTGTTCATCGCTGCCCTGCAGAGCCCTCGTGTCTGCACGAC	1344
Qy	578	TATTTTATCACGCTTCAGTGTGCTCGGGATGAGGTTTACAGTAGCCATGTGCCATPATGATT	637
Db	1345	TACTTCACATCTGCTTCGTACAGTGGCATGAGGATCAAGACCGCTGTCAATTTGGGCGTGC	1404
Qy	638	TATCGGAGGCCACTTCGCTTTAGTAACTATGCCATGGCCATGGGAAGACAACACAGGCCACATA	697
Db	1405	TATCGGAGGCCCTTGGTATCACCNAATTCAGCCAGAAATCCTCCACGGTGGGGAGATT	1464
Qy	698	GTCAATCTGCTGTCCAAATGATGTGAACAAGTTTGATCAGGTGCACAGTGTCTTACACTTC	757
Db	1465	GTCAACCTCATGTCTGGACGCTCAGAGGTTTCATGGACTTGGCCACGTACATTAACATG	1524
Qy	758	CTGTGGCAGGACCACTGCAGCGATCGGAGTACTGCCCTACTCTCGATGGAGATAGGA	817
Db	1525	ATCTGTACGCCCCCTCGAAGTCATCTTCTCTACCTCCCTGTGGCTGAATCTGGCG	1584
Qy	818	ATATCTGCTTGTCTGGGATGGCAGTCTTAATCATCTCCCTGCCCTGCAAAAGCTGTTTT	877
Db	1585	CTTCCGCTCCTGGCTGGATGGCGTGATGGTCTCTATGTGCCCCGTCAATGCTGTGATG	1644
Qy	878	GGGAAGTTGTTCTCATCTAGGAGTAAACTGCACTTTCACGGATGCCAGATCAGG	937
Db	1645	GCATGAAGACCAAGACGCTATCAGGTGGCCACATGAAGACAAAGACAATCGGATCAAG	1704
Qy	938	ACCATCAATGAAGTTATTAAC TGGTATAAGGATAATAAAATGTACGCCCTGGAAAACTCA	997
Db	1705	CTCATCAACGAATCTCAATGGGATCAAGTGTAAAGCTTTATGGCTGGGAGCTGGCA	1764
Qy	998	TTTTCAAAATCTTATTACCAATTTGAGAAGAGGAGATTTTCCAAAGATCTCTGAGAAGTTCC	1057
Db	1765	TTCAAGGACAAGTGCTGGCCATCAGCAGGAGAGAGCTGAAGGTGCTGAAGAAGCTCTGCC	1824
Qy	1058	TGCTCAGGGGATGNAATTTGGCTTCGTTTTTCAGTCAAGCAAAATCATCGTGTGTGTG	1117
Db	1825	TACCTGTACGCGTGGGCACCTTCACTTGGGTCTGCAGCGCCCTTTCCTGGTGGGCTGTGTC	1884
Qy	1118	ACCTTCCACCACCTTAGTGTCTCTCGGCAGTGTGATCATCAGCCAGCCGCGTGTCTGTGGCA	1177
Db	1885	ACATTTTCCGCTCTACGTGACCATTGACGAGAACAACATCTCGATGCCAGACAGCCTTC	1944
Qy	1178	GTGACGCTGTATGGGGCTGTGGGCTGACGGTTACCTT---TCTTCTCCCTCAGGCATT	1234
Db	1945	GTGCTTTGGCCCTTGTCAACATCTCCGGTTTCCCTTGAACATCTCCCATGGTGCATC	2004

CLASSIFICATION: 424
PRIOR APPLICATION DATA: 08/029,340
FILING DATE: 8-MAR-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA: 08/141,893
FILING DATE: 26-OCT-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA: 08/407,207
FILING DATE: 20-MAR-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: Q1551
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 196..4788
US-08-460-907B-1

Query Match 9.2%; Score 390.4; DB 2; Length 5011;
Best Local Similarity 47.1%; Pred. No. 3.7e-102;
Matches 1659; Conservative 0; Mismatches 1786; Indels 77; Gaps 12;

QY 518 TACGCTATGCCCGGTGCTGACTTTTGGCAGCTCATTTTGGCTATACCTGATCATTCA 577
DB 1285 TACTTCTACACCGGTGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1344
QY 578 TATTTTATCACGCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 637
DB 1345 TACTTCCACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1404
QY 638 TATCGAAGGACCTTCTGCTTGTAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 697
DB 1405 TATCGAAGGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1464
QY 698 GTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 757
DB 1465 GTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1524
QY 758 CTGTGGCAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 817
DB 1525 ATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1584
QY 818 ATATCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 877
DB 1585 CTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1644
QY 878 GGAAGTTGTTCTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 937
DB 1645 GCATGAAGACCAAGAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1704
QY 938 ACCATGAATGAAGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 997
DB 1705 CTGCTGACCAAGTTCTCAATGGATCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1764
QY 998 TTTTAAATCTTATACCAATTTGAGAAAGAGGATTTTCCAAAGATTTCTGAAAGTTCC 1057
DB 1765 TTCAAGGACCAAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1824
QY 1058 TGCTCAGGGGATGAATTTGGCTTCGCTTTTTCAGTCAAGCAAAATCATCGTTTGTG 1117

DB 1825 TACCTGTGAGCGGTGGGCAACCTTACCTGGGTCTGACGCCCTTCTGCTGGCTTGTGC 1884
QY 1118 ACCCTTACACCTAGTGTCTCTCGGAGTGTGATCACAGCCAGCGGTGTTCTGGGCA 1177
DB 1885 ACATTTGCGGTCTAGTGTACCATTTGACGAGAACACATCTCTGATGCGGAGAGCTTTC 1944
QY 1178 GTGAGCTGTATGGGGCTGTGGGCTGACGGTTTACCTT---CTTCTTCCCTCAGCAAT 1234
DB 1945 GTGTCTTTGGCTTGTTCACATCTCTCGGTTTCCCTTGAACATTTCTCCCATGCTCATC 2004
QY 1235 GAGAGGTGTGAGAGGCAATGTGATCCGAGATCCGAGACCTTTTGTACTTGTAT 1294
DB 2005 AGCAGATCTGTCAGGCGAGTGTCTCCCTCAACGCTTGAAGATTTCTCTCCCATGAG 2064
QY 1295 GAGATATCACAGCGCAACCTGTCAGTCCGTCAGATGTGTAAGAAATGTTGATGTGAG 1354
DB 2065 GAGTGGAACTGACAGCATCGAGC-GACGGCTCTCAAGACGCGGGGCGACGAACAG 2123
QY 1355 GATTTTACTGCTTTTGGGATA-----AGCATCACAGACCCCAACTTCTACAAGG 1404
DB 2124 CATCACGCTGAGGAATGCCACATTCACCTGGCCAGAGGACCTTCCACACTGAATGG 2183
QY 1405 CCTTTCCTTTACTGTGACACCTGGGAAATTTAGTGTGCTGCTGCTGCTGCTGCTGCTG 1464
DB 2184 CATCACCTTCTCCATCCCGAAGGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2243
QY 1465 GAAGTCATCACTGTGTAAGTCCGTCGCGGAAATTTGCCCCCAAGTACAGGGCTGCTGAG 1524
DB 2244 AAGTTGCTCCTGCTCTCAGCCCTTGTGGCTGAGATGGACAAAGTGGAGGGGCGACGGC 2303
QY 1525 CGTGCATGGAAAGAAATTTGCTATGCTCTCAGCAGCGCTGGGTGTTCTCGGAACTCTGAG 1584
DB 2304 TATCAAGGGCTCCGCTGCTATGTGCCACAGCGGCTGGATTCAGATGATTTCTCTCG 2363
QY 1585 GAGTAATATTTTATTTGGGAAAGAAATATGAAAAGAACAGATATGAAAAGTCAATAAGGC 1644
DB 2364 AGAAACATCTCTTTTGGATGCTAGCTGGAGGAACCATATTACAGTCCGCTGATACAGGC 2423
QY 1645 TTGTGCTGTGAAAAGGATTTACAGCTGTTCGAGGATGCTGCTGCTGCTGCTGCTGCTGCTG 1704
DB 2424 CTGTGCTCCTCCACAGCTGGAAATCTCTCCAGTGGGATCGGACAGAGATTGGCGA 2483
QY 1705 TCGGGCAACCACTGATGCTGAGGCGAGAAAGCACGGTAAACCTTTCAGAGAGAGTGA 1764
DB 2484 GAAGGCGTGAACCTGCTGCGGACAGACAGCGGCTGAGCTTGGCCCGGCGTGA 2543
QY 1765 TCAAGATGCTGACATCTATCTCTGGAGGATCTCTCAGTGCAGTGTAGATCGGAAAGTTAG 1824
DB 2544 CTCCAAGCTGACATTTACCTCTTCGATGATCCCTCTCAGCAGTGGATGCCATGTGGG 2603
QY 1825 CAGACCTGTTCGAACCTGTATTTGTCAA-----ATTTTGCATGAGAGATCACAAT 1878
DB 2604 AAACACATCTTTGAAAATGTGATTTGGCCCCAAGGGATGCTGAAGAAACAAGACGCGAT 2663
QY 1879 TTTAGTGACTCATCAGTTGCTGCTACCTCAAGCTGCAAGTCTGATTTCTGATTTGAAAGA 1938
DB 2664 CTGTGTCAGCAGCAGCATGACTACTTGGCCAGCTGGACGCTCATCTGCTGATGAGTGG 2723
QY 1939 TGGTAAATGTCAGAGAGGAGCTTACATGAGTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1998
DB 2724 CGCAAGATCTCTGAGATGGGCTCTACCAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2783
QY 1999 CTCCTTTTA-----AAGAGGATAATGAGAAAGTGAACAACTC 2039
DB 2784 TGAGTTCTCTGCTACCTATGCTCAGCAGACAGAGCAGGATCGAGAGGAGACGGGGT 2843
QY 2040 CAGTTCAGGAACCTCCACACATTAAGGAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2099
DB 2844 CACGGGCTCAGCGTCCAGGAGGAGGAGCAACAAATGAGAGATGGCATGCTGCTGCTG 2903
QY 2100 AACATCTTCTAGACCTCTCTTGAAGATGCTGCTGAGAGGCAAGATACAGAGATG 2159

Db 2904 GGACAGTGCAGGAGCAACTGCAGAGACAGCTCAGACGCTCTCTCTCTATAGTGGGA 2963
QY 2160 TCCAG-----TTACATATCAGAGGAGAACCGTTCTGA-----AGGAAAGCTGGTTTT 2209
Db 2964 CATCAGAGGACCAACACAGACACCGAGAACTGCAGAAAGCTGAGGCCAAGAAGAGGA 3023
QY 2210 CAGGCTATAAGAAATTAATTCAGAGCTGGTGTCTACTGATGTCTTCAATTTTCCTTAT 2269
Db 3024 GACCTGGAAGCTGAGGAGCTGCAAGGCGCAGAGCGAGGCTTCCGTTGTA 3083
QY 2270 CTCCTAACACTGCAGCTCAGTTCGCTATGTGCTTCA-----AGATGGTGGCTTTTAT 2324
Db 3084 CTGGACTACATGAAGGCATCGGACTCTTCATCTCTCTCTCTCAGCATCTTCTCTTTTCA 3143
QY 2325 ACTGGCAACAAACAAGATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCG 2384
Db 3144 GTGTAAACATGTGTCGGCTGGCTTCCAACTATTGGCTCAGCTCTGGACTGATGACCC 3203
QY 2385 AGAAGCTAGATCTTAACCTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTC 2444
Db 3204 CATCTCAACGGGACTCAGGAGCACAGAAAGTCCGGCTGAGCGTCTATGGAGCCCTGGG 3263
QY 2445 TTTTGGGATAGCAAGATCTTATTTG-----GTATCTAGCTCCTTGTTHAA 2490
Db 3264 CATTTCAAGAGGATCGCGCTGTTTGGCTACTTCCATGCGCGTGTCCATCGGGGGATCTT 3323
QY 2491 CTTCTCACAACTTTGCCAACAAATGTTTGAAGTCTTGAAGTCTGAGTCAATTTAT 2550
Db 3324 GGTCTCCCGCTCTGTCAGCTGGAGCTGTCACAGACATCTTGGCTGAGCTTCCATGAGCTT 3383
QY 2551 CTTTGTAGAAATCCAAAGGAAGAAATTTAAATGTTTCTCCAAAGACATTTGGACAT 2610
Db 3384 CTTTGGCGGACCCCGAGTGGAACTGTTGAACCGTCTTCCAAAGGAGCTGGACAGT 3443
QY 2611 GGATGATTTGCGCGCTGACGTTTGTAGATTTCAATTCAGACATTTGCTACAGTGTGG 2670
Db 3444 GGACTCCATGATCCGGAGGTCATCAAGATGTTTCACTGGCTCTCTTCAAGCTCATTTG 3503
QY 2671 TGTGCTCTGTCGCTGGCGTGTATCTTGGATCGCAATACCTTGTTCCTCCCTTGG 2730
Db 3504 TGCTGCTATCTGTTATCTCTGCGCACGCGCCATCGCGCGCATCATCTCCGCGCTTGG 3563
QY 2731 AATCATTTTCAATTTTCTTCGCGGATATTTTGGAAAGCTCAAGAGATGTGAAGCGCT 2790
Db 3564 CCTCATCTACTTCTGCTCCAGAGTTCTACGTGGCTTCTTCCCGGAGCTGAAGCGCT 3623
QY 2791 GGAATCTAAGCTGGAGTCCAGTGTTCCTCCACTTGTCTCTCTCCAGGGCTCTG 2850
Db 3624 CGAGTGGTCAAGCGCTCTCCCGCTTATTTCCATTTCAAGAGACCTTGTGGGGTCA 3683
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QY 3091 GTTTCAGTGTGTGTCGAAAGTCTGAAGTTGAGATATGATGATGATCTCAGTAGAAG 3150
Db 3924 CTTGAATGCTGGTTCGGATGTCATCTGNAATGGAACCAACATGTCGCGCTGGAGAG 3983
QY 3151 GGTCTATTGAATACAGACCTTTGAAAGAAAGACCTTGGAA---TATCAGAAAGCC 3207
Db 3984 GCTCAAGGAGTATTCAGAGACTGAGAGGAGGCGCTTGGCAAAATCCAGGAGACAGCTCC 4043

QY 3208 ACCACAGCTGCCCCATCAAGAGTGTAAATCTTTGCAATGTGAATCTCATGTACAG 3267
Db 4044 GCCACAGCTGCCCCAGTGGCGGAGTGGAAATTCGGAACTACTGCTGGCTACCG 4103
QY 3268 TCCAGTGGCTCTGCTGTAAGCATCTGACAGCACTCAATTAATCAAGAAAGGT 3327
Db 4104 AGAGGACCTGGCTGCTTCTCAGGCACATCAATGTCAGATCAATGGGGGAGAAAGGT 4163
QY 3328 TGCGATTTGGGAAGAACCGAGCTGGAAGTTCCTTCATCTCAGCCCTTTAGATT 3387
Db 4164 CGGATCTGGGGGAGCGGAGCTGGAGTCTCCCTGACCTGGCTTATTCGGAT 4223
QY 3388 GTCAGA---ACCCGAAGTAAATTTGGATTGATAAGATCTTGACAACTGAAATTTGACT 3444
Db 4224 CACAGTCTGCCGAGGAGAGATCATCTGATGSCATCAACATGCCCAAGATCGCCT 4283
QY 3445 TCAGATTTAAGGAAGAAATGTCAATCATACCTCAGGAACCTGTTTGTCTACTGGAAC 3504
Db 4284 GCACGACCTCGCTTCAAGATCACCATCATCCCCAGGACCTGTTTGTTCGGGTT 4343
QY 3505 AATGAGAAACCTCGATCCCTTTAAGGAGCACGAGTGAAGTGTGGATGCTT 3564
Db 4344 CCTCCGAATGAACCTGGACCCATTCAGCCAGTACTCGGATGAAGAGTCTGGACGCTCC 4403
QY 3565 ACAAGAGGTACAACTTTAAAGAAACCATTTGAAGATCTTCTGTTAAATGATGACTGAAT 3624
Db 4404 GGAGTGGCCCTCAGGACTTCTGTGAGCCCTTCTGACANGCTAGACCATGAATG 4463
QY 3625 AGCAGATCAGGATCAATTTTGTGTTGACAAAGACAACTGTTGCTTGGCAGGGC 3684
Db 4464 TGCAGAGGCGGGAGAACCTCAGTGTGGGCGAGCGCAGCTTGTGCTAGCCCGGC 4523
QY 3685 AATCTCAGAAATACAGATTTGATTTATGATGAGCGACGCAATCTGGATCCAAG 3744
Db 4524 CTTGCTGAGGAAGCAAGATCTTGTGTTGATGAGCCACGCGCTGGACCTTGA 4583
QY 3745 AACTGATGATTAATACAAAAAATTCGGGAGAAATTTGCCACTGCACTGCTTAAC 3804
Db 4584 AACGAGGACCTCATCCAGTCCACCATCCGACACAGTTCGAGGACTGCACTCCCTC 4643
QY 3805 CATTCACAGATTTGAACACCATTTATGACAGGACAGATATGTTTGTAGTTCAGG 3864
Db 4644 CATCGCCACCGCTCAACACCATCATGAGTACTACAAAGGCTGATCGCTTGGCAAGG 4703
QY 3865 AAGACTGAAGAATATGATGAGCGGTATGTTGCTGCAAAATAAAGAGAGCTTATTTA 3924
Db 4704 AGAATCCAGAGTACGCGCCCTCATCGGACCTCTCTCGACAGAGAG---GTCCTTTCTA 4760
QY 3925 CAAGATGGTGCAACAACTGGGCAAGGAGGAGCGCTGCGCT 3966
Db 4761 CAGCATGGCCAAAGACGCGCTTGTGTCAGCCCAAGCT 4802

RESULT 13

US-08-463-179A-1
; Sequence 1, Application US/08463179A
; Patent No. 6001563
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING CHEMOSENSITIZERS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,179A
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PQI-002CPB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..4788
; US-08-463-179A-1

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Query Match          9.2%; Score 390.4; DB 3; Length 5011;
Best Local Similarity 47.1%; Pred. No. 3.7e-102;
Matches 1659; Conservative 0; Mismatches 1786; Indels 77; Gaps 12;

QY 518 TAGCGCATATGCCAGCGTGTGCTACTTTTGCACGCTCAATTTTGGCTATACCTGCATCACATTA 577
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1285 TACTTCTACACCGCTGCTGCTGTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1344

QY 578 TATTTTATCAGTTCAGTGTGCTGGGATGAGGTACGAGTACGACATGTCACATATGATT 637
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1345 TACTTCCACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1404

QY 638 TATCGGAAGGCACTTCTGCTTAGTAACATGGCCATGGGGAAGCAACACACAGCGCAGATA 697
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1405 TATCGGAAGGCGCTGGTGATCACCATTTCAGCCAGAAATCTCCACGGTGGGAGATT 1464

QY 698 GTCAATCTGCTGCTCAATGATGTGAACAAGTTTGTATCATAGTGCACAGTGTCTTACACTTC 757
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Db 1465 GTCAACCTCATCTGCTGACGCTCAGAGGTTCTGAGGATCAAGACCGCTGTCAATTGGGCTGTC 1524

QY 758 CTGTGGGAGGACCACTGCTGAGCGGATCGCAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCT 817
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1525 ATCTGTGAGCGCCCTGCAAGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1584

QY 818 ATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 877
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Db 1585 CTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1644

QY 878 GGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 937
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1645 GCGATGAAGCAACCAAGACGTTATCAGTGGGCCACATGAGAGCAAAAGACAAATCGGATCAAG 1704

QY 938 ACCATGAATGAAGTTATTAAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGT 997
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1705 CTGATGAAGCAAAATCTCAATGGGATCAAGTGTCAAGGCTTATGCTGCTGCTGCTGCTGCTG 1764

QY 998 TTTTCAAAATCTTTTACCAATTTGAGAGAGGAGGATTTCCAAAGATTCTGAGAGTTCC 1057
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QY 1058 TGCCTCAGGGGATGAAATTTGGCTTCGTTTTCAGTCAAGCAAAATCATCGTGTGTTGTG 1117
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Db 1825 TACTGTACAGCGTGGCAGCTTTCACCTGGTCTGACGCGCTTTCGTTGGTGGCTTGTGC 1884

QY 1118 ACCTTACACACCTACGTGCTTCGCGCAGTGTATACAGCCAGCCGCTGTTGCTGGCA 1177
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1885 ACATTTGCGCTCTACGTGACCATTTGACGAGAACAACTCTGATGCTGACAGACGCTTC 1944

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Db 1945 GTGCTTTGGCCTTGTTCACATCTCCGCTTCCCTGAACATCTCCCATGGTCTATC 2004

QY 1235 GAGAGGCTGTACAGGCAATCTGTCAGCATCCGAAGATCCAGACCTTTTTCCTACTTGTAT 1294
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QY 1405 CCTTCTCTTACTGTACAGCTGGCGAATTTGTAGCTGTGCTGCGCCCTGCGGAGCAGG 1464
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Db 2304 TATCAAGGCTCGTGGCTGATGTGCCACAGCAGCGCTGGATTCAGAAATGATTTCTCCG 2363

QY 1585 GAGTAATATTTTATTTGGGAAGAAATATGAAAGGAACGATATGAAAGTGCATAAAGGC 1644
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Db 2364 AGAAACATCTTTTGGATGTGCTGAGTGGAGAACCATATTACAGTCCCTGATACAGGC 2423

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Db 2784 TGAGTTCTCTGCTGCTATGCTCCAGCAGCAGAGGAGGAGTGCAGAGAGAGAGCGGGT 2843

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RESULT 14

US-08-461-384B-1

; Sequence 1, Application US/08461384B

; Patent No. 6025473

; GENERAL INFORMATION:

; APPLICANT: Cole, Susan P.C.

; APPLICANT: Deeley, Roger G.

; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS

; STREET: Queen's University at Kingston

; CITY: Kingston

; STATE: Ontario

; COUNTRY: CANADA

; ZIP: K7L 3N6

; COMPUTER READABLE FORM:

QY 2100 AACAACTCTTAGACCTCTCTGAAAGATGGTCTCTGGAGAGCCGAAATACAGAGAAATG 2159
Db 2904 GGACAGTGCAGGAAGCAACTGCAGAGACAGCTCAGCAGCTCTCTCTCTATAGTGGGA 2963
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RESULT 15

US-08-407-207A-1

; Sequence 1, Application US/08407207A

; Patent No. 6063621

; GENERAL INFORMATION:

; APPLICANT: Deeley, Roger G.

; APPLICANT: Cole, Susan P.C.

; TITLE OF INVENTION: ANTIBODIES TO A MULTIDRUG RESISTANCE PROTEIN

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS

; STREET: Queen's University at Kingston

; CITY: Kingston

; STATE: Ontario

; COUNTRY: CANADA

; ZIP: K7L 3N6

QY 2100 AACAAATCTTCTAGACCTCCTTGAAGATGCTGCTGGAGAGCAAGATACAGAGATG 2159
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 Job time : 181.375 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:49:35 ; Search time 102.455 Seconds
(without alignments)
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Title: US-09-647-140A-1

Perfect score: 4231

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 356696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 713392

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4211	99.5	6082	9	US-10-012-896-535
2	4211	99.5	6082	10	US-09-759-143-535
3	4211	99.5	6082	10	US-09-780-669-535
4	4211	99.5	6082	10	US-09-822-827-535
5	3910.2	92.4	6140	9	US-10-012-896-536
6	3910.2	92.4	6140	10	US-09-759-143-536
7	3910.2	92.4	6140	10	US-09-780-669-536
8	3910.2	92.4	6140	10	US-09-822-827-536
9	3739.2	88.4	4395	9	US-10-012-896-1007
10	3738.6	88.4	3786	9	US-10-012-896-1006
11	1218	28.8	1427	10	US-09-925-300-613
12	1045.4	24.7	1074	9	US-10-012-896-824
13	1045.4	24.7	1074	10	US-09-759-143-824
14	1045.4	24.7	1074	10	US-09-780-669-824
15	1045.4	24.7	1074	10	US-09-822-827-824
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17	430.2	10.2	5300	10	US-09-880-107-3373
18	371.2	8.8	4551	9	US-09-938-842A-1674
19	363.8	8.6	4872	9	US-09-938-842A-436

20	360.6	8.5	4545	9	US-09-938-842A-55	Sequence 55, Appl
21	351.8	8.3	4869	9	US-09-938-842A-1392	Sequence 1392, Ap
22	292.6	6.9	5728	10	US-09-917-800A-479	Sequence 479, App
23	274.6	6.5	3069	10	US-09-756-095-105	Sequence 105, App
24	274.6	6.5	6129	10	US-09-782-378A-24	Sequence 24, Appl
25	216.8	5.1	291	9	US-10-012-896-823	Sequence 823, App
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27	216.8	5.1	291	10	US-09-780-669-823	Sequence 823, App
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35	184.4	4.4	1977	10	US-09-880-107-3407	Sequence 3407, Ap
36	184.4	4.4	1977	10	US-09-967-768A-190	Sequence 190, App
37	181.4	4.3	1448	10	US-09-925-299-157	Sequence 157, App
38	124.8	2.9	453	10	US-09-924-035A-271	Sequence 271, App
39	123.2	2.9	697	10	US-09-770-149-277	Sequence 277, App
40	119.6	2.8	380	10	US-09-878-574-1080	Sequence 1080, Ap
41	115.8	2.7	473	10	US-09-560-863-603	Sequence 603, App
42	115.4	2.7	640881	10	US-09-790-988-1	Sequence 1, Appl
43	106	2.5	939	10	US-09-974-300-6511	Sequence 6511, Ap
44	101.6	2.4	1980	10	US-09-841-132-462	Sequence 462, App
45	100.4	2.4	1584	10	US-09-756-095-101	Sequence 101, App

ALIGNMENTS

RESULT 1
US-10-012-896-535
; Sequence 535, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepier, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-535

Query Match 99.5%; Score 4211; DB 9; Length 6082;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4225; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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Db	2591	TGAGTCAATTCGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGAATTTT	2650
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RESULT 2
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; Sequence 535, Application US/09759143

Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-535

Query Match 99.5%; Score 4211; DB 10; Length 6082;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4225; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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DB 791 GAACAAGTTTGTATCAGGTGACAGTGTCTTACACTTCTGTGGGAGGACCACTGCAGGC 850
QY 781 GATCGCAGTACTGCCCTACTCTGGATGAGATAGGAATATCGTGCCTTGTCTGGGATGTC 840
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QY 841 AGTTCTAATCATTTCTCTCCCTTGCAGAGCTGTTTGGGAAAGTCTTCTCATCACTGAG 900
DB 911 AGTTCTAATCATTTCTCTCCCTTGCAGAGCTGTTTGGGAAAGTCTTCTCATCACTGAG 970
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DB 971 GAGTAAAGTGCACACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATAACTGG 1030
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Qy	2521	TGAGTCAATTTCTGAAAGCTCCGGTATTATCTTTGATAGAAATCCNAATAGGAGAATTTT	2580
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DB	3491	GATCTTGACAACCTGAAATTTGGACTTCCACGATTTAAGGAAGAAAATGTCAATCATACCTCA	3550
QY	3481	GGAACTGTTTTGTTTCACTGGAAACAATGAGGAAAAAACCTGGATCCCTTTTAAAGGAGCACAC	3540
DB	3551	GGAACTGTTTTGTTTCACTGGAAACAATGAGGAAAAAACCTGGATCCCTTTTAAAGGAGCACAC	3610
QY	3541	GGATGAGGAACCTGTGAATGCCCTTACAGAGGTACAACTTAAAGAAACCACTTGAAGATCT	3600
DB	3611	GGATGAGGAACCTGTGAATGCCCTTACAGAGGTACAACTTAAAGAAACCACTTGAAGATCT	3670
QY	3601	TCTCGTAAAAATGGATACTGAAATTAGCAGAAATCAGGATCCAAATTTTATGTTTGACAAAG	3660
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RESULT 3

US-09-780-669-535

; Sequence 535, Application US/09780669

; Patent No. US20020051977A1

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; APPLICANT: Houghton, Raymond L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C24

; CURRENT APPLICATION NUMBER: US/09780,669

; CURRENT FILING DATE: 2001-02-09

; NUMBER OF SEQ ID NOS: 943

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 535

; LENGTH: 6082

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-780-669-535

Query Match

Best Local Similarity 99.5%; Score 4211; DB 10; Length 6082;

Matches 4225; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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 DB 3251 AGCACCTTGGGAATATCAGAAACCCGCCACACAGCTTGGCCCCATGAAGAGTGATAAT 3310
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 QY 3301 AGCACTCATTAATACAGAAAAAGTTGGCATTTGTGGGAAGAACCGGAGCTGAAAAAG 3360

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QY 4201 CAAGATCTAGTTTCAATTTGAATATTTCTCCC 4231
Db 4270 CAAGATCTAGTTTCAATTTGAATATTTCTCCC 4300
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RESULT 4

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US-09-822-827-535
; Sequence 535, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
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; CURRENT APPLICATION NUMBER: us/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-535
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Query Match 99.5%; Score 4211; DB 10; Length 6082;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4225; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
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Db 131 GGCCACTCGCGCTGATCAGCGCGACCCCGCGCGCGCGCGCGCGCGCGCGCAAGATGCT 190
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QY 181 GTTCTTCTGTGGTGCATCAATCCCTTCTTTAAATTTGGCCATAAACGGAGATTAGAGGA 240
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QY 241 TGATATGATTCAGTGTGCCAGAGACCGCTCAGACGACCTTTGGAGAGGAGTTGCAAG 300
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QY 301 GTTCTGGGATAAAGAGTTTAAAGAGCTGAGAACTGACGACACAGAGCCCTCTTTAAACA 360
Db 371 GTTCTGGGATAAAGAGTTTAAAGAGCTGAGAACTGACGACACAGAGCCCTCTTTAAACA 430
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QY 421 GGAAAGTCCCAAGTAATCCAGCCCATATTTTGGGAAAAATTTAAATTTTGA 480
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Db 851 GATCGCAGTGAATCCCTTACTCTGATGGAGATAGGAATATCGTCCCTTGTGGATGAC 910
QY 841 AGTTCTAATCAATCTCTGCGCCCTTGCAGAGCTGTTTGGGAAGTTGTTCTCATCTAG 900
Db 911 AGTTCTAATCAATCTCTGCGCCCTTGCAGAGCTGTTTGGGAAGTTGTTCTCATCTAG 970
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Qy	901	GAGTAAAACTGCAACTTTTACGGATGCCAGGATCAGGACCATGAATGAAGTTATAACTGG	960
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	961	TATAAGGATAATAAAAAATGTACGGCTGGGAAAAGTCAATTTTCAAATCTTTATTAACCAATTT	1020
	1031	TATAAGGATAATAAAAAATGTACGGCTGGGAAAAGTCAATTTTCAAATCTTTATTAACCAATTT	1090
Qy	1021	GAGAAAGAGAGATTTTCCAAGATTTCTAGAAAGTTCTTCCCTCAGGGGGATGAATTTGGC	1080
Db	1091	GAGAAAGAGAGATTTTCCAAGATTTCTAGAAAGTTCTTCCCTCAGGGGGATGAATTTGGC	1150
	1081	TTTCGTTTTTTCAGTGCACGCAAAATCATCGTGTTCGTGACACTTTCACCAACCTACGTGCTCCT	1140
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Qy	1141	CGCGAGTGTGATCACAGCAGCGCGGTGTTCGTGGCAGTGACGCTGTATGGGGCTGTGGC	1200
Db	1211	CGCGAGTGTGATCACAGCAGCGCGGTGTTCGTGGCAGTGACGCTGTATGGGGCTGTGGC	1270
	1201	GCTGACGGTTACCCCTTCTTCCCTCAGCCATTCAGAGGGTGTTCAGAGGCAATCGTCAG	1260
	1271	GCTGACGGTTACCCCTTCTTCCCTCAGCCATTCAGAGGGTGTTCAGAGGCAATCGTCAG	1330
Qy	1261	CATCCGAAGAATCCAGACCTTTTTCCTACTTCGATGAGATATCACAGCGCAACCGTCAGCT	1320
Db	1331	CATCCGAAGAATCCAGACCTTTTTCCTACTTCGATGAGATATCACAGCGCAACCGTCAGCT	1390
	1321	GCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGTTTTTGGGATAAAGC	1380
	1391	GCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGTTTTTGGGATAAAGC	1450
Qy	1381	ATCAGAGACCCCAACTCTACAGGGCCTTTCCTTTACTGTCAGACCTGGCGAATTTGTTAGC	1440
Db	1451	ATCAGAGACCCCAACTCTACAGGGCCTTTCCTTTACTGTCAGACCTGGCGAATTTGTTAGC	1510
	1441	TGTGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTTAACTGGCGTCTCGGGGAAT	1500
	1511	TGTGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTTAACTGGCGTCTCGGGGAAT	1570
Qy	1501	GGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGGAAGATTTGCTGTCTCAGCAGCC	1560
Db	1571	GGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGGAAGATTTGCTGTCTCAGCAGCC	1630
	1561	CTGGGTGTTCCTGGGAACCTCTCAGCAGTAAATTTTATTTGGGAGAANAATGCAAAAGGA	1620
	1631	CTGGGTGTTCCTGGGAACCTCTCAGCAGTAAATTTTATTTGGGAGAANAATGCAAAAGGA	1690
Qy	1621	ACGATATGAAAAAGTCATAAAGCCTTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGA	1680
Db	1691	ACGATATGAAAAAGTCATAAAGCCTTGCTCTGAAAAAGGATTTACAGCTGTTGGAGGA	1750
	1681	TGGTGATCTGACTGTATAGGAGATCGGGGAACCGCTGTAGTGGAGGGCAGAAACGACG	1740
	1751	TGGTGATCTGACTGTATAGGAGATCGGGGAACCGCTGTAGTGGAGGGCAGAAACGACG	1810
Qy	1741	GGTAAACCTTGCAGAGCAGTGTATCAAGATCGTGACATCTATCTCCTGCACGATCCTCT	1800
Db	1811	GGTAAACCTTGCAGAGCAGTGTATCAAGATCGTGACATCTATCTCCTGCACGATCCTCT	1870
	1801	CAGTGCAGTGTAGTGGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAAAATTTT	1860
	1871	CAGTGCAGTGTAGTGGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAAAATTTT	1930
Qy	1861	GCATGAGAAAGATCACAAATTTTATGTACTCATCAGTTGCGAGTACCTCAAAGCTGCAAGTCA	1920
Db	1931	GCATGAGAAAGATCACAAATTTTATGTACTCATCAGTTGCGAGTACCTCAAAGCTGCAAGTCA	1990
	1921	GATTCGTGATATTGAAAGATGGTAAAAATGGTGCAGAGGGGACTTACACTGAGTTCCTAAA	1980
	1991	GATTCGTGATATTGAAAGATGGTAAAAATGGTGCAGAGGGGACTTACACTGAGTTCCTAAA	2050

QY	1981	AFCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATAATAGAGAAAGTGAACAACCTCC	2040
DB	2051	AFCTGGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATAATAGAGAAAGTGAACAACCTCC	2110
QY	2041	AGTTCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCA	2100
DB	2111	AGTTCAGGAACCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCA	2170
QY	2101	ACAATCTTCTAGACCTCCTTGAAAGATGGTCTCTGGAGAGCCAAAGATACAGAGAATGT	2160
DB	2171	ACAATCTTCTAGACCTCCTTGAAAGATGGTCTCTGGAGAGCCAAAGATACAGAGAATGT	2230
QY	2161	CCAGTTACACTATCAGAGGAAACCGTTCTGAAGAAAAGTTGGTTTTCAGGCCATATAA	2220
DB	2231	CCAGTTACACTATCAGAGGAAACCGTTCTGAAGAAAAGTTGGTTTTCAGGCCATATAA	2290
QY	2221	GAATTACTTCAGAGCTGGTGCTCACTGGGATGTCTTCATTTTCCCTTATCTCCCTAAACAC	2280
DB	2291	GAATTACTTCAGAGCTGGTGCTCACTGGGATGTCTTCATTTTCCCTTATCTCCCTAAACAC	2350
QY	2281	TGCAGCTCAGGTTGGCTATGTGCTTCAAGATTGGTGGCTTTTCATCTAGGGCAACAAACA	2340
DB	2351	TGCAGCTCAGGTTGGCTATGTGCTTCAAGATTGGTGGCTTTTCATCTAGGGCAACAAACA	2410
QY	2341	AAAGTATGCTAAATGTCATCTGTAATGAGGAGGAAATGTAACCGAGAAGCTAGATCTTAA	2400
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DB	3011	GACAACGTCGGTGGTTTGGCCGTCTGGATGCCATCTGTGCCATGTTTGTTCATCAT	3070
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Db 4210 TTTGGACTATGTAACACCATTTGATCTACTTTTTTACTTTGGCAACAATATTTATACATA 4369
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Db 4270 CAAGATGCTAGTTCATTTCGAATATTTCTCCC 4300
RESULT 5
US-10-012-896-536
; Sequence 536, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Megaher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 536
; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4535
; OTHER INFORMATION: n = A,T,C or G
US-10-012-896-536

Query Match 92.4%; Score 3910.2; DB 9; Length 6140;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 4040; Conservative 0; Mismatches 3; Indels 118; Gaps 1;

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Db 233 GGTGCTCAATCCCTGTTTAAATTTGCCATAAACGGAGATTAGAGGATGATATGT 292
Qy 249 ATTCACTGCTCCGAGAACCGCTCACAGACCTTTGGAGAGGAGTTGCAAGGTTCTGGG 308
Db 293 ATTCACTGCTCCGAGAACCGCTCACAGACCTTTGGAGAGGAGTTGCAAGGTTCTGGG 352
Qy 309 ATAAGAAGTTTAAAGAGCTGAGAAATGAGCAAGACCTTTCTTTAAACAGAGCAATCA 368
Db 353 ATAAGAAGTTTAAAGAGCTGAGAAATGAGCAAGACCTTTCTTTAAACAGAGCAATCA 412
Qy 369 TAAAGTGTACTGGAAATCTTATTTAGTTTGGGAATTTTACGTTAATTGAGGAAAGTG 428
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QY 429 CCAAGTAATCCAGCCCATATTTTGGGAAAAATTAATTAATTTTGAATAATATGATC 488
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Db 473 CCAAGTAATCCAGCCCATATTTTGGGAAAAATTAATTAATTTTGAATAATATGATC 532
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QY 549 CGCTAATTTGGCTATACATGCACTATATATTTTATCACGTTTCACTGTTGGGATGA 608
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Db 773 TTGATCAGGTGACAGTGTCTTACACTTCTGTGGGAGGACCACTGCAGGCGCATGCGAG 832
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QY 2409 TAGGAATTTTATCAGGTTTAACTAGTACCGTTCTTTTGGCATAGCAAGATCTCTAT 2468
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Db 2453 TAGGAATTTTATCAGGTTTAACTAGTACCGTTCTTTTGGCATAGCAAGATCTCTAT 2512
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QY 2469 TGTATTTCTAGTCCCTTTGTTAACTCTTCACAAACTTTTGCACAAACAAATGTTTGGTCA 2528
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Db 2513 TGTATTTCTAGTCCCTTTGTTAACTCTTCACAAACTTTTGCACAAACAAATGTTTGGTCA 2572
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QY 2529 TTCTGAAAGCTCCGGTATTTCTTTTGTATAGAAATCCAATAGGAGAAATTTTAAATCGTT 2588
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; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 536
; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(6140)
; OTHER INFORMATION: n-A,T,C or G
; US-09-759-143-536

Query Match      92.48; Score 3910.2; DB 10; Length 6140;
Best Local Similarity 97.18; Pred. No. 0;
Matches 4040; Conservative 0; Mismatches 3; Indels 118; Gaps 1;

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QY 609 GGTTCAGAGTACCCATGTGCCATATGATTTATCGGAAGCACTTCTGTACTTACATGG 668
DB 653 GGTTCAGAGTACCCATGTGCCATATGATTTATCGGAAGCACTTCTGTACTTACATGG 712
QY 669 CCATGGGAAGACACACAGCCAGATAGTCAATCTGCTGCCAATGATGTGAACAAGT 728
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QY 729 TTGATCAGGTGACAGTGTCTTACACTTCCCTGTGGCAGGACCACTGACGGGATGCGCAG 788
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QY 789 TGACTGCCCTACTCTGGATGGAGATAGGAATATCGCTTCCCTGGGATGGCAGTTCTAA 848
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QY 849 TCATTTCTCTGCTTGTGAAAGCTCTTTTGGGAAGTTGTTCTCATCAGTGGAGGTAA 908
DB 893 TCATTTCTCTGCTTGTGAAAGCTCTTTTGGGAAGTTGTTCTCATCAGTGGAGTAA 952
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Db	3653	AAATGATGATCTGAATTTAGCAGAAATCTCAGGAAATCAGATATTTGATTATTTGATGAAGCGACGG	3712
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Db	3713	TGTGCTTCTGCCAGGGCAATTTCTCAGGAAATCAGATATTTGATTATTTGATGAAGCGACGG	3772
QY	3729	CAAAATGTGATCCAGAACTGATGATTTAATACAAAATAATCCGGGAGAAATTTTGCCC	3788
Db	3773	CAAAATGTGATCCAGAACTGATGATTTAATACAAAATAATCCGGGAGAAATTTTGCCC	3832
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Db	3833	ACTGCACCCGTGTATCACTTGCACACAGATTTGAACACCATTTATTGACAGGACAAAGATAA	3892
QY	3849	TGGTTTTAGATTCAGGAAGACTGAAAGAAATATGATGAGCGGTATGTTTTCGTGCAAAATA	3908
Db	3893	TGGTTTTAGATTCAGGAAGACTGAAAGAAATATGATGAGCGGTATGTTTTCGTGCAAAATA	3952
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Db	3953	AAAGAGGCTTATTTACAAAGTGGTCCAACTGGGCAAGGACGAGCGCTGCCCCCTCA	4012
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Db	4013	CTGAACACAGCAAAACAGATGGGGTTTCCACATGTTGGCCAGGCTGTTCTCAAACCTCT	4072
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RESULT 7
US-09-780-669-536
; Sequence 536, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 536
; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(6140)
; OTHER INFORMATION: n=A,T,C or G
US-09-780-669-536

Query Match 92.4%; Score 3910.2; DB 10; Length 6140;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 4040; Conservative 0; Mismatches 3; Indels 118; Gaps 1;

QY 189 GTGGCTCAATCCCTGTGTTAAATTTGGCCATAAACGGAGATTAGAGGAAGATGATATGT 248
Db 233 GTGGCTCAATCCCTGTGTTAAATTTGGCCATAAACGGAGATTAGAGGAAGATGATATGT 292

QY 249 ATTCAAGTCTGCCAAGAACCCCTCACAGCACCTTTGGAGAGAGTTGCCAAGGTTCTGGG 308
Db 293 ATTCAAGTCTGCCAAGAACCCCTCACAGCACCTTTGGAGAGAGTTGCCAAGGTTCTGGG 352

QY 309 ATAAAGAAGTTTAAAGAGCTGAGATGAGCAGACAGCCTTCTTTAAAGAGCAATCA 368
Db 353 ATAAAGAAGTTTAAAGAGCTGAGATGAGCAGACAGCCTTCTTTAAAGAGCAATCA 412

QY 369 TAAAGTGTTACTGGAAATCTATTATTAGTTTGGGAATTTTACGTTAATTGAGGAAGTG 428
Db 413 TAAAGTGTTACTGGAAATCTATTATTAGTTTGGGAATTTTACGTTAATTGAGGAAGTG 472

QY 429 CCAGAAGTATCCAGCCCATATTTTGGGAAATTTATTAATTTTGAATAATTTATGATC 488
Db 473 CCAGAAGTATCCAGCCCATATTTTGGGAAATTTATTAATTTTGAATAATTTATGATC 532

QY 489 CCATGGATTCGTGGCTTTGAACACAGCGTACGCCATATGCCACGGTGTGACTTTTGA 548
Db 1613 TCTCGGAACTCTGAGGAGTAAATATTTTATTGGGAAGAAATACGAAAGGACGATATG 1672

Db 533 CCATGGATTCGTGGCTTTGAACACACAGCGTACGCCATATGCCACGGTGTGACTTTTGTCA 592
QY 549 CGCTCATTTTGGCTATACTGCATCAGCTTATATTTTATCATAGTTCAGTGTGCTGGGATGA 608
Db 593 CGCTCATTTTGGCTATACTGCATCAGCTTATATTTTATCATAGTTCAGTGTGCTGGGATGA 652
QY 609 GTTTACAGTAGCATGTGCCATATGATTTATCGGAAGGACACTTCGTCTTTAGTAACATGG 668
Db 653 GTTTACAGTAGCATGTGCCATATGATTTATCGGAAGGACACTTCGTCTTTAGTAACATGG 712
QY 669 CCATGGGAAGACACACACAGGCGAGATAGTCAATCTGCTGTCCAAATGATGTGAACAGT 728
Db 713 CCATGGGAAGACACACACAGGCGAGATAGTCAATCTGCTGTCCAAATGATGTGAACAGT 772
QY 729 TTGATCAGGTGACAGTGTCTTACATCTCTGCGGAGGACCACTCCAGCGGATCCAG 788
Db 773 TTGATCAGGTGACAGTGTCTTACATCTCTGCGGAGGACCACTCCAGCGGATCCAG 832
QY 789 TGACTGCCCTACTCTGATGGAGATAGGAATATCGTGCCTTGTCTGGATGGCAGTTCTAA 848
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Db 893 TCATTTCTCTGCCCTTGCAGAAAGCTGTTTGGGAAGTGTCTCATCACTACTGAGGAGTAAA 952
QY 909 CTGCAACTTTCAGGATGCCAGGATCAGGACCATGAATGAAGTTATTAACATGATTAAGGA 968
Db 953 CTGCAACTTTCAGGATGCCAGGATCAGGACCATGAATGAAGTTATTAACATGATTAAGGA 1012
QY 969 TAATAAAATGTACGCTGGGAAAGTCATTTTCAAACTTATTACCAATTTTGAAGAAGA 1028
Db 1013 TAATAAAATGTACGCTGGGAAAGTCATTTTCAAACTTATTACCAATTTTGAAGAAGA 1072
QY 1029 AGGAGATTTTCCAAAGATTCAGAGAGTTCCTGCTCAGGGGAGTGAATTTGGCTTCGTTTT 1088
Db 1073 AGGAGATTTTCCAAAGATTCAGAGAGTTCCTGCTCAGGGGAGTGAATTTGGCTTCGTTTT 1132
QY 1089 TCAGTGCAGCAAGCAAAATCATCGTGTGTTGTACCTTACCACCTACGTCCTCTCGGCAGTG 1148
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QY 1209 TTACCCCTTTTCCCTCAGCCATTGAGAGGTTGTCAGAGGCAATCGTCAGCAATCCGAA 1268
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Db 1373 ATGTTAAAAGATGTGTGCTACTGTGAGGATTTTACTGCTTTTGGGATTAAGGCATCAGAGA 1432
QY 1389 CCCCAACTCTAAGGCCCTTTCCTTTACTGTCTAGACCTGGCGAATTTGTTAGCTGTGGTCG 1448
Db 1433 CCCCAACTCTAAGGCCCTTTCCTTTACTGTCTAGACCTGGCGAATTTGTTAGCTGTGGTCG 1492
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QY 1749 TTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTCTGACGATCCTCTCAGTGAG 1808
DB 1793 TTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGACGATCCTCTCAGTGAG 1852
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DB 1853 TAGATCGGAGTGTAGCAGACACTTGTGCAACTGTGTATTTGCAAAATTTTGGCAGAGA 1912
QY 1869 AGATCACAAATTTAGTGACTCATCAGTTGACAGTCTCAAGCTCAAGCTCAGATCTCTGA 1928
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QY 1929 TATTGAAAGATGGTAAATGGTGCAGAAAGGGACTTACACTGAGTTCCTTAAATCTGGTA 1988
DB 1973 TATTGAAAGATGGTAAATGGTGCAGAAAGGGACTTACACTGAGTTCCTTAAATCTGGTA 2032
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DB 2033 TAGATTTGGCTCCCTTTTAAAGAGGATTAATGAGGAAAGTGAACAACTCCAGTTCAG 2092
QY 2049 GAATCCACACTAGGAATCGTACCTTCTCAGAGTCTTCGGTGTGGTCTCAACAACTCT 2108
DB 2093 GAATCCACACTAGGAATCGTACCTTCTCAGAGTCTTCGGTGTGGTCTCAACAACTCT 2152
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QY 2169 CACTATCAGAGAGAACCGTCTCAAGGAAAGTGGTTTTCAGGCCATPAAAGATTAAT 2228
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QY 2409 TAGGAATTTATTCAGGTTTAACTGTAGCTACCGTCTCTTTTGGCATAGCAGATCTCTAT 2468
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DB 3473 CAACGTAAATTTGGACTTCAAGATTTAAGGAAGAAATGTCAATCATCTCAGGAACCTG 3532
QY 3489 TTTTCTTCTCAGTGGACATGAGAAAACCTGGATCCCTTTAAGGAGCACCGGATGAGG 3548
DB 3533 TTTTCTTCTCAGTGGACATGAGAAAACCTGGATCCCTTTAAGGAGCACCGGATGAGG 3592
QY 3549 AACTGTGAATTTGCCCTTACAAGAGGTACAACTTAAAGAAACCAATTTGAAGATCTTCTGTTA 3608
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DB 3653 AAATGGATCTGAATTTAGCAGAAATCAGATATTTAGTGTGGACAAAGACAACTGG 3712
QY 3669 TGTGCTTCCAGGCAATTTCTCAGAAAATCAGATATTTAGTGTGGACAAAGACAACTGG 3728
DB 3713 TGTGCTTCCAGGCAATTTCTCAGAAAATCAGATATTTAGTGTGGACAAAGACAACTGG 3772
QY 3729 CAATGTGGATCCAAAGAACTGATGATTAATAACAAAAAATCCGGGAGAAATTTGGCC 3788
DB 3773 CAATGTGGATCCAAAGAACTGATGATTAATAACAAAAAATCCGGGAGAAATTTGGCC 3832
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QY ----- 3985
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Db 4133 CCACGCCACCGCTGAGTATACTTCAAAGAAATTTATCCACATATTGGTCACACTGACCCAC 4192
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Db 4313 GTAAACCAATGTACTTTTTTTTACTTTGGCAACAAATATTTATACATACAGATGCTA 4372
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Db 4373 GTTCATTTGAATATTTCTCCC 4393

RESULT 8

US-09-822-827-536
; Sequence 536, Application us/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 536
; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(6140)
; OTHER INFORMATION: n=A,T,C or G
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QY 189 GGTGGCTCAATCCCTGTGTTTAAATTTGGCCATAAACGGAGATTAGAGGAAGATGATATGT 248
Db 233 GGTGGCTCAATCCCTGTGTTTAAATTTGGCCATAAACGGAGATTAGAGGAAGATGATATGT 292
QY 249 ATTCACTGCTGCCAGAACCGCTTCACAGCACCTTGGAGAGGAGTTGCAAGGTTCTGGG 308

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Db	1493	GCCCCGTGGAGCAGGGAAGTCATCACTGTTAAGTGCCTGTCGCGGAATTTGGCCCCAA	1552
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Db	2093	GAATCCCACTAAGGAATCGTCTCTCAGAGCTCTCGGTTTGGTCTCAACAATCTTT	2152
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QY	2589	TCTCCAAGACATTTGGACACTTTGGATGATTTGCTGGCGCTACGTTTATAGATTTTCATCC	2648
DB	2633	TCTCCAAGACATTTGGACACTTTGGATGATTTGCTGGCGCTACGTTTATAGATTTTCATCC	2692
QY	2649	AGCAATTTGCTACAAAGTGGTGGTGTGGCTCTGTGGCTGTGGCGGTGATTCCTTTGGATCG	2708
DB	2693	AGCAATTTGCTACAAAGTGGTGGTGTGGCTCTGTGGCTGTGGCGGTGATTCCTTTGGATCG	2752
QY	2709	CAATACCCTTGGTTCCCTTTGGAAATCATTTTTCATTTTTTCTTCGGCGATATTTTTTGGAAA	2768
DB	2753	CAATACCCTTGGTTCCCTTTGGAAATCATTTTTCATTTTTTCTTCGGCGATATTTTTTGGAAA	2812
QY	2769	CGTCAAGAGATGTGAAGCGCTCGAATCTACAACCTCGGAGTCCAGTGTGTTTCCCACTTGT	2828
DB	2813	CGTCAAGAGATGTGAAGCGCTCGAATCTACAACCTCGGAGTCCAGTGTGTTTCCCACTTGT	2872
QY	2829	CATCTTCTCTCCAGGGCTCTGACCACTCCGGGCATACAAAGCAGAAGAGGTGTCAAG	2888
DB	2873	CATCTTCTCTCCAGGGCTCTGACCACTCCGGGCATACAAAGCAGAAGAGGTGTCAAG	2932
QY	2889	AACGTGTTGATGCACACCAGGATTTACATTCAGAGCTTGGTTCCTTGTGTTGACAACGT	2948
DB	2933	AACGTGTTGATGCACACCAGGATTTACATTCAGAGCTTGGTTCCTTGTGTTGACAACGT	2992
QY	2949	CCGCTGGTTCGGCGTCCGCTCGATCTGCCATCTGTGCCATGTTGTGCATCATCTGTGCCCT	3008
DB	2993	CCGCTGGTTCGGCGTCCGCTCGATCTGCCATGTTGTGCATCATCTGTGCCCT	3052
QY	3009	TTGGGTCCCTGATTCCTGGCAAAACCTCTGGATCCGGGCAGGTGTGTTTGGCACTGTCT	3068
DB	3053	TTGGGTCCCTGATTCCTGGCAAAACCTCTGGATCCGGGCAGGTGTGTTTGGCACTGTCT	3112
QY	3069	ATGCCCTCAGCTCATGSGGATGTTTCACTGGTGTGTTTCGACAAAGTGTGAAGTTGAGA	3128
DB	3113	ATGCCCTCAGCTCATGSGGATGTTTCACTGGTGTGTTTCGACAAAGTGTGAAGTTGAGA	3172
QY	3129	ATATGATGATCTCAGTAGAAAGGTCATTGAAATACACAGACCTTGAAAAAGAGCACCTT	3188
DB	3173	ATATGATGATCTCAGTAGAAAGGTCATTGAAATACACAGACCTTGAAAAAGAGCACCTT	3232
QY	3189	GGGAATATCAGAAACCCACCAGACCTTGCCCCATGAAGGAGTGAATACTTTTGACA	3248
DB	3233	GGGAATATCAGAAACCCACCAGACCTTGCCCCATGAAGGAGTGAATACTTTTGACA	3292
QY	3249	ATGTGAACCTTCATGTACAGTCCAGGTGGCCCTCTGGTACTGAAGCATCTGCACAGCACTCA	3308
DB	3293	ATGTGAACCTTCATGTACAGTCCAGGTGGCCCTCTGGTACTGAAGCATCTGCACAGCACTCA	3352
QY	3309	TTTAAATCACAGAAAGGTTGGCATTGTGGGAAGAACCCGAGCTGGAAAAAGTTCCTCTCA	3368
DB	3353	TTTAAATCACAGAAAGGTTGGCATTGTGGGAAGAACCCGAGCTGGAAAAAGTTCCTCTCA	3412
QY	3369	TCCTAGCCCTTTTATGTTTCAGAACCCGAGGTAAAATTTGGATTTGATTAAGATCTTGA	3428
DB	3413	TCCTAGCCCTTTTATGTTTCAGAACCCGAGGTAAAATTTGGATTTGATTAAGATCTTGA	3472
QY	3429	CAACTGAAATGGAATTCACGATTTAAAGGAAGAAATGTCAATCATACCTCAGGAACCTG	3488
DB	3473	CAACTGAAATGGAATTCACGATTTAAAGGAAGAAATGTCAATCATACCTCAGGAACCTG	3532
QY	3489	TTTTTCTTCACTGGAAATGAGGAAAAACCTTGGATCCCTTTTAAGGAGCACACGGATGAGG	3548
DB	3533	TTTTTCTTCACTGGAAATGAGGAAAAACCTTGGATCCCTTTTAAGGAGCACACGGATGAGG	3592
QY	3549	AACTGTGGAATGCCCTTACAAGAGGTACAACTTTAAAGAAACCAATTTGAAAGATCTTCTCTGTA	3608

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Db 3593 AACGTGGAAATGCGCTTACAGAGGTACAACTAAAGAAACCACTGAAGATCTTCGTGTA 3652
Qy 3609 AAATGGATACGTAAATAGCAGAAATCAGATCCAAATTTAGTGTGGCAAAACAACTGG 3668
Db 3653 AAATGGATACGTAAATAGCAGAAATCAGATCCAAATTTAGTGTGGCAAAACAACTGG 3712
Qy 3669 TGTGCTTGGCAGGCAATCTCAGGAAATATCAGATATTCATTTGATGAAGCGACGG 3728
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Db 3773 CAATGTGGATCCAAAGCACTGATGATTAACAAAAAATCCGGAGAAATTTGCC 3832
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Db 3833 ACTGCACGGTGTAAACATTCACACAGATTTGAACACCAATTTTCACAGCCACAAGATAA 3892
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Db 3893 TGGTTTTAGATTCAGGAAGACTGAAAGAAATATGATGAGCCGTATGTTTGTGCAAAATA 3952
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Db 4013 CTGAAACAGCAAAACAGAGATGGGGTTTTCACCATGTTGGCCAGGCTGTCTCAAACTCCT 4072
Qy 3986 ----- 3985
Db 4073 GACCTCAAGTGATCCACCTGCTTGGCTCCCAAACTGCTGAGATTACAGGTGTGAGCCA 4132
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Db 4253 TGAATCCAAACCAATGCAAGTCCGTTCCGAAGCAATTTCCACTAGTATTTTGGACTAT 4312
Qy 4151 GTAAACCAATTTGACTTTTTTTTACTTTGGCAACAAATATTTATACATAAAGATGCTA 4210
Db 4313 GTAAACCAATTTGACTTTTTTTTACTTTGGCAACAAATATTTATACATAAAGATGCTA 4372
Qy 4211 GTTCAATTTGAATATTTCTCC 4231
Db 4373 GTTCAATTTGAATATTTCTCC 4393
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RESULT 9

US-10-012-896-1007

; Sequence 1007, Application US/10012896

; Publication No. US20020183251A1

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yugu

; APPLICANT: Kalos, Michael D.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedwick, Thomas S.

; APPLICANT: Carter, Darriack

; APPLICANT: Li, Samuel X.

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; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Megher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012.896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1007
; LENGTH: 4395
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-012-896-1007

Query Match 88.4%; Score 3739.2; DB 9; Length 4395;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3744; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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Qy 298 AGGGTCTGGGATAAAGAGTTTAAAGAGCTGAGATGAGCAGACAGCCCTCTTTAAC 357
Db 663 AGGGTCTGGGATAAAGAGTTTAAAGAGCTGAGATGAGCAGACAGCCCTCTTTAAC 722
Qy 358 AAGAGCAATCATAAAGTGTACTGGAAATCTTATTTAGTTTGGGAATTTTACGTTAAT 417
Db 723 AAGAGCAATCATAAAGTGTACTGGAAATCTTATTTAGTTTGGGAATTTTACGTTAAT 782
Qy 418 TGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTGGGAAAAAATTTAATTTATTTGA 477
Db 783 TGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTGGGAAAAAATTTAATTTATTTGA 842
Qy 478 AAATTTATGATCCATCGATCTGTGGCTTTGAACACAGCTAGCCCTATGCCACGGTGCT 537
Db 843 AAATTTATGATCCATCGATCTGTGGCTTTGAACACAGCTAGCCCTATGCCACGGTGCT 902
Qy 538 GACTTTTTGCACGCTCATTTTGGCTATCTGATCATCTATATTTTATCATCAGTTCAAGT 597
Db 903 GACTTTTTGCACGCTCATTTTGGCTATCTGATCATCTATATTTTATCATCAGTTCAAGT 962
Qy 598 TGCTGGATGAGTTTACGAGTAGCCCATGTGCCATATGATTTATCGGAAGCACTTCGTCT 657
Db 963 TGCTGGATGAGTTTACGAGTAGCCCATGTGCCATATGATTTATCGGAAGCACTTCGTCT 1022
Qy 658 TAGTAACATGGCCATGGGGAAGACAACACAGCCAGAGATAGTCAATCTGCTGTCGAATGA 717
Db 1023 TAGTAACATGGCCATGGGGAAGACAACACAGCCAGAGATAGTCAATCTGCTGTCGAATGA 1082
Qy 718 TGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCTCTGGCAGGACCACTGCA 777
Db 1083 TGTGAACAAGTTTGATCAGGTGACAGTGTCTTACACTTCTCTGGCAGGACCACTGCA 1142
Qy 778 GCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTCCCTTCTGGGAT 837
Db 1143 GCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTCCCTTCTGGGAT 1202
Qy 838 GCGATTTCAATCATTTCTCTGCCCTTGCCTTGGAAAGCTGTTTGGGAAGTGTGTTCTCATCACT 897
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QY 958 TGGTATAAGGATAATAAATAATACGCTTGGGAAAGTCATTTTCAAAATCTTATTATACAA 1017
DB 1323 TGGTATAAGGATAATAAATAATACGCTTGGGAAAGTCATTTTCAAAATCTTATTATACAA 1382
QY 1018 TTTTGAGAAAGAGAGATTTCCAAAGATCTGAGAAGTTCCTGCTCAGGGGGATGAATTT 1077
DB 1383 TTTTGAGAAAGAGAGATTTCCAAAGATCTGAGAAGTTCCTGCTCAGGGGGATGAATTT 1442
QY 1078 GGCTTCGTTTTTTCAGTGCAAGCAAAATCATCGTGTGTTGTCACCTTCACCACTACGTGCT 1137
DB 1443 GGCTTCGTTTTTTCAGTGCAAGCAAAATCATCGTGTGTTGTCACCTTCACCACTACGTGCT 1502
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DB 1503 CPTCGGACGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCTGT 1562
QY 1198 GCGGCTGACGGTTTACCGCTTCTTCCCTCAGCCATTTGAGAGGGTGTGAGAGCAATCGT 1257
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QY 1318 GCTGCGCTCAGATGTTAAAGATGTTGCTGTCAGAGGATTTTACTGCTTTTGGGATAA 1377
DB 1683 GCTGCGCTCAGATGTTAAAGATGTTGCTGTCAGAGGATTTTACTGCTTTTGGGATAA 1742
QY 1378 GGCATCAGAGACCCCAACTCTACAAGCCCTTCCCTTACTGTGTCAGACCTGCGGAAATGTT 1437
DB 1743 GGCATCAGAGACCCCAACTCTACAAGCCCTTCCCTTACTGTGTCAGACCTGCGGAAATGTT 1802
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DB 1863 ATTGGCCCCAAGTACGGGCTGGTACGCTGTCATGGAAGAAATGTCCTATGTGCTCAGCA 1922
QY 1558 GCGCTGGGTGTTCTCGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAAGA 1617
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QY 1618 GGAACGATATGAAAGTATGAAAGCTTGTGCTCTGAAAGAGATTTACAGCTGTGGA 1677
DB 1983 GGAACGATATGAAAGTATGAAAGCTTGTGCTCTGAAAGAGATTTACAGCTGTGGA 2042
QY 1678 GGATGTTGATCTGATGATAGGAGATCGGGGAACCCAGCTGAGTGGAGGCGAGAAAGC 1737
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QY 1738 ACGGTTAAACCTTTCGAAGAGAGTGTATCAAGATGCTGACATCTACTCTCGACCATCC 1797
DB 2103 ACGGTTAAACCTTTCGAAGAGAGTGTATCAAGATGCTGACATCTACTCTCGACCATCC 2162
QY 1798 TCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAAGTGTGATTTGTCAAAAT 1857
DB 2163 TCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAAGTGTGATTTGTCAAAAT 2222
QY 1858 TTTTGATGAGAAGATCACAATTTTATGACTCATCATGTTGCTAGTACCTCAAGCTGCAAG 1917
DB 2223 TTTTGATGAGAAGATCACAATTTTATGACTCATCATGTTGCTAGTACCTCAAGCTGCAAG 2282
QY 1918 TCAGATTTCTGATTTGAAGATGGTAAATGTTGAGAGAGGAGCTTACATGAGTTCT 1977
DB 2283 TCAGATTTCTGATTTGAAGATGGTAAATGTTGAGAGAGGAGCTTACATGAGTTCT 2342
QY 1978 AAAATCTGATATAGATTTTGGCTCCCTTTTAAAGAGGATATAGGAAAGTGAACACACC 2037

DB 2343 AAAATCTGATATAGATTTTGGCTCCCTTTTAAAGAGGATAATAGGAAAGTGAACACACC 2402
QY 2038 TCCAGTTCCAGGAACCTCCACACTAAGAAATCGTACCTTCTCAGAGTCTTCGGTTTGGTC 2097
DB 2403 TCCAGTTCCAGGAACCTCCACACTAAGAAATCGTACCTTCTCAGAGTCTTCGGTTTGGTC 2462
QY 2098 TCAACAATCTTCTAGAACCTCCTTGAAGATGGTCTCTGGAGAGCCCAAGATACAGAGAA 2157
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QY 2158 TGTCCAGTTACACTATCAGAGAGAACCGTCTGAAAGAAAGTTGTTTTTCAGGCCCTA 2217
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DB 2823 AAGATCTCTATGCTTATGCTTACGCTTCTGTTTAACTCTTCAAAAACCTTTCACAAACAA 2882
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QY 3658 AAGCAACTGTGTGCTTGCCTGAGGCAATCTCAGGAAATATCAGATATGATATTGA 3717
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QY 3718 TGAAGCAGCGCAATGTGGATCCAAAGAACTGATGAGTTAATACAAAAAATCCGGA 3777
Db 4083 TGAAGCAGCGCAATGTGGATCCAAAGAACTGATGAGTTAATACAAAAAATCCGGA 4142
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QY 3838 CGACAAGATAATGTTTGTAGATCAGGAAGACTGAAGAAATATGATGAGCCGTATGTTT 3897
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QY 3898 GCTCAAAATAAGAGAGCCTATTTTACAAGATGTTGCAACAACTGGGCAAGCGAAGC 3957
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Db 4323 CGTGGCCCTCACTGAAACAGCAAAACAGAT 4354

RESULT 10

US-10-012-896-1006
; Sequence 1006, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu

APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1006
LENGTH: 3786
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-1006

Query Match 88.4%; Score 3738.6; DB 9; Length 3786;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3741; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 245 ATGTATTTCAGTGTGTCAGAAAGACCGCTCACAGCACCTTGGAGAGGAGTTTCAAGGGTTC 304
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QY 305 TGGGATAAAGAGAGTTTAAAGAGCTGAGAAATGACGACAGAGGCTTCTTTAAACAAGAGCA 364
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QY 365 ATCATAAAGTGTACTGGAAATCTTATTTAGTTTGGGAATTTTACGTTAAATGAGGAA 424
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Db 181 AGTGCCAAAGTAATCCAGCCCATATTTTGGGAAAAAATTAATTAATTTTGAATAATAT 240
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QY 605 ATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGACCTTCTCTTAGTAAC 664
Db 361 ATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGACCTTCTCTTAGTAAC 420
QY 665 ATGGCCATGGGAAGAACACACAGGCCAGATAGTCAATCTGCTGCTCAATGATGTAAC 724
Db 421 ATGGCCATGGGAAGAACACACAGGCCAGATAGTCAATCTGCTGCTCAATGATGTAAC 480
QY 725 AAGTTTGATCAGGTGACAGTGTCTTACACTTCCCTGTGGCAGGACACTGCAAGGCGATC 784
Db 481 AAGTTTGATCAGGTGACAGTGTCTTACACTTCCCTGTGGCAGGACACTGCAAGGCGATC 540
QY 785 GCAGTCACTGCCCTACTCTGCTGATGGAGATAGGAATATCGTGCCTTCTGCTGGGATGCGGAT 844

|||||
Db 541 GCAGTACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTCTGGGATGCGAGTT 600
Qy 845 CTAATCATCTCTCCCTCCCTGCAAGCTGTTTGGGAAGTTGTTCTCATCACTGAGGAGT 904
Db 601 CTAATCATCTCTCCCTCCCTGCAAGCTGTTTGGGAAGTTGTTCTCATCACTGAGGAGT 660
Qy 905 AAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATTAAGTGGTATA 964
Db 661 AAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATTAAGTGGTATA 720
Qy 965 AGGATAATAAAATGTAAGCTCGGGAAGTCAATTTTCAAACTTTATTACCAATTTTGAGA 1024
Db 721 AGGATAATAAAATGTAAGCTCGGGAAGTCAATTTTCAAACTTTATTACCAATTTTGAGA 780
Qy 1025 AAGAGGAGATTTCCAAAGATTTCTGAGAAAGTTCTGCTCCCTCAGGGGATGAATTTGSCITCG 1084
Db 781 AAGAGGAGATTTCCAAAGATTTCTGAGAAAGTTCTGCTCCCTCAGGGGATGAATTTGSCITCG 840
Qy 1085 TTTTTCAGTGAAGCAAAATCATCGTGTGTTGTGACCTTCACCACTAGCTGCTCTCGGC 1144
Db 841 TTTTTCAGTGAAGCAAAATCATCGTGTGTTGTGACCTTCACCACTAGCTGCTCTCGGC 900
Qy 1145 AGTGTGATCACAGCAGCCGCTGTTCTGTGCGAGTGAGCGCTGTATGGGCTGTGGCGTG 1204
Db 901 AGTGTGATCACAGCAGCCGCTGTTCTGTGCGAGTGAGCGCTGTATGGGCTGTGGCGTG 960
Qy 1205 ACGETTACCCCTTTCTTCCCTCAGCCATTTGAGAGGTGTGAGAGGCAATCGTCAGCATC 1264
Db 961 ACGETTACCCCTTTCTTCCCTCAGCCATTTGAGAGGTGTGAGAGGCAATCGTCAGCATC 1020
Qy 1265 CGAAGATCCAGACTTTTCTCTACTGTGATGAGATATCACAGCGCAACCGTCAGCTGCGG 1324
Db 1021 CGAAGATCCAGACTTTTCTCTACTGTGATGAGATATCACAGCGCAACCGTCAGCTGCGG 1080
Qy 1325 TCAGATGGTAAAGAGTGGTCATGTGCGAGGATTTTACTGCTTTTGGGATAAGGCATCA 1384
Db 1081 TCAGATGGTAAAGAGTGGTCATGTGCGAGGATTTTACTGCTTTTGGGATAAGGCATCA 1140
Qy 1385 GAGACCCCACTCTACAGGCTTTCTCTTACTCTCAGACCTGCGCAATTTTACTGCTG 1444
Db 1141 GAGACCCCACTCTACAGGCTTTCTCTTACTCTCAGACCTGCGCAATTTTACTGCTG 1200
Qy 1445 GTCGGCCCGTGGGAGCAGGAAGTCATCTGTTAAGTCCGCTGCTCGGGGAATTTGGCC 1504
Db 1201 GTCGGCCCGTGGGAGCAGGAAGTCATCTGTTAAGTCCGCTGCTCGGGGAATTTGGCC 1260
Qy 1505 CCAAGTCACGGCTGGTCAGCGTGCATGGGAAGATTTGCTATGTGCTCAGCAGCCCTGG 1564
Db 1261 CCAAGTCACGGCTGGTCAGCGTGCATGGGAAGATTTGCTATGTGCTCAGCAGCCCTGG 1320
Qy 1565 GTGTTCTGGGAACCTCTGAGAGTAATTTTATTGGGAAGAAATATGAAAGGAACGA 1624
Db 1321 GTGTTCTGGGAACCTCTGAGAGTAATTTTATTGGGAAGAAATACGAAAGGAACGA 1380
Qy 1625 TATCAAAAAGTCATAAAGCTGTGCTCTGAAAAGGATTTACAGCTGTTGGAGGATGGT 1684
Db 1381 TATCAAAAAGTCATAAAGCTGTGCTCTGAAAAGGATTTACAGCTGTTGGAGGATGGT 1440
Qy 1685 GATCTGACTGTGATAGGATCGGGGAACACCGTGTGAGGGCAGAAAGCAGGGTA 1744
Db 1441 GATCTGACTGTGATAGGATCGGGGAACACCGTGTGAGGGCAGAAAGCAGGGTA 1500
Qy 1745 AACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGAGCATCTCTCAGT 1804
Db 1501 AACCTTGAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTGAGCATCTCTCAGT 1560
Qy 1805 GCAGTAGATGGGAAGTTAGCAGACATTTGCGAAGTGTATTTGTCAAAATTTTGCAT 1864
Db 1561 GCAGTAGATGGGAAGTTAGCAGACATTTGCGAAGTGTATTTGTCAAAATTTTGCAT 1620
Qy 1865 GAGAAGATCAAAATTTTACTGACTCATCATGTTGAGTACCTCAAGCTGCAAGTCAGATT 1924
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Db 1621 GAGAAGATCACAAATTTTAGTGACTCATCATAGTTGCAAGTCTCAAAAGTCAAGTCAGATT 1680
Qy 1925 CTGATATTTGAAAGATCGTAAATAGTGTGCAAGAGGGGACTTTACACTGAGTTTCTTAAATCT 1984
Db 1681 CTGATATTTGAAAGATCGTAAATAGTGTGCAAGAGGGGACTTTACACTGAGTTTCTTAAATCT 1740
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Db 1741 GGTATAGATTTTGGCTCCCTTTTAAAGAAAGGATAATAGAGAAAGTGAACAACCTCCAGTT 1800
Qy 2045 CCAGGAATCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAA 2104
Db 1801 CCAGGAATCTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACAA 1860
Qy 2105 TCTTCTAGACCCCTCCCTTGAAGATGGTCTCTGGAGAGCAAGATACAGAGAAATGTCCCA 2164
Db 1861 TCTTCTAGACCCCTCCCTTGAAGATGGTCTCTGGAGAGCAAGATACAGAGAAATGTCCCA 1920
Qy 2165 GTTACACTATCAGAGAGAAACCGTTCTGAAGAAAGTTGGTTTTCAGGCCCTATAGAAT 2224
Db 1921 GTTACACTATCAGAGAGAAACCGTTCTGAAGAAAGTTGGTTTTCAGGCCCTATAGAAT 1980
Qy 2225 TACTTACAGAGCTGGTCTCAGTGGATGTTCTTCATTTTCCCTTATTTCTCTAACTGCA 2284
Db 1981 TACTTACAGAGCTGGTCTCAGTGGATGTTCTTCATTTTCCCTTATTTCTCTAACTGCA 2040
Qy 2285 GCTCAGGTTGCTATGCTTCAAGATTTGGTGGCTTTTCATCTGGGCAACAAACAACT 2344
Db 2041 GCTCAGGTTGCTATGCTTCAAGATTTGGTGGCTTTTCATCTGGGCAACAAACAACT 2100
Qy 2345 ATGCTAAATGTCACGTAAATGGAGAGGAAATGTAACCGAGAAGCTAGATCTTAACCTGG 2404
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Qy 2465 CTATTTGTTATCTACGCTCTTTGTTAACTCTTCAACAACTTTGCACAAACAAATGTTTGG 2524
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Qy 2705 ATCCGAATACCTTGGTTCCTTGGGAATCATTTTCATTTTCTTCGGCGATATTTTGG 2764
Db 2461 ATCCGAATACCTTGGTTCCTTGGGAATCATTTTCATTTTCTTCGGCGATATTTTGG 2520
Qy 2765 GAAACGTCAGAGATGTGAAGCGCTGGAATCTCAAACTCCGAGTCCAGTGTTCCTCCAC 2824
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Db 2881 GAGATATGATGATCTCAGTAAAGGTCATTTGAATACACAGACTTTGAAAAAGACGA 2940
Qy 3185 CCTTGGGAATATCAGAAACGCCACCCAGCCCTGGCCCTGAGAGAGTATGATATCTTT 3244
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Qy 3365 CTCATCTCAGCCCTTTTAGATTTCTCAGAACCCGAAAGGTAAATTTGGATTGATGAAGATC 3424
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Db 3181 TTGCAACTGAAATTTGACCTTCAGATTTAAGGAAGAAATGTCATCATCTCAGGAA 3240
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Qy 3665 CTGTTGTCCTTGCAGGGCAATCTCAGGAAAAATCAGATATTCATTTATGATCAAGCG 3724
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Qy 3725 ACGCAAAATGTGGATCCAAAGACTGATGAGTTAATACAAAAAATCCGGGAGAAATTT 3784
Db 3481 ACGCAAAATGTGGATCCAAAGACTGATGAGTTAATACAAAAAATCCGGGAGAAATTT 3540
Qy 3785 GCCCACTGCACCGTGTAAACATTTGCACAGATGAACACCAATTTATGACAGCACAAG 3844
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Db 3721 CTCACCTGAAACAGCAAAACAGAGAT 3745
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RESULT 11

US-09-925-300-613

; Sequence 613, Application US/09925300

; Patent No. US20020151681A1

; GENERAL INFORMATION:

; APPLICANT: Craig Rosen,

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA101

; CURRENT APPLICATION NUMBER: US/09/925,300

; CURRENT FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05988

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 1890

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 613

; LENGTH: 1427

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (297)

; OTHER INFORMATION: n equals a,t,g, or c

US-09-925-300-613

Query Match

Best Local Similarity 28.8%; Score 1218; DB 10; Length 1427;

Matches 1221; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1430 GAATTTGTTAGCTGTGTCGGCCCCGTGGAGCAGGAAAGTCATCTGTTAAAGTCGGGTG 1489

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Qy 1490 CTCGGGGAAATTCGCCCAAGTCACGGGCTGTCAGCTGCATCGAAGAAATGCTATGTG 1549

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Qy 1550 TCTCAGCAGCCCTGGGTGTTCTCGGGAACCTCTCAGGAGTAATAATTTTGGGAAGAAA 1609

Db 122 TCTCAGCAGCCCTGGGTGTTCTCGGGAACCTCTCAGGAGTAATAATTTTGGGAAGAAA 181

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Qy 1730 CAGAAAGCAGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTG 1789

Db 302 CAGAAAGCAGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCTG 361

Qy 1790 GAGCATCTCTCAGTGCAGTAGATCGGGAAGTTAGCAGACACTTGTTCGACATGTGTATT 1849

Db 362 GAGCATCTCTCAGTGCAGTAGATCGGGAAGTTAGCAGACACTTGTTCGACATGTGTATT 421

Qy 1850 TCTCAAAATTTTCATCAGAAAGATCAAAATTTTAGTCACATCATCAGTTGCAAGTACCAA 1909

Db 422 TCTCAAAATTTTCATCAGAAAGATCAAAATTTTAGTCACATCATCAGTTGCAAGTACCAA 481

Qy 1910 GCTGCAAGTCAGATTTCTGATATTGAAAGATGTTAAATGTTGCAAGGAGGACTTACACT 1969

Db 482 GCTGCAAGTCAGATTTCTGATATTGAAAGATGTTAAATGTTGCAAGGAGGACTTACACT 541

Qy 1970 GAGTTCTTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATGAGGAAAGT 2029

Db 542 GAGTTCTTAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAGGATATGAGGAAAGT 601

Qy 2030 GAACAACCTCCAGTTCCAGGAACCTCCACACTTAAGAAATCGTACCTTCTCAGAGTCTTCG 2089

Db 602 GAACAACCTCCAGTTCCAGGAACCTCCACACTTAAGAAATCGTACCTTCTCAGAGTCTTCG 661

Qy 2090 GTTTGGTCTCAACAATCTTCTAGACCCCTCTTGAAGATGGTGTCTGAGAGACCAAGAT 2149

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Db 662 GTTGGCTCAACAATCTCTAGACCCCTCTGAAGATGGTCTCGAGAGCCAAAGT 721
QY 2150 ACAGAGAAATGTCAGTACACTATCAGAGGAGAACCGTCTGGAAGAAAGTTGGTTTT 2209
Db 722 ACAGAGAAATGTCAGTACACTATCAGAGGAGAACCGTCTGGAAGAAAGTTGGTTTT 781
QY 2210 CAGGCTATAGAAATCTTACAGCTGGTGTCTACTGGATGTCTCATTTTCTTATT 2269
Db 782 CAGGCTATAGAAATCTTACAGCTGGTGTCTACTGGATGTCTCATTTTCTTATT 841
QY 2270 CTCCTAAACACTGCAGCTGAGTTCCTATGCTTCAAGATGGTGTCTTCACTACG 2329
Db 842 CTCCTAAACACTGCAGCTGAGTTCCTATGCTTCAAGATGGTGTCTTCACTACG 901
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Db 902 GCAACAAACAAAGTATCTAAATGTCTACTGTAATGAGGAGGAAATGTAACCGAGAG 961
QY 2390 CTAGATCTTAAGTGTAGTAATTTATTCAGGTTTAACTGTAGCTACCGTCTTTT 2449
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QY 2630 ACGTTTTTAGATTTTCATCCAGACATTTGCTACAAGT 2664
Db 1202 ACGTTTTTAGATTTTCATCCAGGTAACGTTGAGAGT 1236
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RESULT 12

US-10-012-896-824

; Sequence 824, Application US/10012896

; Publication No. US20020183251A1

; GENERAL INFORMATION:

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; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
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; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 824
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-824
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Query Match 24.7%; Score 1045.4; DB 9; Length 1074;
Best Local Similarity 99.9%; Pred. No. 1.3e-291;
Matches 1046; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1226 TCAGCCATTGAGAGGTTGTACAGAGCAATCGTCAGCATCCGGAAGATCCAGACCTTTTGG 1285
Db 4 TCAGCCATTGAGAGGTTGTACAGAGCAATCGTCAGCATCCGGAAGATCCAGACCTTTTGG 63
QY 1286 CTACTGTGATGAGATATCAGAGCGCAACCTCAGCTGCCCTCAGATGGTAAAAAGATGGTG 1345
Db 64 CTACTGTGATGAGATATCAGAGCGCAACCTCAGCTGCCCTCAGATGGTAAAAAGATGGTG 123
QY 1346 CATGTGCAGGATTTTACTGCTTTTGGGATAAGGCATCAGACCCCAACTCTACAAGGC 1405
Db 124 CATGTGCAGGATTTTACTGCTTTTGGGATAAGGCATCAGACCCCAACTCTACAAGGC 183
QY 1406 CTTTCTTTTACTGTCTCAGACCTGGCGAATTTTGTAGCTGTGGTCCGCCCTGGAGCAGGG 1465
Db 184 CTTTCTTTTACTGTCTCAGACCTGGCGAATTTTGTAGCTGTGGTCCGCCCTGGAGCAGGG 243
QY 1466 AAGTCATCACTGTTAAGTGCCTGCTCGGGGAAATTTGGCCCCCAAGTCACGGGCTGGTTCAGC 1525
Db 244 AAGTCATCACTGTTAAGTGCCTGCTCGGGGAAATTTGGCCCCCAAGTCACGGGCTGGTTCAGC 303
QY 1526 GTGCATGGAAGAAATGTCATGCTGTCTCAGCAGCCCTGGGTGTTCTCGGGAACTCTGAGG 1585
Db 304 GTGCATGGAAGAAATGTCATGCTGTCTCAGCAGCCCTGGGTGTTCTCGGGAACTCTGAGG 363
QY 1586 AGTAATATTTTATTTGGGAAGAAATATGAAAGGAACCATATGAAAAAGTCTATAAGGCT 1645
Db 364 AGTAATATTTTATTTGGGAAGAAATACGAAAGGAACCATATGAAAAAGTCTATAAGGCT 423
QY 1646 TGTGCTCTGAAAAAGGATTTACAGCTGTTTGGAGGATGGTGTACTGTATAGAGAT 1705
Db 424 TGTGCTCTGAAAAAGGATTTACAGCTGTTTGGAGGATGGTGTACTGTATAGAGAT 483
QY 1706 CGGGGAACACGCTCAGTGGAGGCGAGAAAGCACCGGTAAACCTTGCAGAGCAGCTGTAT 1765
Db 484 CGGGGAACACGCTCAGTGGAGGCGAGAAAGCACCGGTAAACCTTGCAGAGCAGCTGTAT 543
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Db 544 CAAGATGCTGACATCTATCTCTCGGACGATCCTCTCAGTGCAGTAGATGCGGAAGTTAGC 603
QY 1826 AGACACTGTTTGCAGACTGTATTTGTCAAATTTTGGCAGAGAAAGTACAAATTTTAGTG 1885
Db 604 AGACACTGTTTGCAGACTGTATTTGTCAAATTTTGGCAGAGAAAGTACAAATTTTAGTG 663
QY 1886 ACTCATCAGTTGCACTACCTCAAGCTCAAGTCAAGTCTGATATTTGAAAGATGGTAAA 1945
Db 664 ACTCATCAGTTGCACTACCTCAAGCTCAAGTCAAGTCTGATATTTGAAAGATGGTAAA 723
QY 1946 ATGCTGCAAGAGGAGGACTTACACTGAGTTCTCTAAATCTGCTATAGATTTTGGCTCCCTT 2005
Db 724 ATGCTGCAAGAGGAGGACTTACACTGAGTTCTCTAAATCTGCTATAGATTTTGGCTCCCTT 783
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RESULT 13
US-09-759-143-824
; Sequence 824, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 824
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-824
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Query Match 24.7%; Score 1045.4; DB 10; Length 1074;
Best Local Similarity 99.9%; Pred. No. 1.3e-291;
Matches 1046; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1226 TCAGCCATTGAGAGGTGTGTCAGAGCAATCGTCAGCATCCGAAAGATCCAGACCTTTTGT 1285
      |||
Db 4 TCAGCCATTGAGAGGTGTGTCAGAGCAATCGTCAGCATCCGAAAGATCCAGACCTTTTGT 63
      |||
QY 1286 CTACTTGATGAGATATCACAGCCCAACCGTCAGCTGCCGTGATGTTAAAGATGGTG 1345
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Db 64 CTACTTGATGAGATATCACAGCCCAACCGTCAGCTGCCGTGATGTTAAAGATGGTG 123
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Db 184 CTTTCTCTTACTCTCAGACCTGCGGAATGTTAGCTGTGGTCGCCCGCTGGGAGCAGGG 243
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RESULT 14
US-09-780-669-824
; Sequence 824, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
```

; APPLICANT: Hepler, William
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 824
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-824

Query Match 24.7%; Score 1045.4; DB 10; Length 1074;
Best Local Similarity 99.9%; Pred. No. 1.3e-291;
Matches 1046; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1236 TCAGCCATTGAGAGGTTGTCAGAGGCAATCGTCAGCATCCGAAGATCCAGACCTTTTGG 1285
DB 4 TCAGCCATTGAGAGGTTGTCAGAGGCAATCGTCAGCATCCGAAGATCCAGACCTTTTGG 63
QY 1286 CTACTTGATGAGATATACAGCGCAACCGTCAGCTGCCGTCTAGATGGTAAAGATGGTG 1345
DB 64 CTACTTGATGAGATATACAGCGCAACCGTCAGCTGCCGTCTAGATGGTAAAGATGGTG 123
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DB 184 CTTTCCTTTACTGTCAGACCTGGCGAATTTAGTGTGGTGGCGCCGTCGGGACGAGG 243
QY 1466 AAGTCATCAGTGTAAAGTGGCGGATTTAGTGTGGTGGCGCCGTCGGGACGAGG 1525
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RESULT 15

US-09-822-827-824
; Sequence 824, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 824
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-824

Query Match 24.7%; Score 1045.4; DB 10; Length 1074;
Best Local Similarity 99.9%; Pred. No. 1.3e-291;
Matches 1046; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1236 TCAGCCATTGAGAGGTTGTCAGAGGCAATCGTCAGCATCCGAAGATCCAGACCTTTTGG 1285
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Search completed: December 18, 2002, 21:40:09
Job time : 144.455 secs

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 S', mRNA sequence.
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 BQ225211.1 GI:20406611
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 EMAIL: cgabs-r@mail.nih.gov
 TISSUE: Procurement: ATCC
 CDNA LIBRARY PREPARATION: Life Technologies, Inc.
 CDNA LIBRARY ARRAYED BY: The I.M.A.G.E. Consortium (LNL)
 CDNA SEQUENCING BY: Agencourt Bioscience Corporation
 CLONE DISTRIBUTION: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
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Db 841 TT 842
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RESULT 2

BG697157

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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BG697157.1 GI:13963059

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 880)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA

Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10699 row: a column: 22

High quality sequence stop: 820.

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Location/Qualifiers

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/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.

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Technologies. Note: this is a NCI_CGAP Library."

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Query Match 13.7%; Score 802.2; DB 12; Length 880;

Best Local Similarity 98.0%; Pred. No. 1.8e-115;

Matches 854; Conservative 0; Mismatches 13; Indels 4; Gaps 4;

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AUTHORS	Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, Y.		
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JOURNAL	Unpublished (2000)		
COMMENT	Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute. Location/Qualifiers 1. -862 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="NT2RP3003721" /clone_lib="NT2RP3"		
FEATURES	source		

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 LOCUS AGENCOURT_812242 Lupski_dorsal_root_ganglion Homo sapiens cDNA
 clone IMAGE:6179508 5', mRNA sequence.
 ACCESSION BQ898022
 VERSION BQ898022.1 GI:22290036
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 935)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM13560 row: m column: 13
 High quality sequence stop: 701.
 Location/Qualifiers
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 /sex="male"
 /tissue_type="dorsal root ganglia"
 /dev_stage="adult, 36 yr"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
 Not1; Site_2: SalI; cDNA made by oligo-dr priming.
 Directionally cloned using the following adaptors:
 5'-TCGACCCAGCGGTCG-3' and
 5'-GACTAGTTCTAGATCGGAGCGGCCCT(15)-3'. Size selected >
 1 kb for average insert length 1.7 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine) and is available through Life
 Technologies."
 BASE COUNT 220 a 220 c 230 g 264 t 1 others
 ORIGIN
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 Best Local Similarity 95.9%; Pred. No. 3.7e-113;
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 Qy 3789 AAGATTGGCATTGTGGGCGGACAGATCAGGAAAGTCTCTCGCTGGGATGGCCCTCTTC 3848
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 Qy 3849 GCTCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAAGATCAGTGATATT 3908
 Db 61 GCTCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAAGATCAGTGATATT 120
 Qy 3909 GGCCTTGGCGACCTCCGAGCAACTCTCTATCTTCCTCAAGACCGGCTGTTCAGT 3968
 Db 121 GGCCTTGGCGACCTCCGAGCAACTCTCTATCTTCCTCAAGACCGGCTGTTCAGT 180
 Qy 3969 GGCCTGTGAGATCAAAATTTGGACCCCTCAACAGTACACTGAAGACACAGATTGGGAT 4028
 Db 181 GGCCTGTGAGATCAAAATTTGGACCCCTCAACAGTACACTGAAGACACAGATTGGGAT 240
 Qy 4029 GCCCTGGAGAGACACATGAAGAANTGTATTCCTGAGCTACCTCTGAACCTTGAATCT 4088
 Db 241 GCCCTGGAGAGACACATGAAGAANTGTATTCCTGAGCTACCTCTGAACCTTGAATCT 300

Qy 4089 GAAGTGATGAGAGATGGGATAAATTCTCACTGGGGGAACGGCAGCTCTTGTGATAGCT 4148
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 Qy 4149 AGAGCCCTGCTCCGCCACTCTAAGATTCTGATTTAGATGAAGCCAGCTGCCATGGAC 4208
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 Qy 4568 -ATTGGCTTGTGTCTTCACTTTTAGGAGAGTCATATTTTATT-----ATTGATTT 4620
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 VERSION B1770993.1 GI:15762571
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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 851)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
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 High quality sequence stop: 784.
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 /clone="IMAGE:5204983"

FEATURES
 source

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/lab_host="DH10B"
/Note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dr
primed, and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research genetics tracking code 026. Note:
this is a NIH_MGC Library."
BASE COUNT 197 a 198 c 184 g 272 t
ORIGIN
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Best Local Similarity 98.6%; Pred. No. 2.5e-110;
Matches 818; Conservative 0; Mismatches 8; Indels 4; Gaps 4;
QY 4176 CTGATTTTGTAGTGAAGCCAGCTGCGATGGACACAGACAGACACTTATTGATTCAAGAG 4235
DB 1 CTGATTTTGTAGTGAAGCCAGCTGCGATGGACACAGACAGACACTTATTGATTCAAGAG 60
QY 4236 ACCATCCGAGAACATTTGCGACTGTACATGCTGACCAATGCCATGCCCTGCACAGC 4295
DB 61 ACCATCCGAGAACATTTGCGACTGTACATGCTGACCAATGCCATGCCCTGCACAGC 120
QY 4296 GTTCTAGGCTCCGATAGGATTATGGTGTGCTGGCCAGGACAGGTGGGAGTTGACACC 4355
DB 121 GTTCTAGGCTCCGATAGGATTATGGTGTGCTGGCCCA-GGACAGGTGGGAGTTGACACC 179
QY 4356 CCATCGGTCTCTGTCACACGACAGTCCCGATTCTATGCCATGTTGCTGCTGCAGAG 4415
DB 180 CCATCGGTCTCTGTCACACGACAGTCCCGATTCTATGCCATGTTGCTGCTGCAGAG 239
QY 4416 AACAGGTGCTGTCAGGGCTGACCTCCCTGTTGTGACGAAGTCTCTTTCTTTTAGAGC 4475
DB 240 AACAGGTGCTGTCAGGGCTGACCTCCCTGTTGTGACGAAGTCTCTTTCTTTTAGAGC 299
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QY 4896 GTAG-GAAGAGTAGCATTTTCATTTCTCTAGCTGGTGGTTTTCAGGTGCCAGGTTTTCT 4954
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RESULT 6
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LOCUS
DEFINITION
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5', mRNA sequence.
AGENCOURT_6448278 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5531707
BM541578
VERSION
BM541578.1 GI:18770340
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1083)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM12213 row: m column: 20
High quality sequence stop: 643.
FEATURES
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/Note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
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Average insert size 2.1 kb."
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ORIGIN
Query Match 13.0%; Score 761.6; DB 13; Length 1083;
Best Local Similarity 98.2%; Pred. No. 3.4e-109;
Matches 812; Conservative 0; Mismatches 10; Indels 5; Gaps 4;
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QY 3028 CAGGAGGATTTCAACAGGTTTTTCCAAAGACATGGATGAAGTTGACGTGGCGTCCGCT 3087
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DB 122 TCAGGCCGAGATGTTTCATCCAGAACGTTATCCTGTGGTCTCTCTGTGGGAATGATCG 181
QY 3148 CAGGAGTCTTCCCGTGGTTCTTGTGGCAGTGGGGCCCTTGTGTCATCTCTTTTCAGTCC 3207
DB 182 CAGGAGTCTTCCCGTGGTTCTTGTGGCAGTGGGGCCCTTGTGTCATCTCTTTTCAGTCC 241
QY 3208 TGCACATTTGCTCCAGGGTCTGATTCGGGAGCTGAAGCGTCTGGACAATATCAGCAGT 3267
DB 242 TGCACATTTGCTCCAGGGTCTGATTCGGGAGCTGAAGCGTCTGGACAATATCAGCAGT 301
QY 3268 CACCTTTCTCTCCACATACGTCACGATACAGGCGCTTGGCCACCATCCAGCGCTACA 3327
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[illegible]

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RESULT 11
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DEFINITION sequence.
ACCESSION AUI37090
VERSION AUI37090.1 GI:10597629
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 761)
AUTHORS Ota.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saito.K., Kawai.Y.,
Yamamoto.J., Wakamatsu.A., Nakamura.Y., Nagai.T., Sugano.S. and
Isozaki.T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isozaki
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES
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Best Local Similarity 96.3%; Pred. No. 3.3e-97;
Matches 720; Conservative 0; Mismatches 25; Indels 3; Gaps 2;
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QY 4377 GACAGTTCCCGATTTCTATGCCATGTTG 4404
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RESULT 12
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DEFINITION UI-E-CQ1-aew-h-01-0-UI 3', mRNA sequence.
ACCESSION BM665074
VERSION BM665074.1 GI:18971693
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 716)
AUTHORS Bonaldo.M.F., Lennon.G. and Soares.M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE

COMMENT

97044477
 Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 The following repetitive elements were found in this cDNA
 sequence: 1-41, >AT-rich#Low_complexity (matched complement)
 Seq primer: M13 Forward
 POLYA=Yes.

FEATURES
source

Location/Qualifiers
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 /note="Organ: eye; Vector: p7T3-Pac (Pharmacia) with a
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 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dr primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into p7T3-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dfr)18 tail. The sequence tag for this library is
 CCATTAAAGTG. This library was created for the program, Gene
 Discovery in the Visual System, supported by National Eye
 Institute (NEI).
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 TAG_TISSUE=human optic nerve
 TAG_SEQ=CCATTAAAGTG"
 BASE COUNT 212 a 165 c 185 g 154 t

Query Match 11.78; Score 683.4; DB 13; Length 716;
 Best Local Similarity 99.7%; Pred. No. 6.1e-97;
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 QY 5243 TGTGTTTCTTAAACAAGATCAGTCTATCCACAGAGATGCCATCGCTCAGGTTCCCTAT 5302
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 DB GGCTGGCCACTGCACAGAGCTCTCCAGCTCCAGACCTGTTGGTTCCAGCCCTGGAGCC 458
 QY 5363 AACTGCTGCTTTTGTAGGTGGCACTTTTTCATTGTCCTATTTCACACACCTCCACAGTTCA 5422
 DB AACTGCTGCTTTTGTAGGTGGCACTTTTTCATTGTCCTATTTCACACACCTCCACAGTTCA 398

QY 5423 GTGGCAGGGCTCAGGATTTCTGGTGGTCTGTCTTTCTCTTTCTCACCAGTGTGCGCAGT 5482
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 QY 5483 CTCTCTCTCTCTCTCCCTCAAGTCTGCAACTTTAAGCAGCTCTTCTGCTAATCAGTGTCT 5542
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 QY 5543 CACACTGGCGGTAGAACTTTTGTACTGTAAGAGACCTACCTCAGTGTGCTGTGCTGT 5602
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 DEFINITION prime, mRNA sequence.
 ACCESSION AL543173
 VERSION AL543173.1 GI:12875651
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 889)
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 208 a 218 g 254 t 1 others
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Query Match 11.6%; Score 677.8; DB 9; Length 889;
 Best Local Similarity 99.0%; Pred. No. 4.1e-96;
 Matches 682; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 680)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>,
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgbps-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10599 row: j column: 19
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Matches 678; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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GenCore version 5.1.3
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Searched: 356696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 713392

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	435.8	7.5	3786	9	US-10-012-896-1006
3	435.8	7.5	4395	9	US-10-012-896-1007
4	435.8	7.5	6140	9	US-10-012-896-536
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21	275.6	4.7	418	10	US-09-960-352-4836	Sequence 4836, Ap
22	248.2	4.3	1936	10	US-09-880-107-3832	Sequence 3832, Ap
23	245.8	4.2	1977	10	US-09-954-456-804	Sequence 804, App
24	245.8	4.2	1977	10	US-09-880-107-3407	Sequence 3407, Ap
25	245.8	4.2	1977	10	US-09-967-768A-190	Sequence 190, App
26	218.4	3.7	1448	10	US-09-925-299-157	Sequence 157, App
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37	136.4	2.3	404	10	US-09-833-381-1090	Sequence 1090, Ap
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ALIGNMENTS

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; Sequence 1684, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1684
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1684

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Best Local Similarity 100.0%; Pred. No. 3.3e-91;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 1006, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1006
; LENGTH: 3786
; TYPE: DNA

; ORGANISM: Homo sapiens
us-10-012-896-1006

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QY 3654 AGAATTAAGAAAGCTCCCTCCCTGACTGGCCGAGGAGGAGGAGTGTGCTTTGAG 3713
Db 2944 TGGGAATATCAGAAAGCCCAACACAGCTGCGCCCATGAAGAGTGTAACTTTTGAC 3003
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QY 3774 ATCAACCTTAAGAGAAAGTATGCTATGTTGGGCGGACAGGATCAGGAGTCTCGCTG 3833
Db 3064 ATTAATCAAGAAAGGTTGCTATGTTGGGAGAACCGGAGTGTGAAAGTCTCCCTC 3123
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Db 3124 ATCTAGCGCTTTTATGATGCTAGA---ACCGAGGTTAAATTTGGATGATGATGATC 3180
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QY 4314 ATTATGCTGCTGCCCGAGGACAGGTGGTGGAGTTTGACACACCCCATCGTCTCTGTC 4373
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Db 3661 AATAAAGAGAGCTATTTTACAAGATGGT 3689

RESULT 3

US-10-012-896-1007
; Sequence 1007, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012.896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1007
; LENGTH: 4395
; TYPE: DNA

ORGANISM: Homo sapiens
US-10-012-896-1007

Query Match 7.5%; Score 435.8; DB 9; Length 4395;
Best Local Similarity 48.8%; Pred. No. 2.8e-89;
Matches 1243; Conservative 0; Mismatches 1297; Indels 9; Gaps 2;

QY 1854 ACACGTGCACAGCATCTGGAGATCCAGAGGTAACCTGGTGGAAATCTGGCGGAGT 1913
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DB GTGGAGGAGGAGTCACTACTGTAACTGCCGTGCTGGGAATGGCCCAAGTCAAC 1878
QY 1974 GCGAGCATGTCAATCAGTGGAACTTCCTTATGTGGCCAGCAGCCCTGGATCCTCAAT 2033
DB GCGTGGTCAAGCTGATGGAAGAAATTCCTATGTCTCAGCAGCCCTGGGTCTCG 1938
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DB 2719 GTCACHTGTAAATGGAGGAGAAATGTAACCGAGAAAGCTAGATCTTAACCTGTACTTAGGA 2778
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; LOCATION: (1)...(6140)
; OTHER INFORMATION: n=A,T,C or G
US-09-759-143-536

Query Match      7.5%; Score 435.8; DB 10; Length 6140;
Best Local Similarity 48.8%; pred. No. 3.4e-89;
Matches 1243; Conservative 0; Mismatches 1297; Indels 9; Gaps 2;

QY 1854 ACATGTCACAGATCGATGTGAGATCCAGAGGGTAAACTGGTGGGAATCTGGGGCAGT 1913
Db 1438 ACTTACAAGGCCCTTCCCTTTACTGTGACAGCTGGCGAATGTTAGCTGTGGTGGGCC 1497
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QY 2814 AACGAGACCTCGGTGAGTGACAGCATGAAGGACAAATCTCTATATGCACTACTATCCAGC 2873

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Db 2398 GTCACTGTAAATGGAGGAGAAATGTAAACCGAGAACTAGATCTTAACTGGTACTTAGGA 2457
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Db 3292 AATGTGAATCTCATGTACAGTCCAGTGGGCTCTCTGATGAAGATCTTCAGACAGACT 3351
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Db 3412 ATCTCAGCCCTTTTAGATTGTGACA--ACCGAAGGTAATAATTTGGATTGATAAGATC 3468
QY 3894 AGAATCAGTATTTGGCCCTTGGCCAGCTCCGAGCAAACTCTCTATCTCTCAAGAG 3953

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Db 3469 TTGACAACTGAAATGGACTTCACGATTTAAGGAAGAAAATGTCATCATACCTCAGGAA 3528
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Qy 4014 GACCAAGATTTGGATGCCCTGGAGAGGACACATGAAGAATGATTGCTCAGCTACCT 4073
Db 3589 GAGGAACCTGTGAATGCCCTTACAAGAGGTACAACTTAAGAAGAACCAATTGAAGATCTTCT 3648
Qy 4074 CTGAACCTTTGAATCTGAAGTATGAGAGATGGGATAACTTCTCAGTGGGGGAACGGCAG 4133
Db 3649 GGTAAATGGTACTGAAATAGCAGAAATCAGGATCCAAATTTTAGTGTGGAGACAGACAA 3708
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Db 3709 CTGGTGTGCCCTTGGCAGGGCAATTTCTCAGGAANAATCAGATATTGATTTATGATGAAGCG 3768
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Qy 4314 ATTATGCTGCGCCAGGACAGCTGGTGGAGTTTGACACCCCATCGGTCCTCTGTCPC 4373
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Db 3949 AATAAGAGAGCCATTTTACAAGATGTT 3977

RESULT 6

US-09-780-669-536
; Sequence 536, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Barrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 536
; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (1)....(6140)
; OTHER INFORMATION: n=A,T,C or G
US-09-780-669-536

Query Match 7.5%; Score 435.8; DB 10; Length 6140;
Best Local Similarity 48.8%; Pred. No. 3.4e-89;
Matches 1243; Conservative 0; Mismatches 1297; Indels 9; Gaps 2;

Qy 1854 ACACCTGCACAGATCGATCGAGATCCAAAGAGGTAAATCGTTGGAATCTCGCGCAGT 1913
Db 1438 ACTCTACAAGGCTTTCCTTTACTGTACACCTGGCAATTTGTAGCTGTGTCGGCCCC 1497
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Qy 2514 AAAAAGGAACACAGTGGTTTCACAGAGAAGTCAACAGACAAGGGTCTTAAACAGAGATCA 2573
Db 2098 CCCACATAGGAATCGTACCTTCTCAGAGTCTTCGGTGTTCGTTCTCAACAATCTTCTAGA 2157
Qy 2574 GTAAAGGAAGAAAAGCAGTAAAGCCAGAGGAGGAGGAGCTTGTGCAGCTGGAAGAGAAA 2633
Db 2158 CCCTCCTTGAAGATGTTGCTCTCGAGAGCCAAAGATCAGAGAATGTCCAGTTACACTA 2217
Qy 2634 GGGCAGGTTCAAGTGGCCCTGCTCAGTATATGTTGCTACATCCAGGCTGTGGGGGCCCC 2693
Db 2218 TCAGAGGAGAACCCCTTCTGAAGGAAAAGTTGGTTTTCAGGCTATAAGAAATTTACTTCA 2277
Qy 2694 TTGCAATCTCTGTTTATATGTCCTTTTTCATGCTGATGTAGGAGCAGCAGCCCTTACG 2753
Db 2278 GCTGGTCTCAGTGGATTTGCTTCAATTTTCTTATTTCTCTTAAACACTGACGCTT 2337
Qy 2754 ACCTGGTGGTTGATTTACTGGATCAAGGAAGGAGGAGGAGGAGTGTGCTGACTCGAGG 2813
Db 2338 GCCTATGCTTCAAGATTTGGTGGCTTTCATCTAGTGGGCAACAAACAAAGTATGCTAAT 2397
Qy 2814 AACGAGACCTCGGTGAGTGACGATGAAGGACAATCCTCATATGCTACTATGCTTATGCTCAGC 2873

Db 2398 GTCACTGTAATGGAGGAAATGTAACCGAGAGCTAGATCTTAACCTGGTACTTAGGA 2457
Qy 2874 ATCTACGCCCTCTCCATGGCAGTCACTGATCCTGGAAGCCATTCGAGGAGTTGCTTTT 2933
Db 2458 ATTTATTCAGGTTAACTGTAGTACCTGCTCTTTTGGCATAGCAAGATCTCTATTGGTA 2517
Qy 2934 GTCAAGGCGACGCTCGAGCTTCTCCCGGTGCATGACGAGCTTTTCCGAAGGATCCCT 2993
Db 2518 TTCTACGCTCTTTAACTCTTCACAACTTTGCAACAATAATGTTTCAGTCAATCTG 2577
Qy 2994 CGAAGCCCTATGAAGTTTTTTGACACGACCCACAGGAGGATTTCTCAACAGGTTTTCC 3053
Db 2578 AAAGCTCCGGTATTATCTTTGATAGAAATCCAAATAGGAAGAAATTTAAATCGTTCTCC 2637
Qy 3054 AAAGACATGGATGAAGTTGACGTGGGCTGCGCTGCCAGGCGAGATGTTCAATCCAGAAC 3113
Db 2638 AAAGACATGGACACTTGGATGATTTGCTGCGCTGACCTTTTATGATTTCAATCCAGACA 2697
Qy 3114 GTTATCCTGGTCTTCTGTGTGGAAATGATCGCAGGAGTCTTCCGCTGGTTCCCTTGTG 3173
Db 2698 TTGCTACAGTGGTGGTGTCTCTGTGGCTGTGGCCGTGATTCCTTGGATCGCAATA 2757
Qy 3174 CGAGTGGGCCCCCTTGTATCCTCTTTTCAAGTCCGACATTTGTCPCAGGCTCCTGATT 3233
Db 2758 CCGTTGGTCCCTTGGAAATCATTTTCAATTTTTCGCGGATATTTTGGGAAACGTCA 2817
Qy 3234 CGGAGCTGAAGCGCTGTGCAATATACCGAGTACCTTTCTCTCCACATCAGTCC 3293
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Qy 3294 AGCATACAGGCGCTTGCACCATTCACGCTTACATAAAGGCGAGGATTTCTGACAGA 3353
Db 2878 TCTCTCCAGGCGCTCGACCATCGGGCATACAAAGCAGAGAGGTTCTCAGGACTG 2937
Qy 3354 TACCAGGAGCTGCTGGATGACAAACAGCTCCTTTTTTTTGTATTACGTGCGATGCGG 3413
Db 2938 TTTGATGCACACAGGCTTTACATTCAGAGGCTTGGTTCTTGTGTTGACAACTGCCGC 2997
Qy 3414 TGGCTGGCTGCGGCTGGACCTATCAGCATCGCCCTCATCACACACGGGGCTGATG 3473
Db 2998 TGGTTGCGCGCTCGCTGATGCCATCTGTGCGCATGTTTGTATCATCATCTGCTTGGG 3057
Qy 3474 ATCGTCTTATACACGGGAGATTCGCCAGCTATGCGGGTCTGCCATCTCTATGCT 3533
Db 3058 TCCCTGATCTCGGAAAAAATCTGATGTCGGGAGGTTGGTTGGCACTGCTCTATGCC 3117
Qy 3534 GTCCAGTTAACGGGCTGTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGTCA 3593
Db 3118 CTCACGCTCATGGGATGTTTCAGTGGTGTGTTGCAACAAAGTCTGAAGTTGAGAATG 3177
Qy 3594 TTCACCTCGGTGAGAGGATCAATCACTACATTAAGACTCTGTCTTGAAGCACTGCC 3653
Db 3178 ATGATCTCAGTAAAGGCTTATGAATACACAGACCTT-----GAAAGAAAGCACCT 3231
Qy 3654 AGAATTAAGAAACAGCTCCCTCCCTGACTGGCCCGGAGGAGGAGGCTGACCTTTGAG 3713
Db 3232 TGGGATATCAGAAAGCCACCCAGCCAGCTGGCCCATGAAGGATGATATCTTTGAC 3291
Qy 3714 AACGAGAGATGAGGTACCGAGAAACCTCCCTCTTGTCTTAAAGAAAGTATCCTTACG 3773
Db 3292 AATGTGAACCTTATGATACAGTCCAGTGGGCTCTGTTACTGAAGCATCTGACAGCACTC 3351
Qy 3774 ATCAACCTTAAGAGAGATTTGGCATTTGGGCGGACAGGATCAGGAGTCCCTGCTG 3833
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Qy 3834 GGGATGGCCCTCTCCGCTGCTGGTGAAGTTATCTGAGGCTGTCATCAAGATGATGAGTG 3893
Db 3412 ATCTCAGCCCTTTTATGATTTGTAGTCA---ACCGAAGGTAATAATTTGGATGATAAGATC 3468
Qy 3894 AGAATCAGTGATTTGGCCCTTGGCCAGCTCCGAGCAAACTCTCTATCATTTCTCAGAG 3953

Db 3469 TTGACAACCTGAAATTTGGACTTTCAGATTTTAAGGAAGAAAAATGTCATATACCTCAGAA 3528
Qy 3954 CCGGCTCTGTTCACTAGTGGCATGTGATCAATTAATTTGGACCCCTTCAACCACTACACTGAA 4013
Db 3529 CTTGTTTGTCTACTGGAACAATGAGGAAAACTGGATCCCTTAAATGAGCACACCGAT 3588
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Db 3589 GAGGAACCTGTGGAATGCCTTACAAGAGGTACAACCTTAAAGAAACCAATTGAAGATCTTCT 3648
Qy 4074 CTGAACCTTGAATCTCAAGTGGATGGAGATTAACCTTCTCAGTGGGGGACGCGAG 4133
Db 3649 GGTAAATGGATCTGAATTTAGCAGATCAGATCCCAATTTTGTGTTGGACAAGACAA 3708
Qy 4134 CTCTCTGATAGTACGACCTCGCCGCTCTGTAAGATTTCTGATTTTGTAGATGAAGCC 4193
Db 3709 CTGCTGTGCTGCCAGGCAATTCAGGAAAAATCAGATNTTGTATTTGATGAAGCG 3768
Qy 4194 ACAGCTGCCATGACACAGACAGACTTATTTGATTTCAAGAGACCATCCGAGAGCAATTT 4253
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Qy 4254 GCAGACTGTACATGCTGACCATGCCCCATCGCTGCACACGGTTCTAGGCTCCGATAGG 4313
Db 3829 GCCCACTGCACCGTGTAACTTGCACAGATTTGAACACCAATTTATGACAGCGACAAG 3888
Qy 4314 ATTATGCTGCTGCCAGGACAGGTGGTGGAGTTTTCACACCCCATCGGCTCTCTGTCC 4373
Db 3889 ATNATGTTTATGATTCAGGAAGACTGAAAGATATGATGAGCGGTATGTTTCTGCGAA 3948
Qy 4374 AACGACAGTTCCCGATTTATGCGCATGTT 4402
Db 3949 AATAAAGAGAGCCTATTTTACAAGATGTT 3977

RESULT 7

US-09-822-827-536
; Sequence 536, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121-534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 536
; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(6140)
; OTHER INFORMATION: n=A,T,C or G
US-09-822-827-536

Query Match 7.5%; Score 435.8; DB 10; Length 6140;
Best Local Similarity 48.8%; Pred. No. 3.4e-89;
Matches 1243; Conservative 0; Mismatches 1297; Indels 9; Gaps 2;

Qy 1854 ACACCTCACAGCATCGATCTGGAGATCCAAAGAGGTAAACCTGTTGGAATCTCGGCAGT 1913
Db 1438 ACTCTACAGGCCCTTCTCTTACTGTGTCAGACCTGGCGAATTTAGTGTGGTCGGCCCC 1497
Qy 1914 GTGGAGGTGGAATAACCTCTCTCATTTAGCCCAATTTTAGCCAGATCAGCCTTCTAGAG 1973
Db 1498 GTGGAGGAGGAGTCACTACTGTTAAGTCCGCTGCTCGGGGATTTGGCCCCAAGTCAC 1557
Qy 1974 GGCAGCATTCATCAGTGAACCTTCGCTTATGTGGCCACAGAGGCTTGATCCTCAAT 2033
Db 1558 GGGCTGCTCAGCGTGCATGGAAGAAATTCCTATGTCTCAGACGCTGGGTGTTCTCG 1617

Qy	2034	GCTACTCTGAGACACACATCCCTGGTTTGGGAAGGAATATGATGAAGAAGATACAACACTCT	2093
Db	1618		
		GGAACCTCTGAGGAGTAATAATTTTTATTGGAAGAATAACGAAAAGAACGATATCAAAAA	1677
Qy	2094	GTGCTGAACAGCTGTCGCCCTGAGGCCTGACCTGGCCATCTCTCCAGCAGCGACCTGACG	2153
Db	1678		
		GTCTAATAAGCCTTGCTCTGAATAAAAGGATTTACAGCTGTTGGAGGATGGTGATCTGACT	1737
Qy	2154	GAGATTGGACGAGCAGAGCCAACCTGACGGTGGGCGAGCCGACAGAGATCAGCCTTGCC	2213
Db	1738		
		GTGATAGAGATCGGGAAACCAGCTGATGGAGGCGAGAAAGCACGGGTAAACCTTGCA	1797
Qy	2214	CGGCCCCGTGATAGTGACAGGAGCATCTACATCTCGAGCACCCCCTCAGTGCCTTAGAT	2273
Db	1798		
		AGAGCACTGTATCAAGATGCTGACATCTATCTCTCGAGGATCCCTCAGTGCAGTAGAT	1857
Qy	2274	GCCATGTGGGCACCAACCATCTTTCAATAGTGTATCTCCGGAACAATCTCAAAGTCCAAGACA	2333
Db	1858		
		GCGGAAGTTAGCAGACACTGTTCGAACTGTGTATTTGTCFAAATTTGTCATGAGAAGATC	1917
Qy	2334	GTCTCTGTTCTTACCCACCAGTACAGTACCTGCTTGACTGTGATGAAGTATCTTCATG	2393
Db	1918		
		ACAAATTTAGTGACTCATCAGTTGCACTACCTFCAAGCTGCAAGTCAAGTTCGATATG	1977
Qy	2394	AAAGAGGCCTGTATTACGGAAGAGCGACCCATGAGAACTGATGAATTTAAATGGTGAC	2453
Db	1978		
		AAAGTGTAAATGGTCAGRAGGGACTTACACTGAGTTCCTTAAATCTGGTATAGAT	2037
Qy	2454	TATGCTACCAATTTTTAATACCTGTGCTGGGAGAGACACCGCCAGTTGAGATCAATPCA	2513
Db	2038		
		TTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAGTGAACAACCTCCAGTTCAGGAAC	2097
Qy	2514	AAAAAGGAACCACTGGTTCACAGRAGAGTACARAACRAGGCTCTTAAACAGGATCA	2573
Db	2098		
		CCCACTAAGGAATCGTACCTTCAGAGCTTCGCGTTTGGTCTCAACAAATCTTCFAGA	2157
Qy	2574	GTAAAGAGGAAAAAGCAGTAAAGCCAGAGGAAGGCGAGCTTGTCAGCTGGAAGAGAAA	2633
Db	2158		
		CCCTCCTTGAAGATGGTGCTCTGGAGAGCCAGATACAGAGAATGTCCCAGTTACACTA	2217
Qy	2634	GGGAGGGTTCACTGCCCTGTGATATAGTGTCATATGCTGATGTAGCAGCAGCCGCTCAGC	2693
Db	2218		
		TCAGAGGAGAACCGTCTCTGAAGGAAAAGTTGGTTTTCAGGCTATAAGAATTTACTTCAGA	2277
Qy	2694	TTGGCATCTCGTATTATATGCGCTTTTCATGCTGATGTAGCAGCAGCCGCTTCAGC	2753
Db	2278		
		GCTGGTGCTACPGGAATGTCTCAATTTCCCTTATCTTCCTTAAACACTGCAGCTCAGGTT	2337
Qy	2754	ACCTGTGGTTGAGTTACTCGATCAAGCAAGGAAGCGGGAACACCAGTGTGACTCGAGGG	2813
Db	2338		
		GCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAACAACAAGTATGCTTAAAT	2397
Qy	2814	AACGAGACCTCGGTGAGTGACAGATGAAAGACAATCCTCATATGCACTACTATGCCAGC	2873
Db	2398		
		GTCACTGTAAATGGAGAGGAAATGTAAACCGAGAAGCTAGATCTTAACTGCTACTTAGGA	2457
Qy	2874	ATCTACGCCCTCTCCATGCACTGATGCTGATCCTTGAAAGCCATTCAGGAGTGCTTT	2933
Db	2458		
		ATTTATTCAGTTTAACTGTAGCTACCGTCTCTTTTGGCATAGCAAGATCTCTATTGGTA	2517
Qy	2934	GTCAAGGCGACGTGCGAGCTTCTCCCGGCTGTCATCAGAGCTTTTCCGAAAGATCCCT	2993
Db	2518		
		TTCTAGCTCTGTTAACTCTTCACAACCTTTGCACAACAANAATGTTTGAGTCAATCTG	2577
Qy	2994	CGAAGCCCTATGAAGTTTTTGTACAGACCCGCCACAGGGAGGATTTCAACAGGTTTCC	3053
Db	2578		
		AAAGCTCCGGTATTATCTTTGTAGAAATCCAAATAGGAAGAAATTTTAAATCGTCTCTC	2637
Qy	3054	AAAGACATGGATCAAGTTGACGTGGCGCTGCGGTTCAGGCGCGAGATGTTTCATCCAGAAC	3113
Db	2638		
		AAAGACATTTGACACTTTGATGATGTTTGGCGGTGACGTTTTTTAGATTTTCATCCAGACA	2697

Qy	3114	GTTATCCTGGTCTTCTCTGTGTGGGAATGATCGCAGGAGTCTTCGCGTGGTTCCTTGTG	3173
Db	2698	TTGCTACAAGTGGTGTGGTGTGGTCTCTGTGGCTGTGGCGCTGATCTCCTTGGATCGCAATA	2757
Qy	3174	GCAGTGGGGCCCTTCGTCATCCTCTCTTTTTCAGTCCCTGCACATGTCTCCAGGGTCTCTGATT	3233
Db	2758	CCCTTGGTTCCTCTGGAAATCATTTTCATTTTCTTCGGGGATATTTTGTGGAAACGTCA	2817
Qy	3234	CGGGAGCTGAAGCGTCTGGACAATATACGCGAGTCACCTTTTCTCTCCACATCAGCTCC	3293
Db	2818	AGAGATGTGAAGCGCTGGAACTACAACTCGAGTCCAGTGTTCCTCCACTTGTCTATCT	2877
Qy	3294	AGCATACAGGGCTTCGCCACCAATCCAGCCTACAAATAAAGCGCAGAGTTCCTGACAGA	3353
Db	2878	TCTCTCAGGGGCTCTGGACCACTCCGGCATACAAAGCAGACAGAGAGGTCTCAGGAAC	2937
Qy	3354	TACCAGGAGCTCTGGATGACAAACCAAGCTCTTTTTTTTTTTTGTTCAGTGTGGATGCCG	3413
Db	2938	TTTGATGCAACACAGGATTTACATTCAGAGGCTGTGTTTCTTGTTCATGCAAGCTCCCGC	2997
Qy	3414	TGGCTGGCTGTGGCTGGACCTCATCAGCATCGCCCTCATCACCAACACGGGGCTGATG	3473
Db	2998	TGGTTCGGCGTCCGCTGATGCCATCTGTGCCATGTTTGTCTATCATCTGTTGCTTTGGG	3057
Qy	3474	ATCGTCTTTATGACGGGCGAGATTCGCCAGCCTATGCGGGTCTGCCCATCTCTTATGCT	3533
Db	3058	TCCTTGATTCTGGCAAAAACCTGGATGCGGGCAGTTGGTTTGGCACTGTCTCTATGCC	3117
Qy	3534	GTCCAGTTAACGGGGCTGTTCCAGTTTACGGTCAGACTGGCATCTGACAGAGAAGCTCGA	3593
Db	3118	CTCAGCCTCATGGGATGTTTCAGTGGTGTGTTCGACAAAGTCTGAAGTTGAGAATATG	3177
Qy	3594	TTCACTCGGTGGAGAGGATCAATCACTACATTAAGACTCTGTCTTGAAGACACCTGCC	3653
Db	3178	ATGATCTCAGTAGAAGGCTCATTGATACACAGACCTT-----GAAAAGAGACACCT	3231
Qy	3654	AGAAATTAAGAACAGCTCCCTCCCTGACTGCGCCAGGAGGAGAGGTGACCTTTGAG	3713
Db	3232	TGGGAATATCAGAAACGCCACACCCAGCTGCGCCCATGAAGAGTGTATATCTTTGAC	3291
Qy	3714	AACGAGAGATCAGGTACCGAGAAACCTCCCTCTGTCTCTTAAGAAAGATATCTTCAAG	3773
Db	3292	AATGTGACTTCATGTACAGTCCAGTGGCGCTCTGGTACTGAAGCATCTGACAGACATC	3351
Qy	3774	ATCAAACTTAAGAGAAGATTGGCATTTGGGCGGACAGGATCAGGGAAGTCTCGCTG	3833
Db	3352	ATTAATACAGAAGAAGTTGGCATTTGGGAAGAACCGAGCTGGAAGAGTTCCCTC	3411
Qy	3834	GGATGGCCCTTCGCTGTGTGTGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTG	3893
Db	3412	ATCTCAGCCCTTTTAGATTGTTCAG--ACCCGAAGGTAAAAATTGGATTGATAAGATC	3468
Qy	3894	AGAATCAGTGATTTGGCTTCGCCACCTCCGACCAACTCTCTATCATTTCTCTCAAGAG	3953
Db	3469	TTGCAACTGAAATTTGGACTTCACGATTTAAGGAAGAAATGTCAATCATCTCAGGAA	3528
Qy	3954	CCGTGCTGTTTCAGTGGCACTCTCAGATCAAAATTTGGACCCCTTCAACAGTACACTGAA	4013
Db	3529	CCTGTTTGTCTACTGGAAATGAGGAACAACTGGATCCCTTTAATGAGCACAGGAT	3588
Qy	4014	GACCAATTTGGGATGCCCTGGAGGAGACACATGAAGAATGTATTGCTCAGCTACCT	4073
Db	3589	GAGGAACCTGTGGAATGGCTTTACAAGAGGTACAACTTAAAGAAACCATTTGAAGATCTT	3648
Qy	4074	CTGAACCTTGATCTGAAGTGTGAGATGGGATACTTCTCAGTGGGGAAACGGCAG	4133
Db	3649	GGTAAATGGATPACTGAAATTAGCAAAATCAGGATCCAAATTTTAGTGTGGACAAAGACA	3708
Qy	4134	CTCTGTGCATAGCTAGAGCCCTGCTCGCCACTGTGAAGATCTCATTTTACATGAAGCC	4193
Db	3709	CTGTTGCTGCCCTGCCAGGCAATTTCTCAGGAAGAAATCAGATATTGATTTATGATGAAGC	3768
Qy	4194	ACAGTCCCATGGACACAGACAGACTTTATTGTTTCAAGAGACCATTCGAGAAGCATTT	4253

Db 3769 ACGCAAAATGGATCCAAAGAACTGATGAGTTAATACAAAAAATCCGGAGAAATTT 3828
QY 4254 GCAGACTGTACCATCTGACCATTCGCCATCGCCTGCACACAGTTCTAGGCTCCGATAGG 4313
Db 3829 GCCCACTGCACCGCTCAACCAATTCACACAGATTGAACACCATTTATTGACAGCCACAAG 3888
QY 4314 ATTATGGTGTGGCCAGGACAGAGTGGTGGAGTTTGAACCCCAATCCGTTCTGTGCC 4373
Db 3889 ATAATGGTTTATGATTCAGGAAGACTGAAAGAAATATGATGAGCCCTATGTTTTGCTGCA 3948
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Db 3949 AATAAAGAGAGCCCTATTTTACAAGATGGT 3977

RESULT 8

US-10-012-896-535
; Sequence 535, Application US/10012896
; Publication No. US20020183251A1

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Barrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012.896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-535

Query Match 7.3%; Score 425.4; DB 9; Length 6082;
Best Local Similarity 48.8%; Pred. No. 7.8e-87;
Matches 1243; Conservative 0; Mismatches 1296; Indels 10; Gaps 3;

QY 1854 ACATGACACATCATGATCTGGAGATCCAAAGAGGTAAACTGGTTGGAATCTCGGSCAGT 1913
Db 1464 ACTCTACAAAGCCCTTTCCTTTACTGTACAGCTGGCGAATTTTACTGTGTGCGCCCC 1523
QY 1914 GTGGAACTGGAAAACTCTCTCATTTTCAGCCATTTTAGGCGAGATGACGCTTCTAGAG 1973
Db 1524 GTGGAGAGGGAAGTCACTGTTAAGTGGCGTCTCGGGAATTTGCCCAAGTCAAC 1583
QY 1974 GCGACATTTGCAATCAGTGAACCTTCGCTTATGTGGCCAGCAGCCCTGGAATCTCAAT 2033
Db 1584 GGGCTGGTCAAGCGTGCATGGGAAGATTTGCTATGTCTCAGCAGCCCTGGGTGTTCTCG 1643

QY 2034 GCTACTCTGAGACACAACATCTCTGTTTGGAGGAATATGATGAAGAAAGATACAACTCT 2093
Db 1644 GGAACCTCTGAGGAGTAAATATTTTATTTGGGAAGAAATACGAAAAGGAACGATATGAAAA 1703
QY 2094 GTGCTGAACAGCTGCTGCTGAGGCTGACCTGGCCATCTTCCAGCAGCGACCTGACG 2153
Db 1704 GTCATAAAGGCTTGTCTCTGAAAAAGGATTTTACAGCTGTTGGAGGATGCTGATCTCACT 1763
QY 2154 GAGATGGAGAGCGGAGGAGCAACCTGAGCGGTGGGAGCCGAGAGGATCAGCTTGGCC 2213
Db 1764 GTGATAGGAGATCGGGAACCCAGCTGAGTGGAGGCGAGAAAGCAGCGGTAAACCTTGCA 1823
QY 2214 CGGGCTTGTATAGTGACAGAGGAGCATCTACATCTCGAGACACCCCTCAGTGCCTTAGAT 2273
Db 1824 AGAGCAGTGTATCAAGATGCTGACATCTATCTCTCGACCATCTCTCAGTGCAGTAGAT 1883
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Db 1884 GCGGAAGTTAGCAGACACTTGTTCGAACCTGTGATTTGTCAAAATTTTGCATGAGAAGATC 1943
QY 2334 GTTCTGTTTGTACCACAGTTACAGTACCTGTTGACTGTGATGAAGTATCTTTCATG 2393
Db 1944 ACAATTTTAGTGACTCATCAGTTGCGAGTACCTCAAGCTCAAGTCAAGTCTGATATTG 2003
QY 2394 AAAGAGGCTGTATTACGGAAGAGGACCCATCGAGAACTGATGAATTTAAATTTGTTGAC 2453
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Db 2064 TTTGGCTCCCTTTTAAAGAAAGGATAATGAGGAAGTGAACAACCTCCAGTTCCAGGAAC 2123
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Db 2124 CCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGGTCTCAACACTTCTTAGA 2183
QY 2574 GTAAAGAAGGAAAAAGCAGTAAAGCCAGAGAAAGGGGAGCTTGTGCACTGGGAAGAGAAA 2633
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QY 2634 GGGCAGGTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2693
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Db 2304 GCTGGTCTCACTGGGATGCTTCTTCAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2363
QY 2754 ACCTGCTGTTGAGTTACTGGATCAAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2813
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QY 2814 AACGAGACCTCGGTGAGTGACAGCATGAAGGACAATCCTCATATGCAAGTACTATGCCAGC 2873
Db 2424 GTCACCTGTAATGGAGGAGGAAATGTAAACCGAAGAGTAGATCTTAACTGGTACTTAGA 2483
QY 2874 ATCTACGCCCTCTCCATGGCAGTCACTGCTATCTTGAAGCCATTCGAGGAGTGTCTTT 2933
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Db 2544 TTTCTAGCTCTTCTTAACTCTTCAACACTTTTGCACAAACAAATGTTTGAGTCAATTTCTG 2603
QY 2994 CGAAGCCCTATGAAGTTTGTGACAGACCCCAAGGGAGGAGTTCTCAACAGGTTTTC 3053
Db 2604 AAAGCTCCGCTATTTATTTTGTAGAAATCCCAATAGGAAGATTTTAAATCGTTTCTCC 2663
QY 3054 AAGACATGATGAAGTTGACGTGCGCTGCGCTTCCAGGCCGAGATGTTTCATCCCAAG 3113
Db 2664 AAAGACATTTGGACACTTGGATGATTTGCTGCCGTGACGTTTGTAGATTTTTCATCCAGACA 2723

Db 1704 GTCATAAAGGCTGTGCTCTGTAAGAAAGATTTACAGCTGTGGAGGATGGTGTACTGACT 1763
Qy 2154 GAGATTGGAGGAGGAGGAGCAACCTGAGCGGTGGGCGCCAGAGGATCAGCTTGGCC 2213
Db 1764 GTGATAGGAGATCGGGAAACCGCTGAGTGGAGGCGAAGACCGGTAAACCTTGCA 1823
Qy 2214 CGGGCCCTGTGATAGTGACAGGAGCATCTACATCCTGGAGACGCCCTTCAGTGCCTTAGAT 2273
Db 1824 AGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGATCCTCTCAAGTGCAGTAGAT 1883
Qy 2274 GCCATGTGGGCAACACATCTTCAATAGTGTATCCGGAAACATCTCAAGTCCCAAGACA 2333
Db 1884 GCGGAAGTTAGCAGACATGTTTGCAGACTGTGATTTGTCAAAATTTTGCATGAGAAGATC 1943
Qy 2334 GTTCTGTGTTTACCACACAGTTACAGTACCTGTGTTGACTGTGATGAAGTGTCTTCATG 2393
Db 1944 ACAATTTAGTACTCATCAGTTGCGAGTACTCAAGCTGCAAGTCAAGTCTGATATTG 2003
Qy 2394 AAGAGGGCTGTATTACGGAAGAGGACCCCATGAGGAATGATGAATTTAAATGGTGAC 2453
Db 2004 AAGATGGTAAATGGTGCAGAAAGGACTTACACTGAGTTCTTAAATCTGGTATATAGAT 2063
Qy 2454 TATGCTTACCAATTTTAAATACCTGTGCTGGGAGAGACCGCCAGTTGAGATCAATTCA 2513
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Qy 2514 AAAAAGGAACCACTGGTTCCACAGAAGTCAACAGACAAGGTCCTTAAACAGAGTCA 2573
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RESULT 11

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US-09-822-827-535
; Sequence 535, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 535
; LENGTH: 6082
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-822-827-535
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Query Match 7.3%; Score 425.4; DB 10; Length 6082;
Best Local Similarity 48.8%; Pred. No. 7.8e-87;
Matches 1243; Conservative 0; Mismatches 1296; Indels 10; Gaps 3;
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RESULT 12

US-09-917-800A-1578
; Sequence 1578, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917.800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880

;; PRIOR FILING DATE: 2000-11-02
;; PRIOR APPLICATION NUMBER: US 60/290,029
;; PRIOR FILING DATE: 2001-05-11
;; PRIOR APPLICATION NUMBER: US 60/290,645
;; PRIOR FILING DATE: 2001-05-15
;; PRIOR APPLICATION NUMBER: US 60/292,336
;; PRIOR FILING DATE: 2001-05-22
;; PRIOR APPLICATION NUMBER: US 60/295,798
;; PRIOR FILING DATE: 2001-06-06
;; PRIOR APPLICATION NUMBER: US 60/297,457
;; PRIOR FILING DATE: 2001-06-13
;; PRIOR APPLICATION NUMBER: US 60/298,884
;; PRIOR FILING DATE: 2001-06-19
;; PRIOR APPLICATION NUMBER: US 60/303,459
;; PRIOR FILING DATE: 2001-07-09
;; NUMBER OF SEQ ID NOS: 1740
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 1578
;; LENGTH: 4918
;; TYPE: DNA
;; ORGANISM: Rattus norvegicus
;; FEATURE:
;; OTHER INFORMATION: Genbank Accession No. US20020119462a1 NM_012833
us-09-917-800A-1578

Query Match 6.78; Score 392; DB 10; Length 4918;
Best Local Similarity 49.4%; Pred. No. 2.8e-79;
Matches 1308; Conservative 0; Mismatches 1235; Indels 105; Gaps 7;
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QY 2755 CC-----TGGTGTGTGATTTACTGATCAAGCAAGGAAGCG 2790
DB 2982 ACCTGAAGTATCTACAGCAGTAGGTGGTGGTCCATCTTTTCATCATCTCTTTCTACG 3041
QY 2791 GGAACACCACTGTGACT-----CGAGGGAACGAGACCTCGGTGA 2829
DB 3042 GATTGAATAATGTGCTTTTATCGGCTCTAAACCTCTGGCTGAGTGTGGACCACTGACT 3101
QY 2830 GTGACAGCATGAAGGACAACTCTCATATGACAGTACTATCCAGCATCTAGCCCTCTCCA 2889
DB 3102 CTGACAACTTGAATGGGACCAACATTCCTCTCTCATAGGACATGAGAAATTTGGGTCT 3161
QY 2890 TGGCAGTCAATGTGATCTCTGAAAGCCATTCGAGGAGTGTCTTTGTCAGAGGACGCTGC 2949
DB 3162 TTGGAGCTCTGGATTAGCAACAAGTATATTTGCTTATTTCAACTCTGTGAGCATAT 3221
QY 2950 GAGCTTCTCCCGGC-----TGCATGACAGAGCTTTTCCAGAGATCTTCGAA 2997
DB 3222 ATGCTTTGCAAAATGCAATCAAAAGCTTTTCAGCGGACGCTGTTAAACCAATCTCCCGG 3281
QY 2998 GCCCTTGAAGTTTGTGACAGCCACACAGGAGGATCTTCAACAGGTTTTCACAAAG 3057
DB 3282 CACCATGAGGTTTGTGACACAACTCCACAGCGCGATTTGACACATTTTCGGTG 3341
QY 3058 ACATGATGAATGTGACGTGCGGCTGCCCTTCCAGGCCAGATGTTTCATCCAGAACGTTA 3117
DB 3342 ATATTTCTACTTGGAGAGCTTGTCTCCCGCAGACACTTCCAAAGCTGGATGTGTTCT 3401
QY 3118 TCCTGGTGTCTTCTGTGTGGGAATGATCGAGGAGTCTTCCGTTGGTTCCTTGTGGCAG 3177
DB 3402 TTGGCATCGCTGGCACTCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 3461
QY 3178 TGGGCGCCCTTGTCTCTCTTTCAGTCTGACATCTGCTCCAGGCTCTGATTCGGG 3237
DB 3462 TCATTTCTCTCAGATCTTATATTTCCGTCGAGGTTTTTATGTTGGCTACTTCCCGC 3521
QY 3238 AGCTGAAGGCTGTGGCAATATACGACAGTCACTTTCCTCTCCACATCACTGATCCAGCA 3297
DB 3522 AGCTGAGAGGTTGGATTTCTGTACCAAAATCTCCGATCTATTTCTCACTTCACTGAGACTG 3581
QY 3298 TACAGGGCTTCCGACCATCCAGCTTCAATAAAGGGCAGAGGTTTTCACACAGATACC 3357
DB 3582 TCACAGGTTTGGCCATTTATCCGTGCTTTGAGCACGACGAGTCTTAGCTTGAATG 3641
QY 3358 AGGAGCTGTGATGACAAACAGCTCTCTTTTGTGTTTGTGTTGTTGTTGTTGTTGTTGTTG 3417
DB 3642 AGAAGCAGATTTGACATCAACAGAAATGTCTTTCTCGGATTAACCTCCACAGAGTGC 3701
QY 3418 TGGCTGTGGCTGGACCTCATCAGCATCGCCCTCATCACACAGGGGCTGATGATCG 3477
DB 3702 TTGCAATTCGGCTGGAGCTGGTTGGAAGTGTGTCGCTCTTCTTCCGCTTGTCTGCTG 3761
QY 3478 TTCCTTATGACGGGAGATTTCCCGCAGCCTATGCGGGCTTCGCCATCTCTTATGCTGTCC 3537

QY 2603 GGAAGGCGAGCTTGT----- 2617
Db 2838 CTTAGCCGAGTTCTAGGTCCAATGGCAGGACATCGAAGTCCCTGAGAACTCCTTTGAAA 2897
QY 2618 -----GCAGCTGGAAGAGAAAGGCGAGGTTCTAGTGCCTTGGTCAGTA 2660
Db 2898 ACTCGGAATGTGAATAGCCTGAAGGAAGACGAGAACTAGTGAAGGACAAACTAAT 2957
QY 2661 TATGGTGTCTACATCCAGGCTGTGGGGCCCTTTGGCAATCCTGGTTATTATGCCCCFT 2720
Db 2958 AAGAAGGAATTCATAGAAACTGGAAGGTGAAGTTCTCCATCTACCTGAGTACCTACAA 3017
QY 2721 TTCATGTGATGTAGGAGACACCGCTTCAGCAGCTGGTGTGAGTTACTGGATCAAG 2780
Db 3018 GCAATAGGATTTGTTCATATTTCTTCATCATCTTCCTGGTGTGATGAATTTCTGTGGCT 3077
QY 2781 CAAGGAAGCGGAAACACCACTGTGACTCGAGGGAACGAGACCTCGGTGAGTCACAGCATG 2840
Db 3078 TTTATTGGATCAACCTCTGGCTAGTCTGGACGAGTACTCTAATACTTCAATAGC 3137
QY 2841 AAGGCAATC-----CTCATATGCACTACTATGCCAGCATCTACGCCCTCTCCATGGCA 2894
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QY 3315 ATCCAGGCTACATAAAGGCGAGGATTTCTGACAGATACAGGAGCTGCTGGATGAC 3374
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QY 3375 AACCAAGCTCTTTTGTGTTTACGTGTGCGATGCGGTGGCTGGCTGTGCGGTGGAC 3434
Db 3678 AACCAAGAAATGTCTTTTCTGATGATCCTCCACAGAGTGGCTTGAATTCGCTGGAG 3737
QY 3435 CTCATCAGCATGCGCTCATCACCAGCAGGCGGTGATGATGCTTCTATGACAGGGCAG 3494
Db 3738 CTGTTGGGAACCTGACGTCTCTTTTTCAGCTTTGATGATGATTTATAGATACAC 3797
QY 3495 ATCCCCAGCCTATGCGGGTCTCCCATCTCTTATGTCTGCTCAAGTTAACGGGCTGTTC 3554
Db 3798 CTAAGTGGGACATGTTGGGCTTTCTGCTCCAAATGACCTCAATATACACAAACCTTG 3857
QY 3555 CAGTTTACGACTGCACTGCACTGAGACAGAGCTCGATTCACCTCGGTGGAGAGATC 3614
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QY 3615 AATCACTACATTAAGACTCTGTCTTGGAGACACCTGCCAGAAATTAAGAACAGGCTCCC 3674
Db 3918 ACTGAGTACACAAAGTG-----GAAATGAGGCACCCCTGGGTGACTGATAAGAGGCT 3971
QY 3675 TCCCTGACTGGCCCCAGGAGGAGGTGACCTTTTGGAGAACGAGAGATGAGGTACCGA 3734
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QY 3795 GGCATTTGGGGCGGACAGGATCAGGAAGTCTCTGCTGGGATGGCCCTTCTCCGCTG 3854
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QY 3975 GTCAGATCAAAATTTGACCCCTTCAACCACTGATGAGAGATTTGGGATGCCCTG 4034
Db 4272 CTGAGATGAATCTGACCCCTTTCAACAACTACTCACTGATGAGGAGATTTGGAAGGCCCTG 4331
QY 4035 GAGAGACACATGAAGAATGATTTGCTCAGTACTCTCTGAACTTGAATCTGAAGTG 4094
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QY 4095 ATGGAGAAATGGGATTAACCTTCTCAGTGGGGAACGGCAGCTTCTGTCATAGTAGGCC 4154
Db 4392 ACAGAGGCTGGTGGCACTGAGCAGTAGGAGGAGGAGCTGCTGCTGGGCGAGGCT 4451
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QY 4275 ATFGCCATCGCTCGACAGGTTCTAGGCTCCGATAGGATTTAGTGTGGGCCAGGGA 4334
Db 4572 ATGCCCCAGGCTGATACCATCATGAGCAGTGAAGGTAATGTTCTCTAGACACGGG 4631
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Db 4632 AGATTATAGAGTACGCGACCCCTCGAAGAACTGCT 4666

RESULT 14

US-09-917-800A-479
; Sequence 479, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castile, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44971-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029


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; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 479
; LENGTH: 5728
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 AB010466
US-09-917-800A-79

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Query Match 6.4%; Score 373.8; DB 10; Length 5728;
Best Local Similarity 47.7%; Pred. No. 4.2e-75;
Matches 1209; Conservative 0; Mismatches 1307; Indels 21; Gaps 3;

Qy	1957	CTGCACAGCATCATCGAGATCCAGAGGTTAACTGGTTGGAAATCTCGCGCAGTGTG	1916
Db	1954	CTGCACGGGATAACCTCACCTACCGCTGGCCAGCGGCTCTCTCGTGGTGTGTGGTGGTCCAAGT	2013
Qy	1917	GGAAGTGGAAAAACCTCTCATATTCAGCCATTTTAGCCAGATGACGCTTCTAGAGGGC	1976
Db	2014	GGGCTGGAAAGTCTCTCCCTGCTGCTGCCCTGCTTGGGAGCTGTGTGAAGTTAGAAGGG	2073
Qy	1977	AGCATTTGCAATCAGTGGAAACCTTCGCTTATGTGGCCCCAGCAGGCGCTGGATCCTCAATGCT	2036
Db	2074	TCTCTGAGCATTCAGGGTTTCCGTGGCTACGTGCTCAGGAGGCTTGGTCTCCAATACC	2133
Qy	2037	ACTCTGAGAGACAACTCTCTGTTTGGGAGGAATATGATGAAGAAGATACAACTCTGTG	2096
Db	2134	TCGTGTGGTGAAGATGTGTCTTCAGCGAGAGCTGGATCTGCCATGGTTGTCAGGAAGTT	2193
Qy	2097	CTGAACAGCTGCTCCCTGAGGGCTGACCTGGCCATCTTCCACAGCAGCGACCTCAGCGAG	2156
Db	2194	CTAGAAGCCTGTGCTTGGGTCGTATGTGGCCAGCTTCCCTGCAGGAGTTACACACCCCA	2253
Qy	2157	ATTGGAGAGGAGGAGGCCAACCTGACGGTGGGCGAGCGCCAGAGGATCAGCCTTGGCCCGG	2216
Db	2254	GTAGGGGAGCAGGGCATGAATCTTCTGGGGGCCAAGACGACGCGCTGAGCTTGGCTCGG	2313
Qy	2217	GCCTTGTATAGTCACAGGAGCATCTACATCTCTGGACGACCCCTCAGTGCCTTAGATGCC	2276
Db	2314	GCTGTGTACAGAAGGGCTGCTGTGTACCTGTATGGATACCCCCCTAGCAGCGCTGAGTGGC	2373
Qy	2277	CATGTGGGCAACCATCTTCAATAGTGTAT-----CCGGAAACATCTCAAGTCCAAG	2330
Db	2374	CATGTCAGCCAGGAAGTCTTCAACACAGGTCATTGSCCCCACTGCCAAGGTACG	2433
Qy	2331	ACAGTTCTGTGTATCCCAACAGTTACAGTACCTTGTGTACTGTGATGAAGTGAATCTTC	2390
Db	2434	ACTCGGATCCTTGTATACACACACGCTGTATGCTTCGCCCCCAAGCTGACCCAGATCCTGGTG	2493
Qy	2391	ATGAAAGAGGGCTGTATTACGAAAGAGGSCCCATGAGGAACATGATGAATTTAAATGGT	2450
Db	2494	CTGGCCATGGGACCATCCAGAGATGGGCTCTTACCAAGACCTTCTGCTATGAGGAACGGA	2553
Qy	2451	GACTATGCTACCATTTTAACTAACTGTGTGGGAGAGACACCGCAGCTTGTGATCAAT	2510
Db	2554	GCCCTGGTGGTCTTCTGGATGGACCCACAGAGCTGCAGCGGAGGAGGAGGAGACA	2613
Qy	2511	TCAAAAAGGAACCACTGGTTTCACAGAAGAGTCAAGAACAAGGTCCTTAAACAGGA	2570

Db	2614	CATGCTGCACCCACCACTGATGACCTTGGAGGCTTTCTTGGAGTGGGACGCCACCGCGC	2617
Qy	2571	TCAGTAAGAAGAAAGACAGTAAAGCCAGAGGAAGGCAGCTTGTGCAGCTGGRAGAG	2630
Db	2674	AGACCAGAGAGGCCACAGACCCAGTGACGACGACCCCTGTGNAAGGCAGTACTTCAGAGGCA	2733
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Db	2734	CAGATGGAGCCCTCTCTGCTGACGTTGAGTCTACTGGACTGCACAGGAGGACAGT	2793
Qy	2691	CCCTTTGGCATTCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGCAGCACCGCCTTC	2750
Db	2794	GTGCAGTATGGCCGGGTGAAGAGCGCACATACCTGAGCTACCTGCGGGCGTGGGCACA	2853
Qy	2751	AGCACTGGTGTGTGAGTTACTTGGATCAAGCAAGGAAGCGGAACAACCACTGTGACTCGA	2810
Db	2854	CGGCTCTGCACCTACACCCTGTTCCTCTTCCTCTGCCAAGTGGCGTCTCTTCGCGCAA	2913
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Db	2914	GGCTACTGGCTGAGCCTCTGGCCGACGACCCGGTCTGATGGGAAGCAGATGCATTCA	2973
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Db	3094	CTCTGGGAGTGGCTCGCTCTCCCATTTGGCTTCTTTGAGGCACACACCGTCGGGAACCTG	3153
Qy	3039	CTCAACAGGTTTCCAAAGACATGGATGAAGTGTGACGTGGGCTGCGGTTCAGGCCGAG	3098
Db	3154	CTGAACCTTTTTCACAGGAGACGACATATGGATGTGGACATCCACAGACAAGATGAGG	3213
Qy	3099	ATGTTATCCAGAACGTTATCCTGGTGTCTTCTGTGTGGGAATGATCCAGGAGTCTTC	3158
Db	3214	ACCCCTGACCTATGCGCTTTGGACTCTGAGAGTTGGCCCTGGCAGTGTGATGGCCACA	3273
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Db	3274	CCACTGGCTATTGTGGCCATCCTACCTCTTATGCTCTCTTATGCTGGTTTCAGAGCCCTC	3333
Qy	3219	TCCAGGTCCTGATTTCGGGAGCTGAAGCTCTGGACAATATCACGCAAGTACCTTCTCTC	3278
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Qy	3279	TCCACATACGTCACAGATACAGGSCCTTGGCCACCATCCAGCCCTACAAATAAAGGCGAG	3338
Db	3394	TCCATCTGGCTGAGACCTTCACGGGCAGTCAAGTGGTCAGGECCTTCCAGGCCACAGGGG	3453
Qy	3339	GAGTTTCTGCACAGATACCAAGAGCTGCTGGATGACAACAAGACTCCTTTTGTGTTT	3398
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Qy	3399	ACGTGTGGATGCGGTGGCTGGCTGTGGGCTGGACCTCATCAGCATATCGCCCTCATCACC	3458
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Qy	3459	ACCAGGGGCTGATGATGCTTCTTATGCAAGGCAGATTCGCCAGCCATATCGGGTCTC	3518
Db	3574	GTGGCGGTACATGTGCTGTCTGAGCAAGGCTCACTGAGTGTGGCTCGCGGCTTC	3633
Qy	3519	GCCATCTTTATGCTGTCCAGTTAACGGGGCTGTTCAGATTACGGTCAAGCTGGCATCT	3578
Db	3634	TCGGTTTCTGCTGCCCTCCAGTAACACAGACTCTGCAGTGGGTGTCGCGAGCTGGACA	3693
Qy	3579	GAGACAGAGCTCGATTACCTTCGGTGGAGAGGATCAATCATATTAAGACTCTGTCTC	3638
Db	3694	GATCTGGAGAACAGCATGGTGGCCCTGGAGCGAGTACAGGATACGTTTCACACCC---CC	3750

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DB 3751 AAGGAGCTCCCTGGAGCTCCCTCTCTGAGCCAGCCTCTCTGGCCCTGTGGGGA 3810
QY 3699 GAGGTGACCTTTGAGACGACAGATGAGTACCGAGAAACCTCCCTCTTCTCTAAAG 3758
DB 3811 CAGATTGATCCGAGACTTTGGCTCAGACACCGACAGCTGCCATGCTGTGAG 3870
QY 3759 AAAGTATCTTACAGCAACCACTAAAGAGAAATTTGGCATTTGGGGCGGAGGATCA 3818
DB 3871 GGTGTGCTCCCTGAGATCCATCAGGAGGAGAGTGGCATCTGTGGCGGAGGACAGGGCC 3930
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DB 3931 GGAAGTCTCTCCCTGACTTTGGGGCTCTGCTGGCTTTCAGGAGCCCATCAGGGTGTAT 3990
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DB 3991 TGGATCATGGGTCCCATCACCAGATGGGTGACACACTGGGTCCAGATCACC 4050
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DB 4051 ATCATCTCTAAGAGCCGCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4110
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QY 4059 ATTGCTCAGTACCTCTGAATCTGAATCTGAATCTGAATCTGAATCTGAATCTGAAT 4118
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DB 4411 ATGAATCGCCAGGTTCTAGTCATGATGATGATGATGATGATGATGATGATGATGATGAT 4470
QY 4359 TCGGTCTCTGTGCTCA 4375
DB 4471 GCACAGCTGTGGCCCA 4487

RESULT 15
US-09-938-842A-1392
; Sequence 1392, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krepis, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1392
; LENGTH: 4869
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1392

Query Match 6.0%; Score 349.2; DB 9; Length 4869;
Best Local Similarity 48.5%; Pred. No. 1.5e-69;
Matches 1237; Conservative 0; Mismatches 1233; Indels 78; Gaps 7;

QY 1854 ACATCTCAGACATCATCTCGAGATCCAGAGGGTAAACTGTTGGAATCTCGGCGAGT 1913
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QY 1914 GTGGGAAGTGGAAAAACCTCTCTCATTTTCAGCCATTTTAGGCCAGATGACGCTCTTA-- 1970
DB 1951 ACAGGAGAAGAAAAACCTCCCTGATATCTGCTATGCTTGGGGAATCTCTTCGATGATCT 2010
QY 1971 GAGGGCAGCATTTGCAATCAGTGGAACTTTCGCTTATGTTGGCCAGCAGGCTGATCCTC 2030
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[illegible]

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QY	3930	AAACTCTATATCATTTCTCAAGAGCGGGTGCTGTTCAGTGGCAGCTCTCAGATCAAAATTTG	3989
DB	3937	GTGCTCGGAATTTATACCGCAAGCGCCAGTCTTTTCTCAGGTACCGTGAGATTCATCTTT	3996
QY	3990	GACCCCTTCAACCGACTACACTGAAGACCAGATTTGGATGCCCTGGAGAGGACACACATG	4049
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QY	4170	AAGATTCTGATTTTATAGTAAGCCACAGCTGCCATGGACACAGAGACAGACTTATTGATT	4229
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DB	4237	CAAAAGACCATCCCGAGAGAAATTTCAAGTCATGCACAATGCTTAATCATCGCTCATCGTCTC	4296
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DB	4297	AATACTATCATCGACTGTGACAAAGTTCTTGTGCTTGATCTGGAAAGATTCAGGAATTC	4356
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Search completed: December 18, 2002, 21:41:29
Job time : 221.369 secs

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RESULT 2

US-09-001-273-1
; Sequence 1, Application US/09001273
; Patent No. 5954130
; GENERAL INFORMATION:
; APPLICANT: SHYJAN, Andrew
; TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/001,273
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: PENTON, Gillian M
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: MIL-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4781 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..4360
US-09-001-273-1

Query Match 80.9%; Score 4724.2; DB 2; Length 4781;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 4737; Conservative 6; Mismatches 9; Indels 1; Gaps 1;
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Db 1 TGATGTGAAACTAACACAGTCTCTGTGAGCCCTGGAACCTCCGCTCAGAGAAGATGAAGATAT 60
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DB 3301 CCAAGCTCCTTTTTTTTTTTTGTAGCTGTCGATGCGGCTGGCTGCGCTGGACCT 3360
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DB 3361 CATCAGATCCCTCATCACACACGCGGCTGATGATCTTATATGACGACGGCAGAT 3420
QY 3497 TCCGCCAGCTATGCGGCTCTCGCATCTCTATGCTCTCCAGTTAAAGGGCTGTTCCA 3556
DB 3421 TCCGCCAGCTATGCGGCTCTCGCATCTCTATGCTCTCCAGTTAAAGGGCTGTTCCA 3480
QY 3557 GTTTACGCTCAGACTGCGCATCTGACAGAGAAGCTCGATTCACCTCGGTCGAGAGGATCAA 3616
DB 3481 GTTTACGCTCAGACTGCGCATCTGACAGAGAAGCTCGATTCACCTCGGTCGAGAGGATCAA 3540
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RESULT 3

US-08-843-459A-1
; Sequence 1, Application US/08843459A
; Patent No. 6162616
; GENERAL INFORMATION:
; APPLICANT: SHYJAN, Andrew
; TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED
; TITLE OF INVENTION: POLYPEPTIDE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/843,459A
; FILING DATE: 16-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanley, Elizabeth A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-056 (formerly MIL-001)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4781 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS

LOCATION: 2...4360
US-08-843-459A-1

Query Match 80.9%; Score 4724.2; DB 4; Length 4781;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 4737; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

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DB 61 CGACATAGGAAGAGATATATCATCCCCAGTCCCTGGGTATAGAAAGTGTGAGGAGAGAAC 120
QY 197 CAGCACTTCTGGGACGACAGAGACCGGTGAAGATTCCAAAGTTCAGGAGAATCCGACCGTT 256
DB 121 CAGCACTTCTGGGACGACAGAGACCGGTGAAGATTCCAAAGTTCAGGAGAATCCGACCGTT 180
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QY 317 CATGCATTTCTCAGCTCAGAACTCCGAGTGGAGGAGCATCCCAAGGGAAGATACCATCATGG 376
DB 241 CATGCATTTCTCAGCTCAGAACTCCGAGTGGAGGAGCATCCCAAGGGAAGATACCATCATGG 300
QY 377 CTTGAGTGTCTGAAGCCCATCCGAGTACTTCCAAACACAGCACCCAGTGGCAATGCG 436
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QY 437 TGGCTTTTTCCTGTATGACTTTTTCGTGGCTTTCTCTGCGCCGCTGTGGCCCAAA 496
DB 361 TGGCTTTTTCCTGTATGACTTTTTCGTGGCTTTCTCTGCGCCGCTGTGGCCCAAA 420
QY 497 GAAGGGGAGCTCTCAATGGGAAGAGCTGTGCTCTGCTCCAAAGACAGAGTCTTCTGAGCT 556
DB 421 GAAGGGGAGCTCTCAATGGGAAGAGCTGTGCTCTGCTCCAAAGACAGAGTCTTCTGAGCT 480
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DB 901 GCAGAGAAATTTGAGGACAGCGCTTGGAGCGCTGTGCTGGAGAGACCGCTTGTGTC 960
QY 1037 CATCTTAGCATGATTTATATGTAATTTATCTGGGACCAACAGGCTTCTGGGATCAGC 1096
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DB 1141 CATTTAAATTTATCAAAATGATGTCCTGGGTCAAAGCATTTTCTCAGAGTGTTCAGAAAT 1200
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DB 1201 CCGCAGGAGGAGCGTCCGATATTGAAAAAGCCGGGTACTTCCAGAGCATCACTGTGGG 1260
QY 1337 TGTGGCTCCCATTTGTTGGTGTGATTTGCCAGCGTGTGACCTTCTCTGTTTCATATGACCT 1396
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DB 1321 GGGCTTTCGATCTGACAGCAGCAGGCTTTTACAGTGTGTGACAGTCTTCAATTTCCATGAC 1380
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Db 4741 TGTGCTAATAAAA 4753

RESULT 4
US-08-463-092B-3
; Sequence 3, Application 05/08463092B
; Patent No. 5766880
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,092B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1546
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..4788
US-08-463-092B-3

Query Match 8.7%; Score 510; DB 1; Length 5011;
Best Local Similarity 52.2%; Pred. No. 3.7e-121;
Matches 1360; Conservative 0; Mismatches 1185; Indels 59; Gaps 8;

Qy 1821 CACATCCACCTGGCCACCTGGCTTACAGAGGACACTGCACAGCATCGATCTGGAGCAT 1880
Db 2142 CACATTCACCTGGGCCA--GGAGCGACCTCCCACTGATGGCATCACCTTCTCCATC 2199
Qy 1881 CAAGAGGTAAATGTTGGAACTCTCGGCAGTGTGGGAAGTGGAAAAAACCCTCTCTCAT 1940
Db 2200 CCCGAAGTGTCTTGGTGGCGGTGGCCAGGTGGCTGCGGAAAGTGTCCCTGCTC 2259
Qy 1941 TCAGCCATTTAGGCCAGATGAGCGTTCTAGAGGGGAGCATTCATCATGATGGAACCTTC 2000
Db 2260 TCAGCCCTCTTGGCTGAGATGGACAAAGTGGAGGGGACGTGCTATCAAGGGCTCCGTG 2319
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Db 2320 GCCTATGTCACAGCAGCGCTGGATTGAGATGATCTCTCGGAAACATCCTCTTTT 2379
Qy 2061 GGAAGGAATATGATGAAGAAAGATACAACTCTGTCTGAACAGCTGCTGCTGAGGCT 2120
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Db 2440 GACCTGGAAATCTGCCAGTGGGGATCGACAGAGATTGGCGAAGAGCGGTGAACCTG 2499
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 Db 4717 TACGGCGCCCATCGGACCTCTG 4740

RESULT 5
 US-08-462-109A-3
 : Sequence 3, Application US/08462109A
 : Patent No. 5882875
 : GENERAL INFORMATION:
 : APPLICANT: Cole, Susan P.C.
 : APPLICANT: Deeley, Roger G.
 : TITLE OF INVENTION: METHODS FOR IDENTIFYING
 : TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
 : NUMBER OF SEQUENCES: 6
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: LAHIVE & COCKFIELD
 : STREET: 60 State Street, suite 510
 : CITY: Boston

Db 2200 CCCGAAGTGTCTTGGTGGCCGCTGGTGGCCAGGTGGGCTGGGAAAGTCTGCCCTGCTC 2259
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RESULT 7

US-08-463-179A-3
Sequence 3, Application US/08463179A
Patent No. 6001563
GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: METHODS FOR IDENTIFYING CHEMOSENSITIZERS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,179A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-Oct-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-OCT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Deconti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PQI-002CP8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA

QY 2739 AGCAGCGCTTCAGCAGCTGGTGGTTAGTTACTGATCAACGAAGAGCGGAACACC 2798
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 QY 4347 TTTGACACCCATCGTCTCTCTG 4370
 DB 4717 TACGGCGCCCATCGAGCTCTCTG 4740

RESULT 8
 US-08-461-384B-3
 ; Sequence 3, Application US/08461384B
 ; Patent No. 6025473
 ; GENERAL INFORMATION:
 ; APPLICANT: Cole, Susan P.C.
 ; APPLICANT: Deeley, Roger G.
 ; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
 ; STREET: Queen's University at Kingston
 ; CITY: Kingston
 ; STATE: Ontario
 ; COUNTRY: CANADA
 ; ZIP: K7L 3N6
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/461.384B
 ; FILING DATE: 05-JUN-95
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/966.923
 ; FILING DATE: 27-OCT-1992
 ; APPLICATION NUMBER: 08/029.340
 ; FILING DATE: 8-MAR-1993
 ; APPLICATION NUMBER: 08/141.893
 ; FILING DATE: 26-OCT-1993
 ; APPLICATION NUMBER: 08/407.207
 ; FILING DATE: 20-MAR-1995

QY 3627 AAGACTCTCTCTTGGAGCACCCTGCCAGAAATTAGAACAGGCTCCCTCCCTGACTGG 3686
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Db 4000 GAGACTGAGAA---GGAGGCGCTTGGCAAAATCCAGAGACAGCTCCGCGCCAGCTGG 4056
QY 3687 CCCCAGGAGGAGAGGTGACCTTTTGAGACCGCAGAGATGAGGTACCGAGAAACCTCCCT 3746
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Db 4057 CCCCAGGTGGCCGAGTGAATTCGGAACTACTGCGCTACCGAGAGACCTGGAC 4116
QY 3747 CTTGTCTTAAGAAAGTATCTTACGATCAAACTAAAGAGAGATTGGCAATGTGGGG 3806
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Db 4117 TTCAGTCTCAGGCACATCAATGTACAGATCAATGGGGGAGAAAGGTGCGCATCTGGGG 4176
QY 3807 CGGACGAGTACAGGAAGTCTCGTGGGGATGGGCTCTCCGTTCTGGTGAGTATCT 3866
|||||
Db 4177 CGGAGGGAGCTGGGAAGTCTCGCTGAGCTCTATTCGGATCAACAGTCTGCC 4236
QY 3867 GGAGCTCATCAAGATTGATGGAGTGAGATCACTGATATTTGGCTTGGCCACCTCGA 3926
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Db 4237 GAAGGAGATCATCATGATGGATCAACATCGCAAGATCGGCTGCAGACCTCGC 4296
QY 3927 AGCAACTCTTATCATCTCAAGAGCGGTGCTGTTCAGTGGCACTGTTCAGATCAAT 3986
|||||
Db 4297 TTCAGATCACCATCATCCGCCAGGACCTGTTTGTTCGGGTTCCTCCGATGAAC 4356
QY 3987 TTGACCCCTTCAACAGTACACTGAAGACCATGTTGGGATGCCCTGGAGAGGACAC 4046
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Db 4357 CTGGACCATTTACGCACTACTCGGATGAAGAAGTCTCGGAGCTGCCGAGCTGCCAC 4416
QY 4047 ATGAAGAAATCTATTGCTCAGCTACTCTGAACTTTGAATCTGAAGTATGAGAAATGG 4106
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Db 4417 CTGAAGACTCTGCTCAGCCCTTCTGCAAGCTAGACCATGATGTGCAAGAGCGGG 4476
QY 4107 GATAACTTCTCAGTGGGGAAACGACGCTCTTGTGCAATGATAGTAGAGTCTGCTCGCCAC 4166
|||||
Db 4477 GAGAACTCTAGTCTCGGACGCGCAGCTTGTGTGCTAGCCGCGCTCTGCTGAGGAG 4536
QY 4167 TGTAGATCTGATTTAGATGAGCCACAGCTGCGCATGAGTATGAGTATGAGTATG 4226
Db 4537 ACGAAGATCTTGTGTTGATGAGCCACGCGCAGCTGGAGCTGGAAACGAGACACTC 4596
QY 4227 ATCAAGAGACATCCGAGAGACATTTGACAGCTGTACCATGCTGACCATGCCCATCGC 4286
|||||
Db 4597 ATCCAGTCCACCATCCGACACAGTTCGAGGACTGCACCTCTCACCATGCCACCGG 4656
QY 4287 CTGACACGGTCTTAGCTCCGATAGGATGATGTTGCTGGCCCGCAGGACAGGTGTTGAG 4346
|||||
Db 4657 CTCACACCATCATGGACTACACAAGGTGATGCTCTTGGACAAAGAGAGAAATCCAGGAG 4716
QY 4347 TTTGACACCCCATCGTCTCTCTG 4370
Db 4717 TACGGCGCCCATCGGACCTCTG 4740

RESULT 9

US-08-141-893-1

; Sequence 1, Application US/08141893

; Patent No. 5489519

; GENERAL INFORMATION:

; APPLICANT: Cole, Susan P.C.

; APPLICANT: Deley, Roger G.

; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEIN

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESSES:

; ADDRESS: LAHIVE & COCKFIELD

; STREET: 60 STATE STREET, SUITE 510

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/141,893

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/966,923; 08/029,340

; FILING DATE: 27-OCT-1992; 8-MAR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: DeConti, Giulio A. Jr.

; REGISTRATION NUMBER: 31,503

; REFERENCE/DOCKET NUMBER: PQ1-002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5149

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5011 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 196..4788

; US-08-141-893-1

Query Match

8.7%; Score 505.2; DB 1; Length 5011;

Best Local Similarity 52.1%; Pred. No. 6.3e-120;

Matches 1357; Conservative 0; Mismatches 1188; Indels 59; Gaps 8;

QY 1821 CACATCCACTGGCCACCTGGCTTACAGAGGACACTGCACAGCATCGATCTGGAGATC 1880

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2142 CACATTCACCTGGGCA--GGAGCGACCTCCACACTGAATGSCATCACCCTTCTCCATC 2199

QY 1881 CAAGAGGTAACTGGTTGGAATCTCGGCGAGTGTGGGAGTGGGAAACACTCTCTCATTT 1940

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2200 CCCGAAGTGTCTTGGTGGCCGTGGTGGCCAGGTGGCGGAAGTTGTCCCTGCTC 2259

QY 1941 TCAGCATTTTAGCGCAGATGACGCTTCTAGAGGCGCAGATTGCAATTCAGTGGAACTTC 2000

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2260 TCAGCCCTCTTGGCTGAGATGGACAAGTGGAGGCGACGTGGCTATCAAGGCTCGGTG 2319

QY 2001 GCTTATGTGGCCAGCAGGCTGGATCTCAATGTCTACCTGTAGAGACAAACATCTCTTT 2060

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2320 GCTATGTGCCACAGCAGGCTGGATTCAGAATGATCTCTCCGAGAAACACATCTCTTTT 2379

QY 2061 GGAAGGATATGATGAAGAAAGATACAACCTCTGTCTGAACAGCTGTGCTGAGGCT 2120

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2380 GGATGTGCTGGAGGAACTATTACAGGTCCGTGATACAGGCTGTGCCCTCTCTCCCA 2439

QY 2121 GACCTGGCCATCTTCCACAGCAGCAGCTGACGAGATTGGAGCGAGGAGCAACCTG 2180

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2440 GACCTGGAAATCTGCCCCAGTGGGATCGGACAGAGATTGGCGAGAGGCGGTGAACCTG 2499

QY 2181 AGCGTGGGCGACGCCAGAGGATCAGCCTTGGCCGGCCCTGTGTATAGTACAGAGGATC 2240

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2500 TCTGGGGACAGACAGCGCGCTGAGCCTGGCCGGCCGCTGTACTCCACGCTGACATT 2559

QY 2241 TACATCTGGAGCAGCCCTCTAGTGCCTTAGATGCCCATGTGGGCAACACATCTTCAAT 2300

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2560 TACCTCTTTCGATGATCCCTCTCAGCAGTGGATGCCCATGTGGGAAACACATCTTTGAA 2619

QY 2301 AGTGTAT-----CCGGAACATCTCAAGTCCAAGACAGTTCTGTCTTACCCACAG 2354

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2620 AATGTGATGGCCCCAAGGGATGCTGAAGCAACAGAGGAGTGTGTGTCAGCAGCAGC 2679

QY 2355 TTACAGTACCTGTTGACTGTGTGATGAAGTATCTTTCATGAAAGAGGCTCTATTACGGAA 2414

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2680 ATGAGCTACTTCCCGCAGGTGACGCTCATCATCGTATCAGTGGCGGCAAGATCTCTGAG 2739

QY 2415 AGAGCACCACATGAGGAAGTATGAATTTAAATGGTGTATGCTATGCTTACCATTCTTTAATAC 2474

Db 2740 ATGGGCTCTACAGGAGCTGCTGGCTGAGACGGCGCTTCGCTGAGTCTCTGGGTACC 2799
 QY 2475 CTGTTGCTGGGAGAGACACCGCCAGTT---GAGATCAATTCATAAAGAGAACAGTGGT 2531
 Db 2800 TATGCCACAGACAGACAGGAGCAGATGAGAGAGAAACGGGGTACAGCGGT 2859
 QY 2532 TCACAGAAGAAGTACACAGACA-----AGGGTCTTAAAA 2565
 Db 2860 CCAGGGAAGGAGCAAGCAATGGAGATGGCATGGCTGCTGAGGACAGTGCAGGGAG 2919
 QY 2566 CAGGATCAGTAAGAGGAAAAAGCAGTAAGCCAGAGGAGGAGCTTGTGAGCTGG 2625
 Db 2920 CAACGTGAGAGACAGCTCAGCAGCTCCTCCTCTATAGTGGGACATCAGCAGGACACC 2979
 QY 2626 AAGAGAAAGGCGGTTGAGTGGCTGCTGCTGAGTATATGCTGCTACATCAGGCTGCTG 2685
 Db 2980 AACAGCAACCGAGAACTGCAAGAAAGCTGAGGCCAAGAGGAGGAGACCTGGAAGCTGATG 3039
 QY 2686 GGGGC-----CCCTTGGCAATTCCTGTTATATGAGCCCTTTTCATGCTCAATGTAGGC 2738
 Db 3040 GAGGCTGACAAGGCGCAGACAGGCGAGGTCAAGCTTTCCTGTACTGGGACTACATGAG 3099
 QY 2739 AGCACCGCTTCAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2798
 Db 3100 GCCATCGGACTCTTCATCT 3159
 QY 2799 ACTGTGACTCGA-----GGGAAAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2852
 Db 3160 GCGTGGCTTCCAACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3219
 QY 2853 CATATGAGTACTATGCGGAGCTATGCGGCTCTCCATGCGGAGTCACTGCTGCTGCTG 2912
 Db 3220 CAGGAGCACGAAGTCCGCTGAGGCTATGAGGCGCTGGGCTGCTGCTGCTGCTGCTG 3279
 QY 2913 GCCATTCGAG-----AGTTGCTTTTCAAGGGGACGCTGCGAGCTTCTCCCGGCTG 2966
 Db 3280 GCGCTGTTGGCTACTCCATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3339
 QY 2967 CATGACGAGCTTTCCGAGGAGCTCTCGAGGCTATGAGTGTGCTGCTGCTGCTGCTG 3026
 Db 3340 CAGTGGAGCTGCTGCAAGCTCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3399
 QY 3027 ACAGGGAGGATCTCAACAGGCTTTTCAAGAGACATGAGTGAAGTGAAGTGAAGTGA 3086
 Db 3400 AGTGGAACTGCTGAGGAGCTTCCCAAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCT 3459
 QY 3087 TTCAGGCGGAGATGTTATCCCAAGAGCTTATCCTGCTGCTGCTGCTGCTGCTGCTG 3146
 Db 3460 GAGTCAATCAAGATGTTCAATGGGCTCCTGTTCAACGTCATTTGCTGCTGCTGCTG 3519
 QY 3147 GCAGGAGCTTCCGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3206
 Db 3520 CTGCTGCGCAGGCGCTATCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3579
 QY 3207 CTGCAATGCTTCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3266
 Db 3580 GTCCAGAGGTTCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3639
 QY 3267 TCACCTTTCTCCCAATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3326
 Db 3640 TCCCGGCTTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3699
 QY 3327 AATAAGGCGGAGGTTCTGCAAGATACAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 3386
 Db 3700 GAGGAGCAGGAGGCTTCTATCCACAGAGTACCTGAGGCTGCTGCTGCTGCTGCTGCTG 3759
 QY 3387 TTTTGTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3446
 Db 3760 TATTACCCAGCATGCTGGCCACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3819
 QY 3447 GCCTTCATCACACGAGGCTGATGCTGCTTATGCAAGGCGGAGATTCCTCCAGCC 3506

Db 3820 TGCATCGTCTCTGTTGCTGCCCTGTTTGGGGTGATCTCCAGGCACAGCCTCAGTGTGGC 3879
 QY 3507 TATGGGCTCTGCCATCTCTTATGCTGTCCAGTTAACGGGCTGTTCAGTTTACGGTTC 3566
 Db 3880 TTGTTGGGCTCTCTAGTGTCTTACTTATGCAAGTCCACACCTACTTGAACCTGGTGT 3939
 QY 3567 AGACTGGGATCTGAGACAGAGCTGATTCACCTCGGTGGAGGATCAATCACTACAT 3626
 Db 3940 CGATGTCATCTGAAATGGAACCAACATCTGTCGGCGTGGAGAGGCTCAAGGATATT 3999
 QY 3627 AAGACTCTGCTTGGAAAGCACTGCCAGATTAAGAAACAAGGCTCCCTCCCTCAGCTGG 3686
 Db 4000 GAGACTGAGAA---GGAGGCGCTTGGCAATCCAGGAGACAGCTCCGCCACAGCCTGG 4056
 QY 3687 CCCAGGAGGAGAGGTGACCTTTGAGAACGAGAGATGAGTACCGAGAAAACCTCCCT 3746
 Db 4057 CCCAGGTGGGCGAGTGGAAATTCGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4116
 QY 3747 CTGTCCTTAAAGAAAGTATCTCTTACGATCAAAACCTTAAGAGAAAGATTCGGCATTT 3806
 Db 4117 TTCGTTTCAGGCACATCAATGTCACGATCAATGGGGGAGAAAGTTCGGCATCTGGG 4176
 QY 3807 CGACAGGATCAGGAAGTCTCTGCTGGGATGGCCCTCTTCCGCTGCTGCTGCTGCTGCT 3866
 Db 4177 CGGAGGAGCTGGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4236
 QY 3867 GGAGCTCATCAAGATTTGAGAGTGAATGAGATCAATGAGTATTTGGCTTGGCGACCTCC 3926
 Db 4237 GAAGGAGAGATCATCATGATGGCATCAACATCGCAAGATCGGCTGCAACGCTCCGC 4296
 QY 3927 AGCAAACTCTATCATCTTCAAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3986
 Db 4297 TTCAGATCAACATCTCCCGAGGAGCTGTTTCTGCTGCTGCTGCTGCTGCTGCTGCT 4356
 QY 3987 TTGGACCCCTTCAACAGTACACTGAAGACCAAGATTTGGGATGCTGCTGCTGCTGCTG 4046
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 QY 4047 ATGAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4106
 Db 4417 CTGAAGGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4476
 QY 4107 GATAACTTCTCAGTGGGGAACGCGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4166
 Db 4477 GAGAACCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4536
 QY 4167 TGTAGATTCGATTTTATGATGAAGCCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4226
 Db 4537 ACGAAGATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4596
 QY 4227 ATTCAAGAGACCTCCGAGAGACATTTGCAGCTGTACCATGCTGCTGCTGCTGCTGCT 4286
 Db 4597 ATCCAGTCCCATCTCGGACACAGTTCGAGGACTGCACTGCTGCTGCTGCTGCTGCTGCT 4656
 QY 4287 CTGCACAGGTTCTAGGCTCCGATAGGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4346
 Db 4657 CTCAACACCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4716
 QY 4347 TTTGACACCCCATCGTCTTCTG 4370
 Db 4717 TACGGGCGCCCATCGGAGCTCTG 4740

RESULT 10
 US-08-463-092B-1
 ; Sequence 1, Application US/08463092B
 ; Patent No. 5766880
 ; GENERAL INFORMATION:
 ; APPLICANT: Cole, Susan P.C.
 ; APPLICANT: Deeley, Roger G.
 ; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
 ; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
 ; NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESS: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen's University at Kingston
CITY: Kingston
STATE: Ontario
COUNTRY: CANADA
ZIP: K7L 3N6

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,092B
FILING DATE: 05-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/966,923

FILING DATE: 27-OCT-1992

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/029,340

FILING DATE: 8-MAR-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/141,893

FILING DATE: 26-OCT-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/407,207

FILING DATE: 20-MAR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Steeg, Carol Miernicki

REGISTRATION NUMBER: 39,539

REFERENCE/DOCKET NUMBER: Q1546

TELECOMMUNICATION INFORMATION:

TELEPHONE: (613) 545-2342

TELEFAX: (613) 545-6853

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5011 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 196..4788

US-08-463-092B-1

Query Match 8.7%; Score 505.2; DB 1; Length 5011;
Best Local Similarity 52.1%; Pred. No. 6.3e-120;
Matches 1357; Conservative 0; Mismatches 1188; Indels 59; Gaps 8;

QY 1821 CACATCACCTGGCCACCTCGCCTTACAGAGGACACTGCACAGCATCGATCGGAGATC 1880
DB 2142 CACATTCACCTGGGCCA--GGAGGACCTCCACACACTGAATGGCATCCTTCCATC 2199
QY 1881 CAAGAGGGTAAACTGTGGAAATCTGCGCAGTGTGGGAAAGTGGAAAACTCTCTCAT 1940
DB 2200 CCCGAAGTGCTTTGGTGGCGGTGGTGGCCAGGTGGCTGGGAAAGTTGTCCCTGCTC 2259
QY 1941 TCAGCCATTTAGCCAGATGAGCGTCTTACAGGGGAGCATTCGAATCAGTGGAACTTC 2000
DB 2260 TCAGCCCTTTGGCTGAGATGGACAAAGTGGAGGGGACCTGGGCTATCAAGGGCTCCGTG 2319
QY 2001 GCTTATGCGCCAGAGGCTGGATCCTCAATGCTACTCTGAGAGACACATCCTGTTT 2060
DB 2320 GCCTATGTGGCAGCAGGCGCTGGATTTCAGAAATCTCTCCGAGAAAAACATCCTTTT 2379
QY 2061 GGGAAAGAAATATGATGAAGAAGATACAACCTGTGCTGTGAACAGCTCTGCCTGAGGCGCT 2120
DB 3460 GAGTCAATCAAGATGTTTCACTGGGCTCCCTGTTTCAACGTCATTTGGTGCCTGCATCGTTATC 3519

DB 2380 GGATGTCACTGGAGAACCATATTACAGTCCGCTCATACAGCCCTGTGCCCTCCTCCCA 2439
QY 2121 GACCTGGCCATCTTCCAGCAGCAGACCTGACGGAGATTGGAGAGCAGGAGCCAACTG 2180
DB 2440 GACCTGGAATCTGCCAGTGGGATCGACAGAGATTGGCAGGAAGGCGTGAACCTG 2499
QY 2181 AGCGGTGGGCGAGGCGCAGAGGATCAGCCCTGCCCCGGCCCTTGTATAGTACAGAGGATC 2240
DB 2500 TCTGGGGAGACAGAAGCAGCGCTGAGCCCTGGCCCGCCGCTGCTACTCCAAACGCTGACAT 2559
QY 2241 TACATCCTGGAGACGCCCTCAGTGCCTTAGATGCCCATGTGGGCAACACACATCTTCAAT 2300
DB 2560 TACCTCTTCGATGATCCCTCTCAGCAGTGGATGCCCATGTGGGAAAAACACATCTTTGAA 2619
QY 2301 AGTGTAT-----CCGGAACATCTCAAGTCCAAGACAGTCTTGTGTTTGTACCCACCAG 2354
DB 2620 AATGTGATTGGCCCAAGGGGATGCTGAAGAACAAGACGCGGATCTTGTGTCAGCACAGC 2679
QY 2355 TTACAGTACCTGGTGTGACTGTGATGAAGTGTCTTCATGAAAGAGGCGTGTATTACGGAA 2414
DB 2680 ATGAGTACTTGGCCGACGCTGACGTCATCATGAGTGGCGGCAAGATCTCTGAG 2739
QY 2415 AGAGCACCCATGAGGAACTGATGAATTTAAATGGTGAATCTATCTTACCATTTTATAAC 2474
DB 2740 ATGGCTCTTACCAGAGCTGCTGGCTGAGACGGCGCTTCGCTGAGTTTCTGCTGCCTACC 2799
QY 2475 CTGTTGCTGGAGAGACACCGCCAGTT---GAGATCAATTTCAAAAAGGAAACACAGTGT 2531
DB 2800 TATGCCAGCAGACAGCAGGAGCAGGATGACAGAGGAGACGCGGTACAGGCGTACGCGGT 2859
QY 2532 TCACAGAAGAGTCAACAGACA-----AGGTCCTTAAAA 2565
DB 2860 CCAGGGAAGGAAAGCAAAATGAGATGCGATGCTGTCAGCGACAGTGCAGGGAAG 2919
QY 2566 CAGGATCAGTAAAGAAAGAAAGCAGTAAAGCAGAGGAAAGGAGGAGCTTGTGCACCTGG 2625
DB 2920 CACTGACAGACAGCTCAGCAGCTCCTCTCTATAGTGGGAGCATCAGAGGACACAC 2979
QY 2626 AAGAGAAAGGCGAGGTTTCACTGTCCTCAGTATATAGTGTCTTACATCCAGGCTGCTG 2685
DB 2980 AACAGCACCGCAGAACTGCAGAAAGCTGAGGCCAAGAGGAGGAGACCTTGAAGCTGATG 3039
QY 2686 GGGC-----CCCTTGGCATTCTGTTGATTTATATGGCCCTTTTCATGCTGAATGAGC 2738
DB 3040 GAGGCTGACAAAGGCGCAGACAGGCGAGCTCAAGCTTTCCGTACTGGGACTACATGAAG 3099
QY 2739 AGCACCGCTTCAGCACCTGTTGTTGATTTACTGGATCAAGCAAGGAGGAGGAGACAC 2798
DB 3100 GCCATCGACTCTTCATCTCCTCTCAGCATCTTCTCTTTCATGTGTAAACATGTGTCTC 3159
QY 2799 ACTGTGACTCGA-----GGGAACGAGACCTCGGTGAGTGACAGCATGAAGACACATCT 2852
DB 3160 CGCGTGGCTTCCAACTATTGGCTCAGCCCTTGGACTGATGACCCCATCTCAACGGGACT 3219
QY 2853 CATATGAGTACTATGCAGCATCTACGCCCTCTCCATGGGCGAGTCAATGCTGATCTGAAA 2912
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QY 2913 GCCATTCGAGG-----AGTTGTCTTTTCAAGGCGCAGCTCGGAGCTTCTTCCCGGCTG 2966
DB 3280 GCCGTGTTGGCTACTCCATGGCGGTGTCATCGGGGGGATCTTGGCTTCCCGCTGTCTG 3339
QY 2967 CATGACGAGCTTTTCCGAAGGATCTTCCGAAGCCCTATGAAGTTTGTGACACGACCCCC 3026
DB 3340 CACGTGGACCTGTGTCAGCATCTTGGCGGTCAACCCATGAGCTTCTTTGAGGGGACCC 3399
QY 3027 ACAGGAGGATTTCAACAGGTTTTCGAAAGACATGAGTGAAGTTGACGTGCGGCTGCG 3086
DB 3400 AGTGGAACTGTGGTGAACCGCTTCTCCAAAGGAGCTGGACACAGTGCATGATGATCCG 3459
QY 3087 TTCAGGCGCGAGATGTTCAATCCAGACGTTTATCTCTGGTGTCTTCTGTGTGGAATGATC 3146
DB 3460 GAGTCAATCAAGATGTTTCACTGGGCTCCCTGTTTCAACGTCATTTGGTGCCTGCATCGTTATC 3519

QY	3147	GCAGAGGCTCTCCGCTGGTTCCCTTGTGTCGAGTGGGGCCCTTGTCTCATCTCTTTTCAGTC	3200
DB	3520	CTGCTGGCCAGGCCATCGCGGCCATCATATCCCGGCCCTTGGGCTCATCTACTTCTTC	3579
QY	3207	CTGCACATTTGCTCCAGGGTCCCTGATTCCGGGAGCTGAAGCGTCTGGACAATATCACGCG	3266
DB	3580	GTCCAGAGGTTCTAGGTGGCTTCCCTCCGCGAGCTGAAGGCCCTCGAGTCGGTCAGCCGC	3639
QY	3267	TCACCTTTCTCTCCACATCATCAGTCCAGCATACAGGGCTTGGCCACATCCAGCCCTAC	3326
DB	3640	TCCCGGCTCTATTCCCATTTCAACGAGACCTTGTCTGGGGTTCAGCGTCAITTCGAGAGCTTC	3699
QY	3327	AATAAAGCGCAGGAGTTTCTGCAACATACACAGGAGCTGCTGGGATGACAACCAAGCTCCT	3386
DB	3700	GAGGAGCAGAGCGCTTCATCCACAGAGTGACTGAAGGTGGACGAGAACCAAGAGGCC	3759
QY	3387	TTTTTTTTTTTACGTGTCGGATGCGGTGGCTGTCCGGCTGGAGCTCATCAGCATC	3446
DB	3760	TATTACCCAGCATCGTGGCCAAACAGTGGCTGGCGCTGCGCTGGAGTGTGTGGCAAC	3819
QY	3447	GCCCTCATCACCAACGAGGGCTGATGATCGTTCTATTGACAGGGCAGATTCGCCAGCC	3506
DB	3820	TGCATCGTCTGTGTCGCTCGCTTGTGGGTGATCTCCAGGCACAGCCTCAGTGTCTGGC	3879
QY	3507	TATCGGGTCTCGCCATCTCTTATGCTGTCACAGTTAAACGGGGCTGTCCAGTTTACCGTC	3566
DB	3880	TTGTTGGGCTCTCAGTGTCTTACTCATTTGCAGGTCAACAGTACTTTGAATGGCTGGTT	3939
QY	3567	AGACTGGCATCTGAGACAGAAGCTCGATTTCACCTCGGTGGAGAGGATCAATCACTACATT	3626
DB	3940	CGGATGTCATCTGAATTGGAACCAACATCGTGGCGGTGGAGAGCTCAAGGAGTATTCA	3999
QY	3627	AAGACTCTGTCTTGAAGCAGCTGCCAGATTTAGAACAAAGGCTCCCTCCCTGACTGG	3686
DB	4000	GAGACTGAGAA---GGAGCGCCCTGGCAATTCACAGSAGACACCTGCGGCCACGACGTGG	4056
QY	3687	CCCCAGGAGGAGGTGACCTTTGAGACGCAGAGATGAGSTACCGAGAAACCTCCCT	3746
DB	4057	CCCCAGTGGCCGAGTGGAAATTCGGAATCTACTCCCTGCGCTACCGAGAGGACCTGGAC	4116
QY	3747	CTTGTCTTAAAGAAGTATCTTTCAGATCAAACTTAAAGAGAAGATTTGCACTTTGGGG	3806
DB	4117	TTCTGTTCTCAGGCACATCAATGTCAGATCAATGGGGGAGAAAAGTTCGCATCGTGGGG	4176
QY	3807	CGACAGGATCAGGGAAGTCTCTCGCTGGGGATGGCCCTTTCCTCTGTGTGGAGTATTCT	3866
DB	4177	CGACGGAAGTGGGAAGTGTCTCTGACCCCTGGGCTTATTTCGGATCAACGAGCTGGC	4236
QY	3867	GGAGGTGTCATCAAGATTGATGGAGTGAATATGATGTCCTGCGCTTGGCGACCTCCGA	3926
DB	4237	GAAGGAGATCATCATCATGGCATCAACATCGCCAGATTCGCGCTGACGACCTCCGC	4296
QY	3927	AGCAACTCTCTATCATTCCTCAAGAGCCGGTGTGTTCAGTGGCACTGTGAGATCAAAAT	3986
DB	4297	TTCAAGATCACTATCCCCAGGACCTGTGTGTGTTTTCGGGTTCCCTCCCAATGAAC	4356
QY	3987	TTGACCCCTTCAACCAGTACACTGAACACCATTTGGGATGCCCTGGAGAGGACACAC	4046
DB	4357	CTGAGCCCATTCAGCCGACTCTGCGATGAAGAAGTCTGGAGCTCCCTGGAGCTGGCCAC	4416
QY	4047	ATGAAGAATGATTGCTCAGCTACTCTGAAACTTGAATCTGAAGTATGGAGATGG	4106
DB	4417	CTGAAGGACTTCGTGTACGCCCTTCTCAGCAAGCTAGACCATGAATGTGCAGAAGCGGG	4476
QY	4107	GATAACTTCTAGTGGGGAGCGGAGCTCTTGTGTCATAGCTAGAGCCCTGCTCCGCCAC	4166
DB	4477	GAGAAGCTCAGTGTGGGCGAGCCAGCTTGTGTGCTAGTCCCGGGCCCTGCTGAGGAG	4536
QY	4167	TGTAAGATCTGATTTAGATGAAGCCACACTGCCATGGACACAGACAGACTTATTG	4226
DB	4537	ACGAAGACTCTTGTGTGTGATGAGCCACGCGACGCGCTGGACCTTGAACCGGACGACTTC	4596

QY	4227	ATTTCAGACACCATCCGAGAACGATTTTGACAGACTGTACCATGCTGACCATTTGCCCATTCG	4288
DB	4597	ATTCAGTCCACCATCCGAGACACACATTCGAGGACTGCACCGTCTCTCACCATTCGCCACCG	4656
QY	4287	CTGCACACGGTCTAGGCTCCGATAGATTATGGTGTCTGSCCCACGAGGAGGTGGTGGAG	4346
DB	4657	CTCAACACCATCATGACTATACACAGGGTGATCGTCTTGACAAAGAGAAATCCAGGAG	4716
QY	4347	TTTGACACCCCATCGGTCCTCTCTG	4370
DB	4717	TACGGCGCCCATCGACGACTCTG	4740
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US-08-462-109A-1			
; Sequence 1, Application US/08462109A			
; Patent No. 5882875			
; GENERAL INFORMATION:			
; APPLICANT: Cole, Susan P.C.			
; APPLICANT: Deeley, Roger G.			
; TITLE OF INVENTION: METHODS FOR IDENTIFYING			
; TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS			
; NUMBER OF SEQUENCES: 6			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: LAHIVE & COCKFIELD			
; STREET: 60 State Street, suite 510			
; CITY: Boston			
; STATE: Massachusetts			
; COUNTRY: USA			
; ZIP: 02109			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: ASCII text			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/462.109A			
; FILING DATE:			
; CLASSIFICATION: 435			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 07/966,923			
; FILING DATE: 27-OCT-1992			
; APPLICATION NUMBER: 08/029,340			
; FILING DATE: 8-MAR-1993			
; APPLICATION NUMBER: 08/141,893			
; FILING DATE: 26-OCT-1993			
; APPLICATION NUMBER: 08/407,207			
; FILING DATE: 20-MAR-1995			
; ATTORNEY/AGENT INFORMATION:			
; NAME: DeConti, Giulio A. Jr.			
; REGISTRATION NUMBER: 31,503			
; REFERENCE/DOCKET NUMBER: POI-002CP4			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (617) 227-7400			
; TELEFAX: (617) 227-5941			
; INFORMATION FOR SEQ ID NO: 1:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 5011 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: double			
; TOPOLOGY: linear			
; MOLECULE TYPE: CDNA			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: 196..4788			
; US-08-462-109A-1			
Query Match 8.7%; Score 505.2; DB 2; Length 5011;			
Best Local Similarity 52.1%; Pred. No. 6.3e-120;			
Matches 1357; Conservative 0; Mismatches 1188; Indels 59; Gaps			
QY	1821	CACATCCACCTGGGCCACCTGGCTGTACAGAGACACTGCACAGCATCGATCTGGAGATC	1880

Db 2142 CACATTCACCTGGGCCA--GGAGGAGACCCCTCCACACTGAATGGCATCACCTTCTCCATC 2199
Qy 1881 CAAGAGGTAAACTGGTTGGAACTCTGCGCAGTGTGGCAAGTGGAAACCTCTCTCATTT 1940
Db 2200 CCCGAGGTGCTTGGTGGCGTGGTGCCAGGTGGGCTGCGGAAAGTTGTCCCTGTCTC 2259
Qy 1941 TCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGCGACATTTGCAATCAGTGGAACTTC 2000
Db 2260 TCAGCCCTCTTGGCTGAGATGGACAAGTGGAGGGCAGCTGGCTATCAAGGGCTCCGTG 2319
Qy 2001 GCTTATGTGGCCAGCAGGCTGTGATCTCAATGCTACTGTGAGAGACAATCCTGTTT 2060
Db 2320 GCTTATGTGGCCAGCAGGCTGTGATCTCAATGCTACTGTGAGAGACAATCCTGTTT 2379
Qy 2061 GGGAGGATATGATGAGAAAGATACAACTCTGTCTGACAGCTGTCTGCTGAGGCT 2120
Db 2380 GGATGTAGCTGGAGGAACCATATTACAGGTCCGTGTACAGGCTGTGCCCTCCTCCCA 2439
Qy 2121 GACCTGGCCATTTCTCCAGCAGCGACTGACGGAGATTGGAGAGGAGGAGCCAACTG 2180
Db 2440 GACCTGGAAATCTTCCCGAGTGGGATCGGACAGAGATTGGCAGAGGGCGTGAACCTG 2499
Qy 2181 AGCGTGGGAGCGCCAGAGAGATCAGCCTTTCGCCGGGCTTTGTATAGTGACAGGAGCATC 2240
Db 2500 TCTGGGGACAGAGACAGCGGCTGAGCCTGGCCGGGCGGTACTCCAAACGCTGACATT 2559
Qy 2241 TACATCTGGACGACCCCTCAGTGCCTTAGATGCCATGTGGGGAACCAATCTTCAAT 2300
Db 2560 TACCTCTCGATGATGCCCTCTACGAGTGGATGCCATGTGGGAAACACATCTTTGAA 2619
Qy 2301 AGTGCTAT-----CCGGAACATCTCAAGTCCAAAGCAGTCTCTGTTTGTACCCACAGC 2354
Db 2620 AATGTGATGGCCCAAGGGATCTGAGAGCAAGACGCGGATCTTGGTCACGACAGC 2679
Qy 2355 TTACAGTACCTGGTTGACTGTGATGATGATCTTCAATGAAAGAGGCTGTATTACGGAA 2414
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Db 2800 TATCCAGCACAGAGGAGGACGATGTCAGAGGAGACGGGTACCGGGCGTCAGCGGT 2859
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Db 2860 CCAGGGAAGGAAGCAAAAGCAAAATGGAAATGGCATGCTGCTGACGGACAGTGCAGGGAAG 2919
Qy 2566 CAGGATCAGTAAAGAAAGCAAGCAGTAAGCCAGAGGAGGAGGCGACTGTGTCAGCTGG 2625
Db 2920 CAATCGAGAGACAGTCAAGAGCTCTCTCTCTATAGTGGGACATCAGCAGGACACAC 2979
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Db 2980 AACAGCACCGCAAGTGCAGAAAGCTGAGGCCAAGAGAGGAGAGCTTGGAACTGATG 3039
Qy 2686 GGGC-----CCCTTGGCATCTCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGG 2738
Db 3040 GAGGCTGACAAGGCGCAGAGAGGCGCATCAAGCTTTTCCGTGCTACTGGGACTACATGAAG 3099
Qy 2739 AGCACCCCTTACGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2798
Db 3100 GCCATGGACTTTCATCT 3159
Qy 2799 ACTGTGACTCGA-----GGGAACGAGACCTCGGTGAGTGACAGCATGAAGCAATCCT 2852
Db 3160 GCGTGGCTTCCAACTATTGGCTCAGCCTCTGACATGATGACCCCTCTGCAAGGGACT 3219
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Qy 2913 GCATTCGAGG-----AGTTGCTTTTTCAGAGGGCACGCTGCGAGCTTCTCTCCGGCTG 2966
Db 3280 GCGGTGTTTGGTACTTCCATGGCCGTGCTCATCGGGGGATCTTGGCTCCCGCTGCTG 3339
Qy 2967 CATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATGAGTTTTGTGACAGACCC 3026
Db 3340 CAGGTGGACCTGCTGCACAGCATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3399
Qy 3027 ACAGGAGGATTTCTCAAGAGGTTTTCGAAGACATGATGAAGTTGACGTGCGGCTGCG 3086
Db 3400 AGTGGGAACCTGCTGAACGCTTCTCCAGGAGCTGGACACAGTGAACCTGATGATCC 3459
Qy 3087 TTCAGGCGGAGATGTTTCAATCAGAACGTTATCTCTGCTGCTGCTGCTGCTGCTGCT 3146
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Qy 3327 AATAAGGCGAGGAGTCTTTCACAGATACACAGGAGCTGCTGGATGACAAACCAAGCTCT 3386
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Qy 3387 TTTTTTTGTGTACGTGCGGATGGGTGGCTGTGCGGCTGAGCCTCATCAGCATC 3446
Db 3760 TATTACCCAGCATCTGGCCAAAGTGGCTGCGCTGCGCTGAGTGTGGGCAAC 3819
Qy 3447 SCCCTCATCACCACACGGGCTGATGCTGTTTATGACAGGGGAGATTTCCCCAGGC 3506
Db 3820 TGATCTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3879
Qy 3507 TATGGGCTGCTGCGCATCTTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3566
Db 3880 TTGTTGGCTCTGAGTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3939
Qy 3567 AGACTGGCATCTGACAGAGAGCTCGATTCCTCGGTGGAGAGATCAATCACTACAT 3626
Db 3940 CGGATGCTATCTGAATGGAACCAACATCTGTCGCTGAGAGGCTCAAGAGTATTC 3999
Qy 3627 AAGACTCTGCTTGGAGACCTGCCAGATTAAGAAACAGGCTCCCTCCCTGACTGG 3686
Db 4000 GAGACTGAGAA---GGAGGCGCTTGGAAATCCAGGAGACAGCTCCGCGCCAGCAGCTGG 4056
Qy 3687 CCCAGGAGGAGAGTGGCTGACCTTTGAGAACGACAGAGATGAGTACCGAGAAACCTCCCT 3746
Db 4057 CCCAGGTTGGCGGAGTGGAAATTCGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4116
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Db 4117 TTCGTTCTCAGGCACATCAATGCTACAGTCAATGAGGAGAAAGGTCGGCATCTGGGG 4176
Qy 3807 CCGACAGGATCAGGAAGTCTCTGCTGGGATGGCCCTCTTCCGCTGCTGGTGGAGTATCT 3866
Db 4177 CCGAGGAGGAGTGGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4236
Qy 3867 GGAGGCTCATCAAGATGATGAGTGAATCAGTGAATGAGCTTGGCCTTCCGAGCTCCGA 3926
Db 4237 GAAGGAGATCATCATGATGGCATCAACATCGCAAGATGCGGCTGCAAGCTCCG 4296
Qy 3927 AGCAAACTCTTATCTTCCCTCAAGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3986
Db 4297 TTCAAGATCACCATCATCCCGCAGGACCTGTTTGTGTTTTCGGGTTTCCCTCCGATGAAC 4356

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/463,179A
;; FILING DATE:
;; CLASSIFICATION: 536

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/966,923

;; FILING DATE: 27-OCT-1992

;; APPLICATION NUMBER: 08/029,340

;; FILING DATE: 8-MAR-1993

;; APPLICATION NUMBER: 08/141,893

;; FILING DATE: 26-OCT-1993

;; APPLICATION NUMBER: 08/407,207

;; FILING DATE: 20-MAR-1995

;; ATTORNEY/AGENT INFORMATION:
;; NAME: DeConti, Giulio A. Jr.

;; REGISTRATION NUMBER: 31,503

;; REFERENCE/DOCKET NUMBER: PQI-002CP8

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 227-7400

;; TELEFAX: (617) 227-5941

;; INFORMATION FOR SEQ ID NO. 1:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 5011 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: double

;; TOPOLOGY: linear

;; MOLECULE TYPE: cDNA

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: 196..4788

;; US-08-463-179A-1

Query Match 8.7% Score 505.2; DB 3; Length 5011;
Best Local Similarity 52.1%; Pred. No. 63e-120;
Matches 1357; Conservative 0; Mismatches 1188; Indels 59; Gaps 8;

QY 1821 CACATCCACCTGGGCCACCTGGCTTACAGAGGACACCTGCACAGCATCGATCTGGAGATC 1880
DB 2142 CACATTCACCTGGGCCA--GGAGCGACCTCCACACATGAATGGCATCACCTTCTCCATC 2199
QY 1881 CAAGAGGTAACTGGTTGGATCTGCGCAGTGGGAGTGGGAGGAAACCTCTCTCAT 1940
DB 2200 CCCGAAGGTGTTGGTGGCCGTGTGGGCCAGGTGGGCTGCGGAAAGTTGTCCTGCTC 2259
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DB 2500 TCTGGGGACAGAACGACGCGCTGAGCCTTGCCCGGGCGGTACTCCAACGCTGACAT 2559
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DB 2560 TACCTCTTCGATGATCCCTCTCAGCAGTGGATGCCATGTGGGAAACCACTCTTGA 2619
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QY 3027 ACAGGAGGATTTCAACAGGTTTCCAAAGACATGGATGAAGTTGACGTGGCGTCCG 3086
DB 3400 AGTGGAACTGTGTAACCGCTTCTCCAGGAGCTGACACAGTGGACTCCATGATCCG 3459
QY 3087 TTCAGGCGGAGATGTTCAATCCAGAACGTTATCTGCTGTTCTGTTGTGGGAATGATC 3146
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QY 3327 AATAAGGCGAGGATTTCTGCACAGATACACAGGAGCTGCTGATGACAAACAGCTCT 3386
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Db 3760 TATTACCCAGCATCTGTGGCCAAACAGGTGGCTGGCGGTGGAGTGTGTGGGCAAC 3819
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Db 3820 TGCATCGTCTCTTTTGTGGCTCTTTGGCGGTATCTCCAGGCACAGCCTCAGTCTGCTGC 3879
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Db 3880 TTGGTGGCCCTCTCAGTGTCTTACTCATGTGAGGTACACAGTACTTGAATGGCTGTT 3939
Qy 3567 AGACTGGCATCTGACAGAGAAGCTCGATTACCTCGGTGGAGAGATCAATCACTACAT 3626
Db 3940 CGGATGTCTGAATGGAACCAACATCGTGGCGGTGGAGAGCTCAAGGATATCA 3999
Qy 3627 AAGACTCTGCTTGGAGACACCTGCCAGATTAAGAACAGGCTCCCTCCCTGACTG 3686
Db 4000 GAGACTGAGAA--GGAGGGCCCTGCAATCCAGGAGACACGTCCGCCCCAGCAGCTGG 4056
Qy 3687 CCCAGGAGGAGAGGTGACCTTTGAAACGCAGAGATGAGGTACCCGAGAAAACCTCCCT 3746
Db 4057 CCCAGGTGGCCGAGTGAATCCGGAATCTGCGCTACCCGAGAGACCTGGAC 4116
Qy 3747 CTTGCTCTAAGAAAGTATCTTCCACGATCAAACTTAAAGAAAGATGGCATTTGGGG 3806
Db 4117 TTCGTCTCAGGCACATCAATGTCAAGTCAATGGGGAGAAAGTGGCATCGTGGG 4176
Qy 3807 CGGACAGATCAGGAAGTCTCCTCGCTGGGATGCGCTCTTCCCTGCTGCTGGTATCT 3866
Db 4177 CGGACGGAGCTGGGAAGTCTCCTGACCTGGGCTTATTTCCGATCAACGAGTCTGCC 4236
Qy 3867 GGAGCTCATCAAGATGATGAGTCAATCATGATGATGATGATGATGATGATGATGAT 3926
Db 4237 GAAGGAGATCATCATCGATGGGATCAATCCCAAGATCGGCTGACGAGCTCCG 4296
Qy 3927 AGCAACTCTCTATCTCTCAAGAGCCGCTGCTTTCAGTGGCAGTGTGATGATCAAT 3986
Db 4297 TTCAAGATCACCATCATCCCCAGGACCTCTTTTGTTCGGGTCCCTCCGATGAC 4356
Qy 3987 TTGACCCCTTCAACAGTACATCAAGACAGATTTGGGATGCGCTGGAGAGACAC 4046
Db 4357 CTGACCCATTCAGCCAGTACTCGGATGAAGAAGTCTGGAGTCTCCCTGGAGTGGCCAC 4416
Qy 4047 ATGAAGAATGATTTGCTCAGTCACTCTGAACTTGAATGATGATGATGATGATGATG 4106
Db 4417 CTGAAGATCTGCTGCTCAGCCCTCTCTGACCAAGTACAGCATGATGACAGAGGGG 4476
Qy 4107 GATAACTTCTCAGTGGGGAACGACGCTCTTGTGCTAGTAGAGCCCTGCTCCGCCAC 4166
Db 4477 GAGAACCTCAGTGTGGGCGAGCCAGCTTGTGTGCTAGCCCGGCGCTGCTGAGGAG 4536
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Db 4537 ACGAAGATCTTGTGTGGATGAGGCCACGACGCTGGACCTTGAACAGGAGACCTC 4596
Qy 4227 ATCAAGAGACCATCCGAGAGCATTTGACAGTGTACCATGCTGACCATGCTCCATCGC 4286
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Qy 4287 CTGACACGGTCTTAGGCTCCGATGAGTATGCTGCTGGCCCGAGGACAGGTGGTGG 4346
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Qy 4347 TTTGACACCCCATCGGCTCTCTG 4370
Db 4717 TACGGCGCCCATCGGACCTCTG 4740

RESULT 14

US-08-461-384B-1
; Sequence 1, Application US/08461384B
; Patent No. 6025473
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.

; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,384B
; FILING DATE: 05-JUN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Steed, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1547
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO. 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..4788
; US-08-461-384B-1

Query Match

Best Local Similarity 8.7%; Score 505.2; DB 3; Length 5011;
Best Local Similarity 52.1%; Pred. No. 6.3e-120;
Matches 1357; Conservative 0; Mismatches 1188; Indels 59; Gaps 8;

Qy 1821 CACATCCACCTGGGCGCCACCTGGCTTTACAGAGGACACTGCACAGCATCTGAGATC 1880
Db 2142 CACATTCACCTGGGCCA--GGAGCGACCTCCACACCTGAATGGCATCACCCTCTCCATC 2199
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Db 2200 CCCGAAGTGTGTTGGTGGCGCTGGTGGCGCAGGTGGCGGAAAGTTGCCCTGCTC 2259
Qy 1941 TCAGCATTTTAGGCCAGATGACGCTTCTAGAGGCGAGCATTCGATGCAATGAGCACTTC 2000
Db 2260 TCAGCCCTCTTGGCTGAGATGGACAAAGTGGAGGGGCGACGTGGCTATCAAGGCTCCGTG 2319
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QY 3807 CGGACAGATCAGGAGAGTCTCTCGTGGGATGGCCCTTCTCCGTCTGTTGGATTTACT 3866
DB 4177 CGGACGAGGAGTGGGAGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4236
QY 3867 GGAGGCTCATCAAGATGATGAGTGAATCAGTGAATTTGGCTTGGCGCTGCGACCTCGGA 3926
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RESULT 15

US-08-407-207A-1
; Sequence 1, Application US/08407207A
; Patent No. 6063621
; GENERAL INFORMATION:
; APPLICANT: Deeley, Roger G.
; APPLICANT: Cole, Susan P.C.
; TITLE OF INVENTION: ANTIBODIES TO A MULTIDRUG RESISTANCE PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/407,207A
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: 01512
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196...4788
US-08-407-207A-1

Query Match 8.7%; Score 505.2; DB 3; Length 5011;
Best Local Similarity 52.1%; Pred. No. 6.3e-120;
Matches 1357; Conservative 0; Mismatches 1188; Indels 59; Gaps 8;

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:00:25 ; Search time 730.01 Seconds
(without alignments)
18009.573 Million cell updates/sec

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Perfect score: 5838

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5838	100.0	5838	20	AAZ30079
2	5838	100.0	5838	20	Human ATP binding
3	4792.6	82.1	4847	21	Human MRP-beta cDN
4	4791	82.1	4847	19	Human MRP-beta cDN
5	4724.2	80.9	4781	22	Human multidrug re
6	1936.4	33.2	2167	18	Multidrug-resistan
7	1676	28.7	1761	18	Human multidrug re
8	925.8	15.9	4101	22	Human transporter-
9	790.6	13.5	4008	22	Human transporter-

10	766.4	13.1	4149	22	AAF83643	Novel human transp
11	759.4	13.0	3660	22	AAD14910	Human transporter-
12	757.8	13.0	4074	24	AAD36023	Human adenosine tr
13	753.2	12.9	3753	22	AAD14911	Human transporter-
14	727	12.5	3055	23	ABV21036	Human prostate exp
15	727	12.5	3055	23	ABV26879	Human prostate exp
16	723.8	12.4	3189	22	AAF83637	Novel human transp
17	723.8	12.4	4638	24	AA922270	Human ATP-binding
18	722.2	12.4	4427	24	ABK92211	Prostate cancer-as
19	537.8	9.2	1698	22	AAD14913	Human transporter-
20	522	8.9	3549	23	AAS90084	DNA encoding novel
21	510	8.7	5011	19	AAV31498	Human MRP variant
22	510	8.7	5011	20	AAV31498	Human multidrug re
23	510	8.7	5011	20	AAV31498	Human MDR variant
24	510	8.7	5011	21	AAZ94741	Human ATP binding
25	510	8.7	5011	21	AAZ90193	Multidrug resistan
26	510	8.7	5011	21	AAZ39556	Human MRP variant
27	510	8.7	5011	24	ABK92125	Prostate cancer-as
28	505.2	8.7	4864	17	AAT14911	cDNA encoding mult
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38	471.2	8.1	2699	24	AAD33647	Human TRICH-2 cDNA
39	442	7.6	442	24	ABL66374	Lung cancer relate
40	437.4	7.5	4231	20	AAZ30078	cDNA encoding a hu
41	437.4	7.5	4231	22	AAH81778	Human differential
42	436	7.5	5020	22	AAF83647	Novel human transp
43	435.8	7.5	3978	24	ABK92135	Prostate cancer-as
44	435.8	7.5	6140	22	AAS63922	Human prostate cDN
45	435.8	7.5	6140	22	AAH93829	Human prostate-spe

ALIGNMENTS

RESULT 1

AAZ30079
ID AAZ30079 standard; cDNA; 5838 BP.

XX AAZ30079;

XX AC AAZ30079;

XX 26-JAN-2000 (first entry)

XX cDNA encoding a human MPR-related ABC transporter designated MOAT-C.

XX Human; MPR-related ABC transporter; MOAT protein; MOAT-C;

XX MOAT mediated transport; anticancer drug sensitivity;

XX transporter mediated cellular efflux; anticancer; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 126..4439

XX FT /*tag= a

XX FT /product= "MOAT-C"

XX FT /note= "MPR-related ABC transporter"

XX PN WO9949735-A1.

XX PD 07-OCT-1999.

XX PF 26-MAR-1999; 99WO-US06644.

XX PR 27-MAR-1998; 98US-0079759.

XX PR 03-AUG-1998; 98US-0095153.

XX PA (FOXC-) FOX CHASE CANCER CENT.

XX Kruh G, Lee K, Belinsky M, Bain L;
 XX WPI; 1999-610812/52.
 DR P-PSDB; AAY43542.
 XX
 PT New transporter gene useful for screening for anti-cancer drugs -
 XX
 PS Claim 11; Page 134-135; 153pp; English.
 XX
 CC The present sequence encodes a human MPR-related ABC transporter (MOAT)
 CC protein, designated MOAT-C. The protein comprises a multi-domain
 CC structure including a tandem repeat of nucleotide binding folds
 CC appended C-terminal to a hydrophobic domain, having Walker A and B ATP
 CC binding sites and several potential membrane spanning domains. The MOAT
 CC nucleic acids are useful for screening a test compound for inhibition of
 CC MOAT mediated transport, indicated by restoration of anticancer drug
 CC sensitivity, which in turn causes a reduction of transporter mediated
 CC cellular efflux of anticancer agents. MOAT DNA or RNA may be used as
 CC probes to detect the presence or expression of genes encoding MOAT
 CC proteins. Anti-MOAT antibodies are useful for detecting and quantitating
 CC MOAT proteins.
 XX
 SQ Sequence 5838 BP; 1422 A; 1432 C; 1509 G; 1475 T; 0 other;
 Query Match 100.0%; Score 5838; DB 20; Length 5838;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5838; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGGCAGGTGGCTCATGCTCGGGAGCGTGTGAGCGGCTGGCGGGTGTCTCGAGC 60
 DB 1 CCGGGCAGGTGGCTCATGCTCGGGAGCGTGTGAGCGGCTGGCGGGTGTCTCGAGC 60

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 DB 61 AGGGCCAGGAATTCGTGTGAACTAACAGTCTGTGAGCCCTGGAACCTCCGCTCAG 120

QY 121 AGAAGATGAAGGATATCGACATAGGAAAGAGTATATATCCCGAGTCTGGGTATAGAA 180
 DB 121 AGAAGATGAAGGATATCGACATAGGAAAGAGTATATATCCCGAGTCTGGGTATAGAA 180

QY 181 GTGTAGGAGAGAACAGACACTTCTGGGAGCGACAGACCGTGAAGATTCCAAAGTCA 240
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 DB 481 CCGGTGTGGCCCCAAGAAGGGGAGCTCTCAATGGAGACGTGTGGTCTCTGTGCCAAGC 540

QY 541 ACCAGTCTCTGACGTGAACCTCAGAGACTAGAGACTGTGGCAGAGAGCTGAATG 600
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 DB 721 TCATGGTGAACACACTCTTGGAGTATACCAGGCAACAGAGTCTAACCTGCAGTACAGCT 780

QY 781 TGTGTAGTGTGCTGGGCTCTCTCTGACGGAAATCGTGGGCTTGGTGGCTTGCACATGA 840
 DB 781 TGTGTAGTGTGCTGGGCTCTCTCTGACGGAAATCGTGGGCTTGGTGGCTTGCACATGA 840

QY 841 CTGGGCAATTGAATPACCGAACCGGTGTCGCTTCGGGGGGCCCATCTTAACCATGGCAT 900
 DB 841 CTGGGCAATTGAATPACCGAACCGGTGTCGCTTCGGGGGGCCCATCTTAACCATGGCAT 900

QY 901 TTAGAAGATCCTTAAGTTAAAGAACATTAAGAGAAATCCCTGGGTGAGCTCATCAACA 960
 DB 901 TTAGAAGATCCTTAAGTTAAAGAACATTAAGAGAAATCCCTGGGTGAGCTCATCAACA 960

QY 961 TTTGCTCCAAGCATGGGCGAGAAATGTTTGGGAGCAGACCGTGGCAGCCTGCTGGCTG 1020
 DB 961 TTTGCTCCAAGCATGGGCGAGAAATGTTTGGGAGCAGACCGTGGCAGCCTGCTGGCTG 1020

QY 1021 GAGGACCGTGTGCTGCCATCTTAGGCATGATTAATATTAATTTCTGGGACCAACAG 1080
 DB 1021 GAGGACCGTGTGCTGCCATCTTAGGCATGATTAATATTAATTTCTGGGACCAACAG 1080

QY 1081 GCTTCTCGGATCAGCTGCTTTTATCTCTTTTACCAGCAATGATGTTTGCATCAGGC 1140
 DB 1081 GCTTCTCGGATCAGCTGCTTTTATCTCTTTTACCAGCAATGATGTTTGCATCAGGC 1140

QY 1141 TCACAGCATATTTTCAGGAGAAATCCGTGGCGCCACCGATGAACGTGTCCAGAGATGA 1200
 DB 1141 TCACAGCATATTTTCAGGAGAAATCCGTGGCGCCACCGATGAACGTGTCCAGAGATGA 1200

QY 1201 ATGAAGTCTTCTTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1260
 DB 1201 ATGAAGTCTTCTTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1260

QY 1261 AGAGTGTTCAAAATAATCCCGAGGAGGAGCGTGGGATTTGGAAAAAGCCGGGTACTTCC 1320
 DB 1261 AGAGTGTTCAAAATAATCCCGAGGAGGAGCGTGGGATTTGGAAAAAGCCGGGTACTTCC 1320

QY 1321 AGGTATACACTGTGGTGTGGCTCCCATTTGTTGGTGTGATTTGCCAGCGTGGTACCTTCT 1380
 DB 1321 AGGTATACACTGTGGTGTGGCTCCCATTTGTTGGTGTGATTTGCCAGCGTGGTACCTTCT 1380

QY 1381 CTGTTTCAATATGACCTGGGCTTTCGATCTGACAGCAGCAGCGTTCACAGTGGTGACAG 1440
 DB 1381 CTGTTTCAATATGACCTGGGCTTTCGATCTGACAGCAGCAGCGTTCACAGTGGTGACAG 1440

QY 1441 TCTTCAATTCATGACTTTTGTGAAAGTAAACACCGCTTTTTCAGTAAAGTCCCTCTCAG 1500
 DB 1441 TCTTCAATTCATGACTTTTGTGAAAGTAAACACCGCTTTTTCAGTAAAGTCCCTCTCAG 1500

QY 1501 AAGCTCAGTGGCTGTGACAGATTTAAGAGTTTGTGTTCTAATGAGAGCTTCCACATGA 1560
 DB 1501 AAGCTCAGTGGCTGTGACAGATTTAAGAGTTTGTGTTCTAATGAGAGCTTCCACATGA 1560

QY 1561 TAAAGAAACAAACAGCCAGTCTTCAATCAAGATAGAGATGAAATGCCACCTTGGCAT 1620
 DB 1561 TAAAGAAACAAACAGCCAGTCTTCAATCAAGATAGAGATGAAATGCCACCTTGGCAT 1620

QY 1621 GGGACTCTTCCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCAAAATGAAAAAG 1680
 DB 1621 GGGACTCTTCCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCAAAATGAAAAAG 1680

QY 1681 ACAAGAGGGCTTCCAGGGGCAAGAGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGATC 1740
 DB 1681 ACAAGAGGGCTTCCAGGGGCAAGAGAGAGTGGAGAGTGGAGAGTGGAGAGTGGAGATC 1740

QY 1741 AGGCGTGTGGCAGAGCAGAAAGGCCACCTCTCTTGGACAGTGAACAGCGGCGCCAGTC 1800

Db 1741 AGCGGTGCTGGCAGAGCAGAAAGGCCACCTCTCTCTGGCAGGTGAGCGGCGCCAGTC 1800
QY 1801 CCGAAGAGGAAGAGGCAAGCAGACATCCACCTGGGCCACCTCTGGCAGGTGAGCGGCGCCAGTC 1860
Db 1801 CCGAAGAGGAAGAGGCAAGCAGACATCCACCTGGGCCACCTCTGGCAGGTGAGCGGCGCCAGTC 1860
QY 1861 ACAGCATCGATCTGGAGATCCAGAGGGTAAACTGGTGGAAATCTGGCGGAGGTGGGAA 1920
Db 1861 ACAGCATCGATCTGGAGATCCAGAGGGTAAACTGGTGGAAATCTGGCGGAGGTGGGAA 1920
QY 1921 GTGGAAGAACTCTCTCATTTTCAGCCATTTTAGSCAGATGAGCCTTCTAGAGGGCAGCA 1980
Db 1921 GTGGAAGAACTCTCTCATTTTCAGCCATTTTAGSCAGATGAGCCTTCTAGAGGGCAGCA 1980
QY 1981 TTGCAATCAGTGAACCTCTGCTTATGTGGCCAGCAGAGGCTGATCCTCAATGCTACTC 2040
Db 1981 TTGCAATCAGTGAACCTCTGCTTATGTGGCCAGCAGAGGCTGATCCTCAATGCTACTC 2040
QY 2041 TGAGAGCAACATCTCTGTTTGGGAAGATATGATGAAGAAAGATCAACTCTGTGCTGA 2100
Db 2041 TGAGAGCAACATCTCTGTTTGGGAAGATATGATGAAGAAAGATCAACTCTGTGCTGA 2100
QY 2101 ACAGCTCTGCTGAGGCTGACCTGCCATTTCTTCCACAGCGACTGACGGAGATTG 2160
Db 2101 ACAGCTGCTGCTGAGGCTGACCTGCCATTTCTTCCACAGCGACTGACGGAGATTG 2160
QY 2161 GAGAGGAGGAGCAACCTGAGCGGTGGGAGCGCCAGAGGATCAGCCTTGGCCGGGCT 2220
Db 2161 GAGAGGAGGAGCAACCTGAGCGGTGGGAGCGCCAGAGGATCAGCCTTGGCCGGGCT 2220
QY 2221 TGATAGTGACAGAGATCATCTCTTGAGGACCCCTCAGTGCCCTTAGATGCCCATG 2280
Db 2221 TGATAGTGACAGAGATCATCTCTTGAGGACCCCTCAGTGCCCTTAGATGCCCATG 2280
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Db 2281 TGCGCAACCATCTTCAATAGTGTATCCGGAACATCTCAAGTCCAAAGCAGTCTGT 2340
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Db 2341 TTGTTACCCACCACTGCTGCTGGAGAGACCCGCGAGTTGAGTCAATTTCAAAAAGG 2400
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Db 2401 GCTGTATTACGGAAGGACCCATGAGAACTGATGAATTTAAATGGTGACTATGCTA 2460
QY 2461 CCATTTTAAATAACCTGCTGCTGGAGAGACCCGCGAGTTGAGTCAATTTCAAAAAGG 2520
Db 2461 CCATTTTAAATAACCTGCTGCTGGAGAGACCCGCGAGTTGAGTCAATTTCAAAAAGG 2520
QY 2521 AAACCAAGTGTTCACAGAAGATCAAGACAGAGGCTCTTAAACAGGATCAGTAAAGA 2580
Db 2521 AAACCAAGTGTTCACAGAAGATCAAGACAGAGGCTCTTAAACAGGATCAGTAAAGA 2580
QY 2581 AGAAAAGCAGTAAAGCCAGAGAGGCGAGCTTGTGACGTGGAAGAAAGGGCAGG 2640
Db 2581 AGAAAAGCAGTAAAGCCAGAGAGGCGAGCTTGTGACGTGGAAGAAAGGGCAGG 2640
QY 2641 GTTCAGTGCCTGTGCTAGTATGCTCTACATCCAGGCTGCTGGGGGCCCTTTGGCAT 2700
Db 2641 GTTCAGTGCCTGTGCTAGTATGCTCTACATCCAGGCTGCTGGGGGCCCTTTGGCAT 2700
QY 2701 TCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGCAGCAGCCCTTCAGCACCTGGT 2760
Db 2701 TCCTGGTTATTATGGCCCTTTTCATGCTGAATGTAGCAGCAGCCCTTCAGCACCTGGT 2760
QY 2761 GGTGAGTTACTGATCAAGAGGAGGCGGACACCATCTGTGACTCGAGGGAAACGAGA 2820
Db 2761 GGTGAGTTACTGATCAAGAGGAGGCGGACACCATCTGTGACTCGAGGGAAACGAGA 2820
QY 2821 CCTCGGTGAGTGACAGATCAAGACAACTCTCATATGAGTACTATGCCAGCATCTACG 2880
Db 2821 CCTCGGTGAGTGAGATCAAGACAACTCTCTATCATCTCTATCATCTCTCANGAGCGGCTC 2880

Db 2821 CCTCGGTGAGTGACAGATGAAGGACAACTCTCATATGAGTACTATGCCACATCTACG 2880
QY 2881 CCCTCTCCATGGCAGTCATGCTGATCTGTAAGCCATTCGAGGAGTGTCTTTGTCGAAG 2940
Db 2881 CCCTCTCCATGGCAGTCATGCTGATCTGTAAGCCATTCGAGGAGTGTCTTTGTCGAAG 2940
QY 2941 GCAGCTGCGAGCTCTCTCCCGGCTGCATGACGAGCTTTCCGGAAGGATCTTCGAAGCC 3000
Db 2941 GCAGCTGCGAGCTCTCTCCCGGCTGCATGACGAGCTTTCCGGAAGGATCTTCGAAGCC 3000
QY 3001 CTATGAAGTCTTTTACACAGACCCACAGGAGGATTTCTCAACAGGTTTTCACAAAGACA 3060
Db 3001 CTATGAAGTCTTTTACACAGACCCACAGGAGGATTTCTCAACAGGTTTTCACAAAGACA 3060
QY 3061 TGSATGAAGTGTGAGCTGCGGCTGCCGTTTCCAGGCCGAGATGTTTATCCAGAACTTATCC 3120
Db 3061 TGSATGAAGTGTGAGCTGCGGCTGCCGTTTCCAGGCCGAGATGTTTATCCAGAACTTATCC 3120
QY 3121 TGGTGTCTTCTGTGTGGGAATGATCGCAGGAGTCTTCCGTTGGTTCCTTGTGGCAGTGG 3180
Db 3121 TGGTGTCTTCTGTGTGGGAATGATCGCAGGAGTCTTCCGTTGGTTCCTTGTGGCAGTGG 3180
QY 3181 GGCCCTTGTCTCTCTTTTTCAGTCTGCACATTTCTTCCAGGGTCTTGTTCGGGAGC 3240
Db 3181 GGCCCTTGTCTCTCTTTTTCAGTCTGCACATTTCTTCCAGGGTCTTGTTCGGGAGC 3240
QY 3241 TGAAGCGTCTGGAACAATATACGAGTCACTCTTCTTCCACATCATCGTCCAGCATAC 3300
Db 3241 TGAAGCGTCTGGAACAATATACGAGTCACTCTTCTTCCACATCATCGTCCAGCATAC 3300
QY 3301 AGGCGCTTGCACCATCCACGCTTACATAAAGGCGAGGTTTCTGACAGATACCAAG 3360
Db 3301 AGGCGCTTGCACCATCCACGCTTACATAAAGGCGAGGTTTCTGACAGATACCAAG 3360
QY 3361 AGCTGCTGGATGACAAACCAAGCTCTCTTTTCTTACGTTGCGATGCGGTGGCTGG 3420
Db 3361 AGCTGCTGGATGACAAACCAAGCTCTCTTTTCTTACGTTGCGATGCGGTGGCTGG 3420
QY 3421 CTGTGCGGCTGGACCTCATCAGCATCGCCCTCATCACCACACCGGGCTGATGCTGTC 3480
Db 3421 CTGTGCGGCTGGACCTCATCAGCATCGCCCTCATCACCACACCGGGCTGATGCTGTC 3480
QY 3481 TTATGCAAGGCGAGATCCCGCAGCTATGCGGCTCGCCATCTTATGCTGCTCCAGT 3540
Db 3481 TTATGCAAGGCGAGATCCCGCAGCTATGCGGCTCGCCATCTTATGCTGCTCCAGT 3540
QY 3541 TAACGGGCTCTTCCAGTTTACGCTGAGCTGCGATCTGAGACAGAGCTCGATTCACCT 3600
Db 3541 TAACGGGCTCTTCCAGTTTACGCTGAGCTGCGATCTGAGACAGAGCTCGATTCACCT 3600
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Db 3601 CGGTGGAGAGGATCAATCACTACATTAAGCTCTCTCTTGGAAAGCCTCGCCAGATTA 3660
QY 3661 AGAACAAGGCTCTCTCTCTGCTGAGCTGCGGCGCAGGAGGAGTGTGAGAGGCGAG 3720
Db 3661 AGAACAAGGCTCTCTCTCTGCTGAGCTGCGGCGCAGGAGGAGTGTGAGAGGCGAG 3720
QY 3721 AGATGAGGTACCGAGAAACCTCTCTTGTCTTAAAGAAAGTATCTTCCAGATCAAA 3780
Db 3721 AGATGAGGTACCGAGAAACCTCTCTTGTCTTAAAGAAAGTATCTTCCAGATCAAA 3780
QY 3781 CTAAGAGAAAGATTGGCATTTGTGGGCGCAGAGGATCAGGGAAGTCTCGCTGGGATGG 3840
Db 3781 CTAAGAGAAAGATTGGCATTTGTGGGCGCAGAGGATCAGGGAAGTCTCGCTGGGATGG 3840
QY 3841 CCCTCTTCCGCTCTGGTGGAGTTATCTGGAGGCTGATCAAGATTGATGAGTGAATCA 3900
Db 3841 CCCTCTTCCGCTCTGGTGGAGTTATCTGGAGGCTGATCAAGATTGATGAGTGAATCA 3900
QY 3901 GTGATATTGGCTTGGCCGACCTCCGAAAGCAAACTCTCTATCATCTCTCAAGAGCGGTC 3960
Db 3901 GTGATATTGGCTTGGCCGACCTCCGAAAGCAAACTCTCTATCATCTCTCANGAGCGGTC 3960

QY	3961	TCTTCAGTGGCACTGTCAGATCAAAATTTTGGACCCCTTCAACCAGTACACTGAAGACCAGA	4020
DB	3961	TGTTACAGTGGCACTGTCAGATCAAAATTTTGGACCCCTTCAACCAGTACACTGAAGACCAGA	4020
QY	4021	TTTGGGATGCCCTGGAGAGACACATCAAAAGAATGTATTGCTTCAGCTACCTCTGAAAC	4080
DB	4021	TTTGGGATGCCCTGGAGAGACACACATCAAAAGAATGTATTGCTTCAGCTACCTCTGAAAC	4080
QY	4081	TTGAATCTGAAGTGATGGAGAAATGGGATAAATCTTCAGTGGGGAACGGCAGCTCTTGT	4140
DB	4081	TTGAATCTGAAGTGATGGAGAAATGGGATAAATCTTCAGTGGGGAACGGCAGCTCTTGT	4140
QY	4141	GCATAGCTAGAGCCCTGCTCCGCCACTGTAAAGATTTCTGATTTTAGATGAAGCCACAGCTG	4200
DB	4141	GCATAGCTAGAGCCCTGCTCCGCCACTGTAAAGATTTCTGATTTTAGATGAAGCCACAGCTG	4200
QY	4201	CCATGGACACAGACAGACACTTATTGATTCAAAGAGACCATCCGAGAGCAATTTTCAGACT	4260
DB	4201	CCATGGACACAGACAGACACTTATTGATTCAAAGAGACCATCCGAGAGCAATTTTCAGACT	4260
QY	4261	GTACCATGCTGACCATTTGCCATTCGCTGCACACCCCATCGTCTGTCCCAAGCACA	4320
DB	4261	GTACCATGCTGACCATTTGCCATTCGCTGCACACCCCATCGTCTGTCCCAAGCACA	4320
QY	4321	TGCTGGCCCAAGGACAGGTGGTGGAGTTTTCACACCCCATCGTCTGTCCCAAGCACA	4380
DB	4321	TGCTGGCCCAAGGACAGGTGGTGGAGTTTTCACACCCCATCGTCTGTCCCAAGCACA	4380
QY	4381	GTTCGCCGATTTATGCGCATGTTTGTGCTGTCAGAGAAACAAGTGCCTGCTCAAGGGCTGAC	4440
DB	4381	GTTCGCCGATTTATGCGCATGTTTGTGCTGTCAGAGAAACAAGTGCCTGCTCAAGGGCTGAC	4440
QY	4441	TCCTCCCTGTTGAGGAAGTCTCTTTCTTTAGAGCAATTCCTGCTGCTGGGGGGGG	4500
DB	4441	TCCTCCCTGTTGAGGAAGTCTCTTTCTTTAGAGCAATTCCTGCTGCTGGGGGGGG	4500
QY	4501	CCCTCATGCGTCCCTCCACGAAACCTTGCGTTTTCGATTTTATCTTTCGCACAGCA	4560
DB	4501	CCCTCATGCGTCCCTCCACGAAACCTTGCGTTTTCGATTTTATCTTTCGCACAGCA	4560
QY	4561	GTTCGGGATTTGCTGTGTGTTTTCACCTTTTAGGGAGAGCTATATTTGATTTGATTTT	4620
DB	4561	GTTCGGGATTTGCTGTGTGTTTTCACCTTTTAGGGAGAGCTATATTTGATTTGATTTT	4620
QY	4621	ATTCCCATATTATCATGTAACAAAATTTAGTTTTTGTCTTAATTCGCACTCTAAAGGTTCA	4680
DB	4621	ATTCCCATATTATCATGTAACAAAATTTAGTTTTTGTCTTAATTCGCACTCTAAAGGTTCA	4680
QY	4681	GGGAACCGTTATTATAATTGTATCATAGAGCCCTATAATGAAGCTTTTACGCTAGCTATA	4740
DB	4681	GGGAACCGTTATTATAATTGTATCATAGAGCCCTATAATGAAGCTTTTACGCTAGCTATA	4740
QY	4741	TCATATATAATTCGTACATAGCCTATATTACAGTGAAATCTAGCTGTTTTATTTTA	4800
DB	4741	TCATATATAATTCGTACATAGCCTATATTACAGTGAAATCTAGCTGTTTTATTTTA	4800
QY	4801	TATTAATAATAAGCACTGTGCTAATAACAGTGCATATTCCTTCTATCATTTTTGTACAGT	4860
DB	4801	TATTAATAATAAGCACTGTGCTAATAACAGTGCATATTCCTTCTATCATTTTTGTACAGT	4860
QY	4861	TTGCTGTACTAGAGATCTGGTTTTTCTGCTATTAGACTGTAGGAAGAGTAGCATTTTCATCTT	4920
DB	4861	TTGCTGTACTAGAGATCTGGTTTTTCTGCTATTAGACTGTAGGAAGAGTAGCATTTTCATCTT	4920
QY	4921	CTCTAGCTGGTGTTCAGGTGCCAGGTTTTCTGGGTGTCCCAAGGAAGACGCTGTGGCA	4980
DB	4921	CTCTAGCTGGTGTTCAGGTGCCAGGTTTTCTGGGTGTCCCAAGGAAGACGCTGTGGCA	4980
QY	4981	ATAGTGGGCCCTCCGACAGCCCCCTCTCGCCCTCCCCACAGCCGCTCCAGGGGTGGCTG	5040
DB	4981	ATAGTGGGCCCTCCGACAGCCCCCTCTCGCCCTCCCCACAGCCGCTCCAGGGGTGGCTG	5040

QY	5041	GAGACGGGTGGCGGCTGGAGACCATGCAGAGCCCGTGAATTCTCAGGGCTCTCGCCTT	5100
DB	5041	GAGACGGGTGGCGGCTGGAGACCATGCAGAGCCCGTGAATTCTCAGGGCTCTCGCCTT	5100
QY	5101	CTGTCTCTGGTGTCACATTACTTTCTCTCAGSAGACGCGGGCGGAAGCCCAGGCCCT	5160
DB	5101	CTGTCTCTGGTGTCACATTACTTTCTCTCAGSAGACGCGGGCGGAAGCCCAGGCCCT	5160
QY	5161	TTTCACTCCCTCATCAAGAANTGGGATCACAGAGACATTCCTCCGAGCGGGGAGTTTC	5220
DB	5161	TTTCACTCCCTCATCAAGAANTGGGATCACAGAGACATTCCTCCGAGCGGGGAGTTTC	5220
QY	5221	TTTTCCGCTTCCTCTTTTGTGTTGTTTCTAAACAAGAATACTAGTCTATCCACAGAGAG	5280
DB	5221	TTTTCCGCTTCCTCTTTTGTGTTGTTTCTAAACAAGAATACTAGTCTATCCACAGAGAG	5280
QY	5281	TCCCACTGGCTCAGGTTCCCTATGGCTGGCCACTGCACAGAGCTCTCAGCTCCAAGACCT	5340
DB	5281	TCCCACTGGCTCAGGTTCCCTATGGCTGGCCACTGCACAGAGCTCTCAGCTCCAAGACCT	5340
QY	5341	GTTGGTTCCAAGCCCTGGAGCCAACTGCTGCTTTTGGAGTGGCACATTTTTCATTTGSCCT	5400
DB	5341	GTTGGTTCCAAGCCCTGGAGCCAACTGCTGCTTTTGGAGTGGCACATTTTTCATTTGSCCT	5400
QY	5401	ATTCCACACACCTCCACAGTTCACTGGCAGGGCTCAGGATTTCTGGGTCTGTTTTCCCTT	5460
DB	5401	ATTCCACACACCTCCACAGTTCACTGGCAGGGCTCAGGATTTCTGGGTCTGTTTTCCCTT	5460
QY	5461	CTCACGGCAGTGGTCCACAGTCTCTCTCTCTCTCCCTCAAAGTCTCGAAGTTTAAG	5520
DB	5461	CTCACGGCAGTGGTCCACAGTCTCTCTCTCTCTCCCTCAAAGTCTCGAAGTTTAAG	5520
QY	5521	CAGCTCTTCTCTAATCAGTGTCTCACACTGGCGTAGAAGTTTGTGTCTGTAAGAGACCT	5580
DB	5521	CAGCTCTTCTCTAATCAGTGTCTCACACTGGCGTAGAAGTTTGTGTCTGTAAGAGACCT	5580
QY	5581	ACCTCAGGTTGCTGGTTGCTGTGTGTTGGTGTTCGCGCAAAACCCCTTTGTGCTGT	5640
DB	5581	ACCTCAGGTTGCTGGTTGCTGTGTGTTGGTGTTCGCGCAAAACCCCTTTGTGCTGT	5640
QY	5641	GGGGCTGTAGCTCAGGTGGGGTGGTCACTGCTGTATCAGTTGAATGGTCAAGCTTGC	5700
DB	5641	GGGGCTGTAGCTCAGGTGGGGTGGTCACTGCTGTATCAGTTGAATGGTCAAGCTTGC	5700
QY	5701	ATGTGCTGTACCACATAGACATTTCTGTGCGCTTAGCATGTTTGTCTGAACACCTTTGTGGAAG	5760
DB	5701	ATGTGCTGTACCACATAGACATTTCTGTGCGCTTAGCATGTTTGTCTGAACACCTTTGTGGAAG	5760
QY	5761	CAAAAATCTGAAAAATGTGAATAAAATATTTTGGATTTTGTAAAAAIAAAAAAAAAAAAA	5820
DB	5761	CAAAAATCTGAAAAATGTGAATAAAATATTTTGGATTTTGTAAAAAIAAAAAAAAAAAAA	5820
QY	5821	AAAAAAAAAAAAAAAAAAAA 5838	
DB	5821	AAAAAAAAAAAAAAAAAAAA 5838	
<hr/>			
RESULT 2			
AAZ94745			
ID	AAZ94745 standard; cDNA; 5838 BP.		
XX	AAZ94745;		
XX	(first entry)		
DT	01-AUG-2000		
DE	Human ATP binding cassette ABC5 (MRP5) cDNA.		
KW	ABCC5; ATP binding cassette; human; cholesterol; lipid disorder; lipid disorder; atherosclerosis; lipid disorder; dyslipidemia; psoriasis;		
KW	lupus erythematosus; diagnosis; gene therapy; MRP5;		
KW	multidrug resistance associated protein; chromosome 3q25-27;		
KW	Dubin Johnson syndrome; hyperbilirubinemia; ss.		
XX			

QY 3721 AGATGAGTACCGAGAAACCTCCCTCTGTGCTTAAGAAAGTATCCTTCAGATCAAAC 3780
DB 3721 AGATGAGTACCGAGAAACCTCCCTCTGTGCTTAAGAAAGTATCCTTCAGATCAAAC 3780
QY 3781 CTAAGAGAAGATTGGCAATGTGGGGCGGACAGATCAGGGAAGTCCCTCGCTGGGGATGG 3840
DB 3781 CTAAGAGAAGATTGGCAATGTGGGGCGGACAGATCAGGGAAGTCCCTCGCTGGGGATGG 3840
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DB 3841 CCCCTCTCCGCTGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGAGTGAAGATCA 3900
QY 3901 GTGATATTGGCTTGGCCGACCTCGAAGCAAACTCTCTATCATCTCCTCAAGAGCCGGTGC 3960
DB 3901 GTGATATTGGCTTGGCCGACCTCGAAGCAAACTCTCTATCATCTCCTCAAGAGCCGGTGC 3960
QY 3961 TGTTCAGTGGCACTGTCAAGTCAAAATTGGACCCCTTCAACCACTGACACTGAAGACCAGA 4020
DB 3961 TGTTCAGTGGCACTGTCAAGTCAAAATTGGACCCCTTCAACCACTGACACTGAAGACCAGA 4020
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DB 4201 CCATGGACACAGACAGACTTATTGATTCAGAGACCATCCGAGAAGCATTTGCGAGCT 4260
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DB 4261 GTACATGCTGACCATGCTCGCTGCACAGGTTCTAGGCTCCATAGGATTATGG 4320
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DB 4321 TGCTGGCCAGGACAGGTGGTGGATTGACACCCCATCGCTCTCTGTCACACGACA 4380
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DB 4381 GTTCCCGATTCTATGCCATGTTGCTGCTGCAGAGAACAGGTGCTGTCAGAGGCTGAC 4440
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DB 4441 TCCTCCCTGTTGAGAGTCTCTTTTCTTTTAGAGATTGCCATTCCTGCTGGGGCGGG 4500
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DB 4501 CCCCTCATCGCTCTCCTACCGAAACCTTCCTTCGCTGATTTTATCTTCGACAGCA 4560
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DB 4621 ATTCCATATTGATGAACAAATTTAGTTTGTCTTAAATGGACCTTAAGAGGTTCA 4680
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DB 4681 GGGAAACCTTTATTAATTGATCAGAGGCCCTATAATGAAGCTTTATACGTGACTATA 4740
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DB 4741 TCTATATATATCTGTACATAGCCTATATTACAGTGAAGTGAAGCTGTTTATTTTA 4800

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DB 4861 TTGCTGTACTAGAGATCTGGTTTTGTATTAGACTGTAGGAAGTAGCATTTTCATCTT 4920
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DB 4921 CTCCTAGCTGGTGGTTTCACGGTGCCAGGTTTCTGGGTGTCCTCAAGAGACGCTGGCA 4980
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DB 5161 TTTCACTCCCTCCATCAAGAAATGGGATCACAGAGACATTCCTCCGAGCCGGGAGTTTC 5220
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DB 5221 TTTCTCTGCTCTCTTTTGTGTTTCTAAACAAGAAATCAGTCTATCCACAGAGAG 5280
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DB 5281 TCCCACCTGCTCAGGTTCTATGGCTGGCCACTGCACAGAGCTCTCCAGTCCAAAGACCT 5340
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DB 5401 ATTCCACACCTCCACAGTTTCTAGTGGCAGGCTCAGGATTTTCGTGGTCTGTGTTTCTT 5460
QY 5461 CTCACGCGAGTGTGCGACAGTCTCTCTCTCTCTCCCTCAAGTCTGCAACTTTAAG 5520
DB 5461 CTCACGCGAGTGTGCGACAGTCTCTCTCTCTCTCCCTCAAGTCTGCAACTTTAAG 5520
QY 5521 CAGCTCTTCTAATCAGTCTCACACTGGCGTAGAAGTTTTTGTACTGTAAAGAGACCT 5580
DB 5521 CAGCTCTTCTAATCAGTCTCACACTGGCGTAGAAGTTTTTGTACTGTAAAGAGACCT 5580
QY 5581 ACCTCAGGTTGCTGTTGCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5640
DB 5581 ACCTCAGGTTGCTGTTGCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5640
QY 5641 GGGGCTGTGTAGCTCAGGTGGGGTGTGCTGCTGCTCTCCCTCAAGTGTGAATGTCAGGTTGC 5700
DB 5641 GGGGCTGTGTAGCTCAGGTGGGGTGTGCTGCTGCTCTCCCTCAAGTGTGAATGTCAGGTTGC 5700
QY 5701 ATGTGCTGACCAACTAGACATTCGTGCGCTTAGCATGTTTGTGCTGAACACCTTTGTGGAAG 5760
DB 5701 ATGTGCTGACCAACTAGACATTCGTGCGCTTAGCATGTTTGTGCTGAACACCTTTGTGGAAG 5760
QY 5761 CAAAAATCTGAATGTGAATAAAAATTTTGTGATTTTGTAAAAAATAAAAAA 5820
DB 5761 CAAAAATCTGAATGTGAATAAAAATTTTGTGATTTTGTAAAAAATAAAAAA 5820
QY 5821 AAAAAAATAAAAAA 5838
DB 5821 AAAAAAATAAAAAA 5838

RESULT 3
 AAA40481
 ID AAA40481 standard; cDNA; 4847 BP.
 XX
 AC AAA40481:
 DT 23-NOV-2000 (first entry)
 XX
 DE Human MRP-beta cDNA.
 XX
 KW MRP-beta; multidrug-resistance associated protein; human; cytosolic;
 KW chemotherapy; cancer cell; drug discovery; cytotoxic; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 116..4429
 FT /*tag= a
 FT /product= "MRP-beta"
 XX
 PN US6077936-A.
 XX
 XX 20-JUN-2000.
 XX
 PF 16-APR-1998; 98US-0061400.
 XX
 PR 16-APR-1997; 97US-0843459.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Shyjan A;
 XX
 DR WPI; 2000-430613/37.
 DR P-PSDB; AAB10225.
 XX
 PT Model multidrug-resistance associated polypeptide useful for improving
 PT the effectiveness of a chemotherapeutic regimen to eradicate
 PT multidrug-resistant transformed cells especially cancer cells -
 XX
 PS Claim 6; Fig 1A-D; 43pp; English.
 XX
 CC This invention describes a novel model multidrug-resistance associated
 CC polypeptide, MRP-beta (I) which has cytostatic activity. Inhibitors of
 CC (I) are useful for improving the effectiveness of a chemotherapeutic
 CC regimen to eradicate multidrug-resistant transformed cells, especially
 CC cancer cells, from the body of a mammal, preferably human. (I) is also
 CC useful for drug discovery, especially to the design of novel
 CC chemotherapeutic drugs that are cytotoxic to cells expressing (I). This
 CC sequence encodes the human MRP-beta protein which is described in the
 CC method of the invention.
 XX
 SQ Sequence 4847 BP; 1226 A; 1178 C; 1263 G; 1180 T; 0 other;
 Query Match 82.1%; Score 4792.6; DB 21; Length 4847;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 4809; Conservative 0; Mismatches 9; Indels 1; Gaps 1;
 QY 11 GGCTCATGCTGGGAGCGTGGTGGAGCGGTGGCGCGGTGGTGGAGCGAGGGGCGAG 60
 DB 1 GGCTCATGCTGGGAGCGTGGTGGAGCGGTGGCGCGGTGGTGGAGCGAGGGGCGAG 60
 QY 71 GAATTCGATGTGAACTAACAGTCTGTGAGCCCTGGAACCTCGGCTCAGAGAAGATGAA 130
 DB 61 GAATTCGATGTGAACTAACAGTCTGTGAGCCCTGGAACCTCCACTCAGAGAAGATGAA 120
 QY 131 GGATATCGACATAGGAAAAGATATATCATCCCGAGTCTGGGTATAGAGAGTGTGAGGGA 190
 DB 121 GGATATCGACATAGGAAAAGATATATCATCCCGAGTCTGGGTATAGAGAGTGTGAGGGA 180
 QY 191 GAGAACCGACACTTCTGGGAGCGACAGAGCCGTGAAAGATTCCAAGTTCAGGAGAACTCG 250
 DB 181 GAGAACCGACACTTCTGGGAGCGACAGAGCCGTGAAAGATTCCAAGTTCAGGAGAACTCG 240

QY 251 ACCGTTGGAATGCCAAGATGCTTGGAAACACAGCCGAGCCGAGGGCGCTCTCTTTGA 310
 DB 241 ACCGTTGGAATGCCAAGATGCTTGGAAACACAGCCGAGCCGAGGGCGCTCTCTTTGA 300
 QY 311 TGCCTCCATGCAATTCAGCTCAGAAATCCTGGATGAGGAGCATCCCAAGGAAAGTACCA 370
 DB 301 TGCCTCCATGCAATTCAGCTCAGAAATCCTGGATGAGGAGCATCCCAAGGAAAGTACCA 360
 QY 371 TCATGGCTTGTAGTGTCTGAAGCCCATCGGACTACTTCCAAACACAGCCAGTGGGA 430
 DB 361 TCATGGCTTGTAGTGTCTGAAGCCCATCGGACTACTTCCAAACACAGCCAGTGGGA 420
 QY 431 CAATCTGGGCTTTTCTCTGATGACTTTTCGTCGGCTTTCTCTCTGGCCCGTGTGC 490
 DB 421 CAATCTGGGCTTTTCTCTGATGACTTTTCGTCGGCTTTCTCTCTGGCCCGTGTGC 480
 QY 491 CCACAAGAGGGGAGCTCTCAATGAAGAGCTGTGGTCTCTGTCCAAAGCAGCTCTTC 550
 DB 481 CCACAAGAGGGGAGCTCTCAATGAAGAGCTGTGGTCTCTGTCCAAAGCAGCTCTTC 540
 QY 551 TGACGTGAAGTGCAGAGACTAGAGACTGTGGCAAGAGAGCTGAATGAAGTTGGGCC 610
 DB 541 TGACGTGAAGTGCAGAGACTAGAGACTGTGGCAAGAGAGCTGAATGAAGTTGGGCC 600
 QY 611 AGACGCTCTTCCCTGCGAAGGTTGTGTGGATCTTCTGCGCCACAGGCTCATCTGTC 670
 DB 601 AGACGCTCTTCCCTGCGAAGGTTGTGTGGATCTTCTGCGCCACAGGCTCATCTGTC 660
 QY 671 CATCGTGTGCTGATGATCAGCAGCTGGCTGCTTCAAGTGACAGGCTTTCATGGTGA 730
 DB 661 CATCGTGTGCTGATGATCAGCAGCTGGCTGCTTCAAGTGACAGGCTTTCATGGTGA 720
 QY 731 ACACCTTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTGTAGT 790
 DB 721 ACACCTTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTGTAGT 780
 QY 791 GCTGGGCTCTCTGAGGAAATCGTCGGTCTTGGTCTGGTGCAGTACACTTGGGCATT 850
 DB 781 GCTGGGCTCTCTGAGGAAATCGTCGGTCTTGGTCTGGTGCAGTACACTTGGGCATT 840
 QY 851 GAATTCAGAAACCGGTGTCCGCTTGGGGGGGCGCATCTTAACCATGGCATTTAAGAAGAT 910
 DB 841 GAATTCAGAAACCGGTGTCCGCTTGGGGGGGCGCATCTTAACCATGGCATTTAAGAAGAT 900
 QY 911 CCTTAAGTTAAGAACATTAAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAA 970
 DB 901 CCTTAAGTTAAGAACATTAAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAA 960
 QY 971 CGATGGGCGAGAGATGTTTGGAGGAGCAGCGTGGGAGCCCTGCTGGGAGGAGCCGCT 1030
 DB 961 CGATGGGCGAGAGATGTTTGGAGGAGCAGCGTGGGAGCCCTGCTGGGAGGAGCCGCT 1020
 QY 1031 TGTGGCATCTTAGGCATGATTATTAATGTAATTTCTGGGACCAACAGGCTTCTCTGGG 1090
 DB 1021 TGTGGCATCTTAGGCATGATTATTAATGTAATTTCTGGGACCAACAGGCTTCTCTGGG 1080
 QY 1091 ATCAGCTGTTTTTATCCCTTTTACCCAGCAATGATGTTTCATCAGCGCTCAGAGCATA 1150
 DB 1081 ATCAGCTGTTTTTATCCCTTTTACCCAGCAATGATGTTTCATCAGCGCTCAGAGCATA 1140
 QY 1151 TTTTCCAGGAGAAATGCGTGGCGCCGACGGATGAAGTGTCCAGAGATGAATGAAGTTCT 1210
 DB 1141 TTTTCCAGGAGAAATGCGTGGCGCCGACGGATGAAGTGTCCAGAGATGAATGAAGTTCT 1200
 QY 1211 TACTTACATTAATTTATCAAAATGATGCTCGGTCAAGCATTTTCTCAGAGTGTTC 1270
 DB 1201 TACTTACATTAATTTATCAAAATGATGCTCGGTCAAGCATTTTCTCAGAGTGTTC 1260
 QY 1271 AAAAATCCGAGGAGGAGCGTCGGATATTGAAAAACCGGGTACTTCCAGGGTATCAC 1330
 DB 1261 GAAAAATCCGAGGAGGAGCGTCGGATATTGAAAAACCGGGTACTTCCAGAGCATCAC 1320
 QY 1331 TGTGGGTGTGCTCCCATTTGTTGGTGTGATTTGCCAGCGGTGTGACCTTCTCTGTTTCATAT 1390

Db 1321 TGTGGGTGTGGCTCCCATTTGTTGGTGTGATTGCCAGCGTGGTACCTTCTCTGTTTCATAT 1380
QY 1391 GACCTGGGCTTCGATCTGACAGACAGACAGGCTTTCACAGTGGTGACAGTCTTCAATTC 1450
Db 1381 GACCTGGGCTTCGATCTGACAGACAGACAGGCTTTCACAGTGGTGACAGTCTTCAATTC 1440
QY 1451 CATGACCTTTTGGCTTTGAAACTTAACACCGTTTTCAGTAAAGTCCCTCTCAAGAGCCTCAGT 1510
Db 1441 CATGACCTTTTGGCTTTGAAAGTAAACCGTTTTCAGTAAAGTCCCTCTCAAGAGCCTCAGT 1500
QY 1511 GGCTGTTGACAGATTTAAAGATTTGTTTCTAATGGAAGAGGTTTCACATGATAAAGACAA 1570
Db 1501 GGCTGTTGACAGATTTAAAGATTTGTTTCTAATGGAAGAGGTTTCACATGATAAAGACAA 1560
QY 1571 ACCAGCAGTCTCACATCAAGATAGAGATGAAAATGCCACCTTGGCATGGGACTCCTC 1630
Db 1561 ACCAGCAGTCTCACATCAAGATAGAGATGAAAATGCCACCTTGGCATGGGACTCCTC 1620
QY 1631 CCACTCCAGTATCCAGAACTCGCCCAAGCTGACCGTGAACCCCAAAATGAAAAGACAGAGGGC 1690
Db 1621 CCACTCCAGTATCCAGAACTCGCCCAAGCTGACCGTGAACCCCAAAATGAAAAGACAGAGGGC 1680
QY 1691 TTCCAGGGCAAGAAAGAGAGGTGAGGCAGCTGCGACGCACTGAGCATCAGGGCGGTGCT 1750
Db 1681 TTCCAGGGCAAGAAAGAGAGGTGAGGCAGCTGCGACGCACTGAGCATCAGGGCGGTGCT 1740
QY 1751 GGCAGAGCAAGAGGCCACCTCTCTCTGGACAGTGAAGAGCGGCCAGTCCCGAAGAGGA 1810
Db 1741 GGCAGAGCAAGAGGCCACCTCTCTCTGGACAGTGAAGAGCGGCCAGTCCCGAAGAGGA 1800
QY 1811 AGAAGCAAGCAACATCCACCTGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGA 1870
Db 1801 AGAAGCAAGCAACATCCACCTGGCCACCTGCGCTTACAGAGGACACTGCACAGCATCGA 1860
QY 1871 TCTGGAGATCCAAAGAGGGTAAACTGTTGGAATCTCGCGCAGTGTGGAAAGTGGAAAAAC 1930
Db 1861 TCTGGAGATCCAAAGAGGGTAAACTGTTGGAATCTCGCGCAGTGTGGAAAGTGGAAAAAC 1920
QY 1931 CTCTCTCATTTACGCCATTTAGGCCAGATGACGCTTCTAGAGGCGACATTCGAATCAG 1990
Db 1921 CTCTCTCATTTACGCCATTTAGGCCAGATGACGCTTCTAGAGGCGACATTCGAATCAG 1980
QY 1991 TGAACCTTTCGCTTATGTGCCCCAGCAGCGCTTGATCTCAATCTACTCTGAGAGACAA 2050
Db 1981 TGAACCTTTCGCTTATGTGCCCCAGCAGCGCTTGATCTCAATCTACTCTGAGAGACAA 2040
QY 2051 CATCTCTTTTGGGAAGGAATATGATGAAGAAAGATACAACCTCTGTCTGAACAGCTGCTG 2110
Db 2041 CATCTCTTTTGGGAAGGAATATGATGAAGAAAGATACAACCTCTGTCTGAACAGCTGCTG 2100
QY 2111 CTTGAGCCTTGACCTGGCCATTTCTCCAGACGCGACCTGACGGAGATTGGAGCGAGG 2170
Db 2101 CTTGAGCCTTGACCTGGCCATTTCTCCAGACGCGACCTGACGGAGATTGGAGCGAGG 2160
QY 2171 AGCCAACTCTGAGCGTGGGCGAGCGCCAGAGATCAGCGCTTGCCGGCCCTGTATAGTGA 2230
Db 2161 AGCCAACTCTGAGCGTGGGCGAGCGCCAGAGATCAGCGCTTGCCGGCCCTGTATAGTGA 2220
QY 2231 CAGGAGCATCTACATCTTGAGCAGCCCTCAGTGGCTTAGATGCCCATGTGGSCAACCA 2290
Db 2221 CAGGAGCATCTACATCTTGAGCAGCCCTCAGTGGCTTAGATGCCCATGTGGSCAACCA 2280
QY 2291 CATCTTCAATAGTGTATTCGGAAACATCTCAAGTCCAAGACAGTCTGTTGTTACCCA 2350
Db 2281 CATCTTCAATAGTGTATTCGGAAACATCTCAAGTCCAAGACAGTCTGTTGTTACCCA 2340
QY 2351 CCAGTTACAGTACTGTTGACCTGTGATGAAGTATCTTCAATGAAGAGGGCTGTATTAC 2410
Db 2341 CCAGTTACAGTACTGTTGACCTGTGATGAAGTATCTTCAATGAAGAGGGCTGTATTAC 2400
QY 2411 GGAAGAGGCGCCATGAGGAACATGATGAATTTAAATGGTGACTATCTACCATTTTAA 2470

Db 2401 GGAAGAGGCGCCATGAGGAACATGATGAATTTAAATGGTGACTATGCTACCATTTTAA 2460
QY 2471 TAACTGTTTGTGGAGAGACACCGCCAGTTGAGATCAATTTCAAAAAGGAACAGTGG 2530
Db 2461 TAACTGTTTGTGGAGAGACACCGCCAGTTGAGATCAATTTCAAAAAGGAACAGTGG 2520
QY 2531 TTCACAGAAGAGTTCACAAGACACAGGGTCTTAAACAGGATCAGTAAAGAGGAAGAC 2590
Db 2521 TTCACAGAAGAGTTCACAAGACACAGGGTCTTAAACAGGATCAATAAAGAGGAAGAAC 2580
QY 2591 AGTAAAGCAGAGGAAGGCGCAGCTTGTGAGCTGGAAGAAAGGCGAGGTTCACTGGC 2650
Db 2581 AGTAAAGCAGAGGAAGGCGCAGCTTGTGAGCTGGAAGAAAGGCGAGGTTCACTGGC 2640
QY 2651 CTGGTCACTATATGTTGTCTACATCCAGGCTGCTGGGGGCCCTTTGGCATTTCTGGTTAT 2710
Db 2641 CTGGTCACTATATGTTGTCTACATCCAGGCTGCTGGGGGCCCTTTGGCATTTCTGGTTAT 2700
QY 2711 TATGGCCCTTTTCACTGCTGAATGTAGGACGACACCGCTTTCAGACCTGGTGTGAGTTA 2770
Db 2701 TATGGCCCTTTTCACTGCTGAATGTAGGACGACACCGCTTTCAGACCTGGTGTGAGTTA 2760
QY 2771 CTGATCAAGCAAGGAAGGCGGACACCACTGTGACTCGAGGGAACGACCTCGGTGAG 2830
Db 2761 CTGATCAAGCAAGGAAGGCGGACACCACTGTGACTCGAGGGAACGACCTCGGTGAG 2820
QY 2831 TGACAGCATGAAGGACAATCTCATATGACGTACTATGCCAGCATCTACGCCCTCTCCAT 2890
Db 2821 TGACAGCATGAAGGACAATCTCATATGACGTACTATGCCAGCATCTACGCCCTCTCCAT 2880
QY 2891 GGCAGTCACTGCTGATCTCTGAAGCCATTCGAGGAGTTGTCTTTGTCAGGGGACGCTGCG 2950
Db 2881 GGCAGTCACTGCTGATCTCTGAAGCCATTCGAGGAGTTGTCTTTGTCAGGGGACGCTGCG 2940
QY 2951 AGCTTCTCTCCGGCTGCTGATGACGAGCTTTTCCGAAGGATCTCTCGAAGCCCTATGAAGTT 3010
Db 2941 AGCTTCTCTCCGGCTGCTGATGACGAGCTTTTCCGAAGGATCTCTCGAAGCCCTATGAAGTT 3000
QY 3011 TTTTGCACAGACCCCGCAGGAGGATTCCTCAACAGGTTTTCCAAAGACATGGATGAAGT 3070
Db 3001 TTTTGCACAGACCCCGCAGGAGGATTCCTCAACAGGTTTTCCAAAGACATGGATGAAGT 3060
QY 3071 TGAGTGGCGGTGCGTTCAGGCGGAGATGTTCAATCCAGACGTTATCTTGGTGTCTT 3130
Db 3061 TGAGTGGCGGTGCGTTCAGGCGGAGATGTTCAATCCAGACGTTATCTTGGTGTCTT 3120
QY 3131 CTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGCGCCCTTGT 3190
Db 3121 CTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGCGCCCTTGT 3180
QY 3191 CATCTCTTTTTCAGTCTCGACATTTGCTCCAGGCTCCTGATTCGGGAGCTGAAGCGTCT 3250
Db 3181 CATCTCTTTTTCAGTCTCGACATTTGCTCCAGGCTCCTGATTCGGGAGCTGAAGCGTCT 3240
QY 3251 GGCAATATACGAGTCACTCTTCTCCACATCAGTCCACGATACAGGCGCTTGC 3310
Db 3241 GGCAATATACGAGTCACTCTTCTCCACATCAGTCCACGATACAGGCGCTTGC 3300
QY 3311 CACCATCCAGCCTTACATAAAGGCGAGGTTTTCTGCACAGATACAGGAGCTGCTGGA 3370
Db 3301 CACCATCCAGCCTTACATAAAGGCGAGGTTTTCTGCACAGATACAGGAGCTGCTGGA 3360
QY 3371 TGACAAACAAGCTCTTTTTTTTTTTTACGTGTGCGATGCGGTGGCTGTGCGGCT 3430
Db 3361 TGACAAACAAGCTCTTTTTTTTTTTTACGTGTGCGATGCGGTGGCTGTGCGGCT 3420
QY 3431 GGACTCATACAGTCCGCTCATCACACCGCGGCTGATGCTGTTCTTATCCAGG 3490
Db 3421 GGACTCATACAGTCCGCTCATCACACCGCGGCTGATGCTGTTCTTATCCAGG 3480
QY 3491 GCAGTTCCCGCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGCCAGTTAACGGGCT 3550
Db 3481 GCAGTTCCCGCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGCCAGTTAACGGGCT 3540

QY	3551	GTTCACGTTTACGGTCAGACTGSCATCTCTGAGACAGAAGCTCGATTCCACTCGGTGGGAGAG	3611
Db	3541		
		GTTCACGTTTACGGTCAGACTGSCATCTCTGAGACAGAAGCTCGATTCCACTCGGTGGGAGAG	3600
QY	3611	GATCAATCACTACATTAAGAAGCTCTGTCCTTGAAGACACCTGCGCAGAATTAAAGAACAAGGC	3670
Db	3601		
		GATCAATCACTACATTAAGACTCTGTCTTGGAGCAGCTGCCAGATTAAGACAAGGC	3660
QY	3671	TCCCTCCCTTGACTGCGCCCGAGAGGGAGAGGTGACCTTTGAGAACGCGAGAGATGAGGTA	3730
Db	3661		
		TCCCTCCCTTGACTGCGCCCGAGAGGGAGAGGTGACCTTTGAGAACGCGAGAGATGAGGTA	3720
QY	3731	CCGAGAAACCTCCCTCTGTCTTAAGAAGAAATATCCCTACGATCAACCTTAAGAGAA	3790
Db	3721		
		CCGAGAAACCTCCCTCTCGTCTTAAGAAGAAATATCCCTACGATCAACCTTAAGAGAA	3780
QY	3791	GATTGGCATTTGTGGCGGCACAGGATCAGGGAAGTCCCTCGCTGGGGATGGCCCTCTTCCG	3850
Db	3781		
		GATTGGCATTTGTGGCGGCACAGGATCAGGGAAGTCCCTCGCTGGGGATGGCCCTCTTCCG	3840
QY	3851	TCGTGGAGATTATCTGGAGGTGTCATCAAGATTGATGGAGTGAGAACTAGTGATTTGG	3910
Db	3841		
		TCGTGGAGATTATCTGGAGGTGTCATCAAGATTGATGGAGTGAGAACTAGTGATTTGG	3900
QY	3911	CCTTGGCGACTCCGAAAGCAACTCTCTATCATCTCTCAAGAGCCGTGCTGTTCAGTGG	3970
Db	3901		
		CCTTGGCGACTCCGAAAGCAACTCTCTATCATCTCTCAAGAGCCGTGCTGTTCAGTGG	3960
QY	3971	CACGTGCAGATCAAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGC	4030
Db	3961		
		CACGTGCAGATCAAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGGGATGC	4020
QY	4031	CTGGAGAGGACACACATGAAAGATGTATGTCTCAGCTACCTCTGAAACTGGAATCTGA	4090
Db	4021		
		CCTGGAGAGGACACACATGAAAGATGTATGTCTCAGCTACCTCTGAAACTGGAATCTGA	4080
QY	4091	AGTGATGGAGATGGGATTAACCTCTCAGTGGGGAACGGCAGACTCTGTGCAATAGCTAG	4150
Db	4081		
		AGTGATGGAGATGGGATTAACCTCTCAGTGGGGAACGGCAGACTCTGTGCAATAGCTAG	4140
QY	4151	AGCCCTGCTCCGCCACTGTAAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACAC	4210
Db	4141		
		AGCCCTGCTCCGCCACTGTAAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACAC	4200
QY	4211	AGAGACAGACTTATTTGATTTCAAGAGACCATCGGAGAGCATTTCCGACGTGTACCATGCT	4270
Db	4201		
		AGAGACAGACTTATTTGATTTCAAGAGACCATCGGAGAGCATTTCCGACGTGTACCATGCT	4260
QY	4271	GACCATTGCCCATCGCTCCACACAGTGTCTAGGCTCCGATAGGATTAATGCTGTGGCCCA	4330
Db	4261		
		GACCATTGCCCATCGCTCCACACAGTGTCTAGGCTCCGATAGGATTAATGCTGTGGCCCA	4320
QY	4331	GGACAGGTGGTGGATTGTGACACCCCATCGCTCTCTGTCTGCTCAACGACAGTTCCCGATT	4390
Db	4321		
		GGACAGGTGGTGGATTGTGACACCCCATCGCTCTCTGTCTGCTCAACGACAGTTCCCGATT	4380
QY	4391	CTATGCCATGTTTGTCTGTCGAGAGAACAGGTGCTGTCAAGGGCTGACTCTCCCTGT	4450
Db	4381		
		CTATGCCATGTTTGTCTGTCGAGAGAACAGGTGCTGTCAAGGGCTGACTCTCCCTGT	4440
QY	4451	TGACGAAGTCTCTTTTCTTATAGAGATTGCCATTCCTGCTGGGGGGGGCCCC-TCATC	4509
Db	4441		
		TGACGAAGTCTCTTTTCTTATAGAGATTGCCATTCCTGCTGGGGGGGGCCCC-TCATC	4500
QY	4510	GCCTCCTCTACCGAAACCTTGCCCTTCTCGATTTATCTTTTCGACAGCAGTTCGGGAT	4569
Db	4501		
		GCCTCCTCTACCGAAACCTTGCCCTTCTCGATTTATCTTTTCGACAGCAGTTCGGGAT	4560
QY	4570	TGCGTTGTGTGTTTTCATTTTTHAGGAGAGTCAATATTTTGTATTATGTATTTATTCATAT	4629
Db	4561		
		TGCGTTGTGTGTTTTCATTTTTHAGGAGAGTCAATATTTTGTATTATGTATTTATTCATAT	4620

QY	4630	TCATGTAACACAAATTTAGTTTTTGTCTTAAATGTCACCTCTAAAGAGTTTCAGGAACCGT	4680
DB	4621	TCATGTAACACAAATTTAGTTTTTGTCTTAAATGTCACCTCTAAAGAGTTTCAGGAACCGT	4680
QY	4690	TATTATAAATTTGATCAGAGCCCTAATAATGAAGCTTTATAGCTGTAGCTATATCTATATAT	4749
DB	4681	TATTATAAATTTGATCAGAGCCCTAATAATGAAGCTTTATAGCTGTAGCTATATCTATATAT	4740
QY	4750	AATTCCTGATACATAGCCCTATATTTACAGTGAATAATGTAAGCTGTTTATTTTATATTTAAAT	4809
DB	4741	AATTCCTGATACATAGCCCTATATTTACAGTGAATAATGTAAGCTGTTTATTTTATATTTAAAT	4800
QY	4810	AAGCACTGTCTTAATAACA	4828
DB	4801	AAGCACTGTCTTAATAAAAA	4819
RESULT 4			
ID	AAV65682	standard; cDNA; 4847 BP.	
XX	AC	AAV65682;	
XX	DT	02-FEB-1999 (first entry)	
XX	XX	Human multidrug resistance-associated protein CDNA.	
XX	DE	Multidrug resistance-associated protein; MRP-beta; human; cancer;	
KW	KW	tumour; chemotherapy; therapy; ss.	
XX	OS	Homo sapiens.	
XX	PH	Key	Location/Qualifiers
FT	FT	CDS	116..4429
FT	FT		/*tag= a
XX	PN	WO9846736-A1.	
XX	PD	22-OCT-1998.	
XX	PF	16-APR-1998; 98WO-US07673.	
XX	PR	16-APR-1997; 97US-0843459.	
XX	PA	(MILL-) MILLENNIUM PHARM INC.	
PI	Shyjan A;		
XX	DR	WPI; 1998-568724/48.	
XX	DR	P-PSDB; AAW80597.	
PT	PT	New isolated multidrug resistance-associated polypeptide - used to	
PT	PT	develop products for modulating multidrug resistance, particularly	
XX	XX	for reducing resistance of tumours to chemotherapeutic drugs	
XX	PS	Claim 1; Page 54-59; 93pp; English.	
XX	CC	This nucleotide sequence codes for novel human multidrug resistance	
CC	CC	associated protein (MRP-beta, see AAW80597), over-expression of which	
CC	CC	is thought to be associated with the emergence and/or persistence	
CC	CC	of a multidrug-resistance phenotype in transformed mammalian cells,	
CC	CC	including carcinoma and adenocarcinoma cells. A unique fragment	
CC	CC	(see AAV65683) of the MRP-beta gene was identified by computer	
CC	CC	assisted searching of a nucleic acid database corresponding to a	
CC	CC	human endothelial cell (HUMVEC) expression library. It was used	
CC	CC	to screen the HUMVEC expression library. This yielded a 4.78 kb	
CC	CC	clone, designated fohd013a05m (deposited as ATCC 98409). Two	
CC	CC	independent cDNA clones comprising approximately 60 residues	
CC	CC	upstream from fohd013a05m were isolated by hybridisation screening	
CC	CC	of human brain and liver cDNA libraries using a probe from the 5'	
CC	CC	end of fohd01305m. The presented sequence of MRP-beta cDNA	
CC	CC	comprises fohd01305m and 66 additional upstream nucleotides. The	
CC	CC	invention provides compositions and methods for improving the	

effectiveness of chemotherapeutic regimens to eradicate
 CC multidrug-resistant transformed cells from the body of a mammal,
 CC especially a human. the disclosed compositions include MRP-beta
 CC nucleic acids, including probes and antisense oligonucleotides
 CC (see also AAV65684-88), MRP-beta polypeptides and antibodies,
 CC MRP-beta expressing host cells, and non-human mammals that are
 CC transgenic or nullizygous for MRP-beta. The disclosed methods
 CC include methods for attenuating aberrant MRP-beta gene expression,
 CC protein production and/or protein function, and for improving the
 CC effectiveness of chemotherapy for a mammal afflicted with a
 CC multidrug-resistant tumour, wherein the tumour is of mammary,
 CC respiratory tract, urogenital tract, endocrine system or immune
 CC system origin. In addition, methods are disclosed for identifying
 CC and using a modulator, such as an inhibitor, that is cytotoxic to
 CC cells expressing MRP-beta.

xx
 SQ Sequence 4847 BP; 1225 A; 1179 C; 1263 G; 1180 T; 0 other;

Query Match 82.1%; Score 4791; DB 19; Length 4847;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 4808; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 11 GGCTCATGCTCGGAGCGTGGTTCAGCGCGTGGCGGCTTCTCTGGAGCGGCGCGAG 70
 DB 1 GGCTCATGCTCGGAGCGTGGTTCAGCGCGTGGCGGCTTCTCTGGAGCGGCGCGAG 60

QY 71 GAATTCGTGTGAACCTACAGTCTGTGAGCCCTGGAACCTCGCTCAGAGAGATGAA 130
 DB 61 GAATTCGTGTGAACCTACAGTCTGTGAGCCCTGGAACCTCGCTCAGAGAGATGAA 120

QY 131 GGATTCGACATAGAAAGAGTATATATCCCGAGTCTGGGTATAGAACTGTGAGGA 190
 DB 121 GGATTCGACATAGAAAGAGTATATATCCCGAGTCTGGGTATAGAACTGTGAGGA 180

QY 191 GAGAACAGACATCTCTGGGAGCGACAGACCGTGAAGATTCAGAGAGAACTCG 250
 DB 181 GAGAACAGACATCTCTGGGAGCGACAGACCGTGAAGATTCAGAGAGAACTCG 240

QY 251 ACCGTGGAATGCCAAGATGCTTGGAAACAGACGCGCGAGGCCCTCTCTTTGA 310
 DB 241 ACCGTGGAATGCCAAGATGCTTGGAAACAGACGCGCGAGGCCCTCTCTTTGA 300

QY 311 TGCTCCATCATCTCTCAGCTCAGATTCAGATGAGGAGCATCCCAAGGGAAGTACCA 370
 DB 301 TGCTCCATCATCTCTCAGCTCAGATTCAGATGAGGAGCATCCCAAGGGAAGTACCA 360

QY 371 TCATGGCTTGAGTCTCTGAAGCCCATCCGAGCTACTTCCAAACACACAGCCAGTGA 430
 DB 361 TCATGGCTTGAGTCTCTGAAGCCCATCCGAGCTACTTCCAAACACACAGCCAGTGA 420

QY 431 CAATGCTGGGCTTTTTCCTGTATGACTTTTTCGTGGCTTCTTCTCTGGCCCGTGGC 490
 DB 421 CAATGCTGGGCTTTTTCCTGTATGACTTTTTCGTGGCTTCTTCTCTGGCCCGTGGC 480

QY 491 CCACAAGAGGGGAGCTCTCAATGGAAGAGCTGTGTCTCTGTCACAGACAGAGTCTTC 550
 DB 481 CCACAAGAGGGGAGCTCTCAATGGAAGAGCTGTGTCTCTGTCACAGACAGAGTCTTC 540

QY 551 TGAGCTGAATCGAAGAGCTAGAGAGCTGTGGCAAGAGAGCTGAATGAAGTTGGGCC 610
 DB 541 TGAGCTGAATCGAAGAGCTAGAGAGCTGTGGCAAGAGAGCTGAATGAAGTTGGGCC 600

QY 611 AGAGCTGCTTCCCTGGAAGGTTGTGTGATCTTCTGCGGACACAGGCTCATCCTGTC 670
 DB 601 AGAGCTGCTTCCCTGGAAGGTTGTGTGATCTTCTGCGGACACAGGCTCATCCTGTC 660

QY 671 CATCGTGTGCTGTATGATCATCGAGCTGGCTGGCTTTCAGTGGACAGCAGCTTCATGGTGA 730
 DB 661 CATCGTGTGCTGTATGATCATCGAGCTGGCTGGCTTTCAGTGGACAGCAGCTTCATGGTGA 720

QY 731 ACACCTCTTGGAGTATACCCAGGCAACAGAGCTCTAATCTGAGTACAGCTTGTGTTAGT 790
 DB 721 ACACCTCTTGGAGTATACCCAGGCAACAGAGCTCTAATCTGAGTACAGCTTGTGTTAGT 780

QY 791 GCTGGCCCTCTCTCTGACGGAAATCGTGGCGTCTTGGTCTGCTGACTGACTTGGGCAT 850
 DB 781 GCTGGCCCTCTCTCTGACGGAAATCGTGGCGTCTTGGTCTGCTGACTGACTTGGGCAT 840

QY 851 GAATTAACGAAACCGTGTCCGCTTGGGGGGGCGCATCTTAACCATGSCATTTAAGAAGAT 910
 DB 841 GAATTAACGAAACCGTGTCCGCTTGGGGGGGCGCATCTTAACCATGSCATTTAAGAAGAT 900

QY 911 CTTAAGTTAAAGAAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAA 970
 DB 901 CTTAAGTTAAAGAAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAA 960

QY 971 CGATGGGAGAGAAATGTTTGGGCGAGCAGCCGTTGGCAGCCTGCTGGTGGAGGACCGT 1030
 DB 961 CGATGGGAGAGAAATGTTTGGGCGAGCAGCCGTTGGCAGCCTGCTGGTGGAGGACCGT 1020

QY 1031 TGTTCCTCTCTTAGCATGATTTATAATCTAATTTCTGGGACCAACAGGCTTCTCTGG 1090
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QY 1091 ATCAGCTGTTTATCTCTCTTTTACCCAGCAATGATTTTGCATCAGGCTCACAGCAT 1150
 DB 1081 ATCAGCTGTTTATCTCTCTTTTACCCAGCAATGATTTTGCATCAGGCTCACAGCAT 1140

QY 1151 TTTTACGAGAAATCGTGGCGCCGACGATGAACGTGTCCAGAAAGTGAATGAATCT 1210
 DB 1141 TTTTACGAGAAATCGTGGCGCCGACGATGAACGTGTCCAGAAAGTGAATGAATCT 1200

QY 1211 TACTTACATTAATTTATCAAAATGATGCTTGGGTGGAAGCATTTCTCAGAGTGTCA 1270
 DB 1201 TACTTACATTAATTTATCAAAATGATGCTTGGGTGGAAGCATTTCTCAGAGTGTCA 1260

QY 1271 AAAATCCGCGAGGAGCGCTCGGATATTGGAAGGCGGCTACTTCCAGGCTATCAC 1330
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QY 1331 TGTGGGTGGCTCCCATTTGGTGTGATGCGCAGCGTGGTACCTTCTCTGTTCTAT 1390
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QY 1391 GACCTGGCTTCGATCTGACAGCAGCAGCTTTTACAGTGGTGCACAGTCTTCAATTC 1450
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QY 1451 CATGACTTTTGTGTTGAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAGCCCTCAGT 1510
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QY 1511 GGCTGTTGACAGATTTAAGATTTTCTTAATGGAAGAGTTTACATGATTAAGAACA 1570
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QY 1571 ACCAGCCAGTCTCATCAAGATAGAGATGAAATGCACTTGGCATGGGACTCCCTC 1630
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 DB 1621 CCATCTCAGTATCCAGAACTCGCCCAAGCTGACCCCAAAATGAAAGAGAGAGGCG 1680

QY 1691 TTCCAGGCGCAGAAAGAGAGAGTGGGAGCTGAGCAGCTGAGCCACTGAGCATCAGCGGTGCT 1750
 DB 1681 TTCCAGGCGCAGAAAGAGAGAGTGGGAGCTGAGCAGCTGAGCCACTGAGCATCAGCGGTGCT 1740

QY 1751 GGCAGCAGAAAGCCGACCTCTCTGACAGTGAAGAGCGGCGGAGTCCCGAAGAGGA 1810
 DB 1741 GGCAGCAGAAAGCCGACCTCTCTGACAGTGAAGAGCGGCGGAGTCCCGAAGAGGA 1800

QY 1811 AGAAGGCAAGCATCTCCACCTGGGCGCCTGCTGCTTACAGAGGACACTGCACAGCATCGA 1870
 DB 1801 AGAAGGCAAGCATCTCCACCTGGGCGCCTGCTGCTTACAGAGGACACTGCACAGCATCGA 1860

QY 1871 TCTGGAGATCCAAAGAGGTAACCTGGTTGGAATCTCGGCAGTGTGGAAAGTGGAAAC 1930
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QY 1931 CTCTCTCATTTTCCAGCCATTTAGGCCAGATGAGCTTCTAGAGGGCAGCATGCAATCAG 1990
DB 1921 CTCTCTCATTTTCCAGCCATTTAGGCCAGATGAGCTTCTAGAGGGCAGCATGCAATCAG 1980
QY 1991 TGGAACTCTGCTTATGTGTGCCAGCAGGCTGTGATCCTCAATGCTACTCTGAGAGCAA 2050
DB 1981 TGGAACTCTGCTTATGTGTGCCAGCAGGCTGTGATCCTCAATGCTACTCTGAGAGCAA 2040
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DB 2401 GGAAGAGGCAACCATGAGAACTGATGAATTTAAATGTTGACTATGCTACCATTTTAA 2460
QY 2471 TAACTGTTGCTGGGAGAGACCGCAGTTGAGATCAATTCAAAAGAGAAACCACTGG 2530
DB 2461 TAACTGTTGCTGGGAGAGACCGCAGTTGAGATCAATTCAAAAGAGAAACCACTGG 2520
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DB 2581 AGTAAAGCCAGAGGAGGCGAGCTTGTGAGCTGGAAGAGAAAGGCGAGGTTTCACTGCC 2640
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DB 2641 CTGGTCAGTATATGTTGCTTACATCAGCTCTGGGGGCCCTTGGCATTCCTGTTAT 2700
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DB 2701 TATGGCCCTTTTATGCTCTGAATAGCAGCACCGCTTTCAGCACCTGGTGGTTGAGTTA 2760
QY 2771 CTGGATCAAGCAAGGAGGGAACACCACTGTGACTCGAGGAAACGAGACCTCGGTGAG 2830
DB 2761 CTGGATCAAGCAAGGAGGGAACACCACTGTGACTCGAGGAAACGAGACCTCGGTGAG 2820
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DB 2821 TGACAGCATGAAGGACAATCTCATATGATGAGTACTATGCCAGCATCTAGCCCTCTCCAT 2880
QY 2891 GGCAGTCACTGCTGATCCTGAAGGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGG 2950
DB 2881 GGCAGTCACTGCTGATCCTGAAGGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACGCTGG 2940
QY 2951 AGCTTCTCCCGCTGCTGATGAGAGCTTTTCCGAGGATCCTTCCGAGGCCCTATGAAGTT 3010

DB 2941 AGCTTCTCCCGCTGCTGATGAGAGCTTTTCCGAGGATCCTTCCAGGCCCTATGAAGTT 3000
QY 3011 TTTTGCACAGACCCCCACAGGAGGATTTCTCAACAGGTTTTCACAAAGACATGATGAAGT 3070
DB 3001 TTTTGCACAGACCCCCACAGGAGGATTTCTCAACAGGTTTTCACAAAGACATGATGAAGT 3060
QY 3071 TGAGCTGGGCTGGCTTCCAGGCGAGATTTCTATCCAGACGTTATCTCTGGTCTTCT 3130
DB 3061 TGAGCTGGGCTGGCTTCCAGGCGAGATTTCTATCCAGACGTTATCTCTGGTCTTCT 3120
QY 3131 CTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCTTGTGGCAGTGGGGCCCTTGT 3190
DB 3121 CTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCTTGTGGCAGTGGGGCCCTTGT 3180
QY 3191 CATCTCTTTTTCAGTCTGACATTTCTCCAGGCTCTGATTCGGGAGCTGAAGCGTCT 3250
DB 3181 CATCTCTTTTTCAGTCTGACATTTCTCCAGGCTCTGATTCGGGAGCTGAAGCGTCT 3240
QY 3251 GGACAATATACGAGTACCTTCTCTCCACATCAGCTCCAGCATACAGGGCTTGC 3310
DB 3241 GGACAATATACGAGTACCTTCTCTCCACATCAGCTCCAGCATACAGGGCTTGC 3300
QY 3311 CACCATCCAGCCTTACAAATAAGGCGAGGATTTCTGCACAGATACCAAGGAGCTCTGGA 3370
DB 3301 CACCATCCAGCCTTACAAATAAGGCGAGGATTTCTGCACAGATACCAAGGAGCTCTGGA 3360
QY 3371 TGACAACAAGCTCCTTTTTTTTTTTTGTGTGCTGCGATGCGGTGGCTGTGCGCT 3430
DB 3361 TGACAACAAGCTCCTTTTTTTTTTTTGTGTGCTGCGATGCGGTGGCTGTGCGCT 3420
QY 3431 GGACTCATCAGCATCGCCCTCATCACACACGGGCTGATGCTCTTATGACAGG 3490
DB 3421 GGACTCATCAGCATCGCCCTCATCACACACGGGCTGATGCTCTTATGACAGG 3480
QY 3491 GCAGATTTCCCGCAGCTATGCGGCTCTGCGCATCTCTTATGCTGTGCCAGTTAACGGGCT 3550
DB 3481 GCAGATTTCCCGCAGCTATGCGGCTCTGCGCATCTCTTATGCTGTGCCAGTTAACGGGCT 3540
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DB 3541 GTTCCAGTTTACGCTCAGCTGGCATCTGACACAGAGCTCGATTCACCTCGGTGGAG 3600
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DB 3661 TCCCTCCCTGACTGGCCCGCAGGAGGAGGTTGACCTTTTGAGAACCGCAGAGATGAGTA 3720
QY 3731 CCAGAGAAACCTCCCTCTTGTCTTAAAGAAAGTATCTTACAGATCAAACTTAAGAGAA 3790
DB 3721 CCAGAGAAACCTCCCTCTTGTCTTAAAGAAAGTATCTTACAGATCAAACTTAAGAGAA 3780
QY 3791 GATTGGCATTTGGGGCGGACAGGATCAGGAACTCTCGCTGGGATGGCCCTTCCG 3850
DB 3781 GATTGGCATTTGGGGCGGACAGGATCAGGAACTCTCGCTGGGATGGCCCTTCCG 3840
QY 3851 TCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTTGAGGTGAGATTCAGTATATGG 3910
DB 3841 TCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTTGAGGTGAGATTCAGTATATGG 3900
QY 3911 CTTGGGACCTCGAGAGCAAACTCTATCATTTCTCAAGAGCCGCTGTGTTCACTGG 3970
DB 3901 CTTGGGACCTCGAGAGCAAACTCTATCATTTCTCAAGAGCCGCTGTGTTCACTGG 3960
QY 3971 CACTGTCAAGTAAATTTGGACCCCTTCAACAGTACACTGAAGACAGATTTGGGATGC 4030
DB 3961 CACTGTCAAGTAAATTTGGACCCCTTCAACAGTACACTGAAGACAGATTTGGGATGC 4020
QY 4031 CTTGGAGGAGCACACATGAAGAAATGATTGCTCAGCTACCTCTGAACTTGAATCTGA 4090

Db 4021 CCTGAGAGGACACACATGAAGAATGATTGCTCAGCTACCTCTGAAACTGAAATCTGA 4080
Qy 4091 AGTATGAGAAATGGGATACCTTCTCAGTGGGGGAGCGGAGCTCTTGTGCATAGCTAG 4150
Db 4081 AGTATGAGAAATGGGATACCTTCTCAGTGGGGGAGCGGAGCTCTTGTGCATAGCTAG 4140
Qy 4151 AGCCCTGCTCGCCACCTGAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATGGACAC 4210
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Qy 4211 AGACAGAGACTTATGATTCAGAGACCATCCGAGAGCAATTTGCAGACTGTACCATGCT 4270
Db 4201 AGACAGAGACTTATGATTCAGAGACCATCCGAGAGCAATTTGCAGACTGTACCATGCT 4260
Qy 4271 GACCATTCGCCATCGCCTGCACAGGTTCTAGGCTCCGATAGGATATGGTGTGGGCCCA 4330
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Qy 4391 CTATGCCATGTTTCTGCTGCAGAGAACAGGTCGCTGTCAGGCGTCACTCTCCCTGT 4450
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Qy 4451 TGACGAGTCTCTTCTTTAGACATTTGCCATTCCTGCTGCCGCGGCCCTC-TCATC 4509
Db 4441 TGACGAGTCTCTTCTTTAGACATTTGCCATTCCTGCTGCCGCGGCCCTC-TCATC 4500
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Db 4501 GCGTCTCTTACCGAACCTTGCCTTCTCGATTTTATCTTTTCCACAGCAGTTCCGGAT 4560
Qy 4570 TGGCTTGTGTTTCACTTTTGGGAGAGTCATATTTTGTATTGATTATTTATTTCCATAT 4629
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Db 4621 TCATGTAACAAATTTAGTTTGTCTTAAATTTGCACCTTAAAGGTTTCAAGAACCGT 4680
Qy 4690 TATTATATTTATCAGAGGCTATATTAAGCTTTTATACGTGTAGCTATATCTATATAT 4749
Db 4681 TATTATATTTATCAGAGGCTATATTAAGCTTTTATACGTGTAGCTATATCTATATAT 4740
Qy 4750 AATCTGTACATAGCCTATATTTACAGTGAATAATGTAAAGCTGTTTATTTATTTAAAT 4809
Db 4741 AATCTGTACATAGCCTATATTTACAGTGAATAATGTAAAGCTGTTTATTTATTTAAAT 4800
Qy 4810 AAGCACTGTGCTAATAACA 4828
Db 4801 AAGCACTGTGCTAATAAAAAA 4819

RESULT 5

AAC85287

ID AAC85287 standard; cdna; 4781 BP.

XX XX

AC AC

XX XX

DT 29-MAR-2001 (first entry)

XX XX

DE Multidrug-resistance associated polypeptide-beta coding sequence.

XX XX

KW Multidrug resistance-associated polypeptide; MRP-beta; transporter;

KW P-glycoprotein; chemotherapy; cancer; ss.

XX OS Homo sapiens.

XX XX

XX Key

PH Location/Qualifiers

FT CDS 2..4363

FT /*tag= a

/product= "MRP-beta"

FT US6162616-A.

XX 19-DEC-2000.

XX 16-APR-1997; 97US-0843459.

XX 16-APR-1997; 97US-0843459.

XX (MILL-) MILLENNIUM PHARM INC.

XX Shyjan A;

XX WPI: 2001-111728/12.

XX P-PSDB; AAB47021.

XX Novel nucleic acid encoding multidrug resistance-associated protein

XX MRP-beta, useful for detecting and treating drug-resistant cancers

XX Claim 1; Fig 1; 41pp; English.

XX This sequence encodes a multidrug resistance-associated polypeptide

XX (MRP-beta). MRP-beta is a transporter that can remove

XX chemotherapeutic agents from cells and/or sequester such agents,

XX and it probably accounts for multidrug resistant phenotypes that do

XX not respond to treatments with reversal agents directed against

XX P-glycoprotein or the known MRP. By inactivating MRP-beta, at nucleic

XX acid or protein levels, cells should be rendered sensitive to

XX chemotherapy agents. The MRP-beta coding sequence, or fragments

XX of it, can be used to detect expression of the MRP-beta gene and

XX thus multidrug resistant cells. Fragments of MRP-beta DNA are useful

XX as primers and as antisense (therapeutic) agents for inhibiting

XX expression of the MRP-beta gene. They can also be used for detecting

XX mutations and to treat diseases associated with abnormal MRP-beta

XX gene expression, specifically cancer, particularly for potentiating

XX chemotherapy of fluid or inoperable tumors, or in cases of regrowth

XX after an initial course of chemotherapy.

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Query Match 80.9%; Score 4724.2; DB 22; Length 4781;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 4737; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 77 TGATGTGAACCTAACAGTCTGTGAGCCCTGGAACCTCCGCTCAGAGAAGATGAAGGATAT 136

Db 1 TGATGTGAACCTAACAGTCTGTGAGCCCTGGAACCTCCGCTCAGAGAAGATGAAGGATAT 60

Qy 137 CGACATAGGAAGAAGTATATCATCCCACTCTGGGTATAGAGTGTGAGGAGAGAAC 196

Db 61 CGACATAGGAAGAAGTATATCATCCCACTCTGGGTATAGAGTGTGAGGAGAGAAC 120

Qy 197 CAGCACTTCTGGAGCGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGAACTGACCGTT 256

Db 121 CAGCACTTCTGGAGCGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGAACTGACCGTT 180

Qy 257 GGAATGCCAAGATGCTTGGAAACAGACGCCGAGCGGCGCTCTCTCTTGTATGCCCTC 316

Db 181 GGAATGCCAAGATGCTTGGAAACAGACGCCGAGCGGCGCTCTCTCTTGTATGCCCTC 240

Qy 317 CATGCATCTCAGCTCAGAAATCTCTGGATCAGAGATCCCAAGGGGAAAGTACCATCATGG 376

Db 241 CATGCATCTCAGCTCAGAAATCTCTGGATCAGAGATCCCAAGGGGAAAGTACCATCATGG 300

Qy 377 CTGTAGTCTCTGAAGCCCATCCGGACTACTTCCAAACACAGACCCAGCTGGACAATGC 436

Db 301 CTGTAGTCTCTGAAGCCCATCCGGACTACTTCCAAACACAGACCCAGCTGGACAATGC 360

Qy 437 TGGGCTTTTCTCTGTATGACTTTTTCGFGGCTTTCTCTCTGGCCCGCTGTGGCCCAAA 496

Db 361 TGGGCTTTTCTCTGTATGACTTTTTCGFGGCTTTCTCTCTGGCCCGCTGTGGCCCAAA 420

DR WPI: 2001-514599/56.
DR P-PSDB; AAE08075.
XX Novel polynucleotides encoding novel human proteins with structural
PT similarity to cellular transporters for the diagnosis of disease and
PT use in gene therapy -
XX
XX
PS Claim 4; Page 60-61; 91pp; English.
XX
CC The present sequence is a human transporter-related protein cDNA.
CC The human transporter-related protein share structural similarity with
CC mammalian metabolite or organic cation transporters, multi-drug
CC resistance (MDR) proteins, mammalian sodium-glucose cotransporters and
CC other cellular transporters. The transporter-related protein DNA may be
CC used for the detection of mutant sequences or inappropriately expressed
CC sequences for the diagnosis of disease. They may also be used to screen
CC for drugs effective in the treatment of the symptomatic or phenotypic
CC manifestations of perturbing the normal functions of the sequences of the
CC invention in the body. They may also be used in gene therapy for treating
CC biological conditions.
XX
SQ Sequence 4101 BP; 1046 A; 1023 C; 1048 G; 983 T; 1 other;
Query Match 15.9%; Score 925.8; DB 22; Length 4101;
Best Local Similarity 54.0%; Pred. No. 1e-213;
Matches 2159; Conservative 0; Mismatches 1707; Indels 129; Gaps 8;
QY 421 ACCGAGTGAACAGTGGGCTTTTCCGTGATGACTTTTTCGTGGCTTCTCTCTCG 480
DB 131 ACCGGTGGATGATCGGGGCTACTCTCCCTGCCACATTTTCTGGCTCACGCCGTGA 190
QY 481 CCGGTGGCCACAGAAGGGGAGCTCAATGAGAGAGGTGTGCTCTGTCCAGC 540
DB 191 TGGTGAAGGCTACCGGCAAG--GCTGACCTAGACACCCCTGCCCCCATTTGTGCAT 247
QY 541 ACGAGTCTTCTGAGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 600
DB 248 ATGACTCATCTGACACCAATGCCAAGATTTTCGAGTCTTGGATGAAGAGTAGCAA 307
QY 601 AAGTGGCCAGAGCTGTCTCCCTGGGAGGTTGTGTGATCTTCTGCGCCACAGGC 660
DB 308 GGGTGGCTCTGAGAGGCTCTCTGAGCAGCTGTGTGAAATTTCCAGAGGACAGCG 367
QY 661 TCATCTGTCCATGCTGTGCTGATGATCAGCAGCTGGCTGCTTCAGTGGACAGCT 720
DB 368 TGTGTGAGCATCTGGGCCAATCTCTGTGATCATCTGAGGAGCCATAGGGCCGACAG 427
QY 721 TCATGTGAACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACTGCACTACAGCT 780
DB 428 TTCTCATTCACCAATCTCTCAGCAGACTGAGAGGACCTCTGGAAAGTCTGGTTGCCA 487
QY 781 TGTGTGTAGTGTGGGCTCTCTCCTGAGGAAATCGTGGGCTGTGTGCTGCTGCACTGA 840
DB 488 TTGAGCTGTGCATAGCCCTTTTGGCCACCAGTTTACCAAGTCTTCTTTTGGGCCCTTG 547
QY 841 CTTGGCATTGAATACCGAACGGTGTCCGCTTGGGGGGCCATCTTAACCATGSCAT 900
DB 548 CTTGGGCCATCAACTACCGCAGCGCCATCCGTTGAAGGTGGGCTCTCCACCTTGTGTT 607
QY 901 TTAAGAGATCCCTTAAGTTAAAGAAATTAAGAGAAATCCCTGGGTGAGCTCATCAACA 960
DB 608 TTCAAAACCTAGTGTCTTCAAGACATTTGACCCACATCTCTGTGGGAGGTGCTCAATA 667
QY 961 TTTGTCCACAGATGGCAGAGAAATGTTGAGGACAGCCGTTGGCAGCCTGCTGGCTG 1020
DB 668 TACTGTCAAGTATAGTATCTTTTGTGTTGTTGAGCTGCTTGTGTTGCTTTGGCCAGCCA 727
QY 1021 GAGGACCCGTGTGCTATCTTAGCATGATTTATATGTAATTTCTGGGACCAACAG 1080
DB 728 CCATCCCGATCCATTAATGGTCTTTTGTGGCGGTACGCCCTTTTTCATTTCTGGGGCCACAG 787
QY 1081 GCCTCTGGGATCAGCTGTTTATCTCTTTTACCCAGCAATGATGTTTGTGATCAGCGC 1140

DB 788 CTCTCATCGGATATCATGTATGTATCATATTCATACCCGCTCCAGATGTTTATGGCCAAGC 847
QY 1141 TCACAGCATATTTTCAGGAGAAAATCGTGGCCGCCACGGATGAACCTGTCCAGAGATGA 1200
DB 848 TCAATTCAGCTTTCGGAAGGTCAGCAATTTTGTGTGACACAGCAGGTTTCAGACAATGA 907
QY 1201 ATGAAGTCTTACATTAAATTTATCAAAATGTATGCTGGGTCAAGACATTTTCTC 1260
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QY 1261 AGAGTGTTCAAAATAATCCGAGAGGAGCGTCGGATATTTGAAAAGCCGGTACTTCC 1320
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DB 1028 AAGTGGAAATCTGCTCCCTGGCCCTCGTGTCCACCATAGCCATCGTGTGACATTTAT 1087
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DB 1268 ACATCACCACCAAGAGAGCAGATCTGTCTGCTTTTAGCAATGACACTTGCAT 1327
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DB 1328 GGG-----AGCATGAAGCCAGCAGAAAGTA 1354
QY 1681 ACAGAGGGCTTCCAGGGCAAGAGAGAGAGGTGAGCAGCTGCGCCACTGAGCATC 1740
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QY 1861 ACAGCATCGATCTGAGATCCAAGAGGTAACCTGGTTGGAATCTGCGSCAGTGGGAA 1920
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QY 1921 GTGAAAACCTCTCTCATTTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGCGACGA 1980
DB 1550 GTGAAAAGAGCTCCCTCTCTGAGCTCTCTAGGACAGATGACGATGCAAGAGGTGG 1609
QY 1981 TTGCAATCAGTGAACCTTCTGCTTATGTGGCCAGCAGCGCTGGATCTCTCAATGCTACTC 2040
DB 1610 TGGCAGTCAATGGAACCTTGGCTTACGTTTTCACAGCAGCATGGATCTTTCATGGAATG 1669
QY 2041 TGAGAGCAACATCTCTGTTTGGGAGGAATATGATGAAGAAAGATACAACTCTGTGCTGA 2100
DB 1670 TGAGAGAAAACATACTCTTTGGAGAAAAGTATGATCAACAAAGGTATCAGCACAGTCC 1729
QY 2101 ACAGCTGCTGCTGAGGCTCACCTGCGCATTTCTCCAGCAGCAGCACTGACGGAGATTG 2160
DB 1730 CGCTCTTGGGCTCCAGAGGACCTGAGCAACCTCCCTTATGGAGACCTGACTGAGATTG 1789
QY 2161 GAGAGCGAGGAGCAACCTGAGCGTGGCGCAGAGGATGACCTTGGCCCGGCT 2220
DB 1790 GGGAGCGGGCTCAACCTCTCTGCGGGGACAGGAGGATTAGCCTTGGCCCGGCTG 1849

QY 2221 TGTATAGTGACAGGAGCATCTACATCCTTGACGACGCCCTCAGTGTCTAGATGCCCATG 2280
DB 1850 TCTACTCCGACCGCTAGCTCTACTGCTGGACGACCCCTGTCGGCGGTGGAGCCGACG 1909
QY 2281 TGGGCAACACACATCTTCAATAGTGTCTATCCGGAACATCTCAAGTCCAAAGACAGTCTGT 2340
DB 1910 TGGGGAAGCAGCTCTTGGAGAGTGCATTAAGAAGAGCGCTCAGGGGAAAGACAGTCTGTC 1969
QY 2341 TTGTTACCCACAGTTTACAGTACCTGGTTGACTGTGATGAAGTATCTTCATGAAAGAGG 2400
DB 1970 TGGTGACCCACAGCTACAGTCTTCTAGAGTCTTGTGATGAAGTATTTATTAGAAGATG 2029
QY 2401 GCTGTATTACGGAAGAGCACCCTATGAGGAACTGATGAATTTAAATGTGACTATGCTA 2460
DB 2030 GAGAGATTTGTGAAGAGGAACCCCAAGAGATTAATGAGGAGAGGGCGCTATGCAA 2089
QY 2461 CCATTTTTAATACCTGTGTCTGGGAGACACCCGCGAGTTGAGATCAATTCAAAAAAGG 2520
DB 2090 AACTGATTACAACTGCGAGGATTGCAAGTCAAGGATCCTGAACACCTTTACAATGCAG 2149
QY 2521 AAACAGTGGTTACAGAGAGAGTCACTAC-----AAGACAGGGTCTCCTAAACAGGAT 2571
DB 2150 CAAATGGTGAAGGCTTCAAGGAGAGCCCTGCTGAGAGAGAGGAAGATGCTGTTTTGGCTC 2209
QY 2572 CAGTAAAGAAAGAAAGCAGTAAGCCAGAGGAA----- 2606
DB 2210 CAGGAATGAGAAAGATGAAGGAAGAAAGATCTGNAACAGGCTCAGAAATTTGAGACACAA 2269
QY 2607 -----GGGAGCTTGTCCAGCTGGAAGAGAAAGGCGAGGTTTCAGTGCCTCGGT 2655
DB 2270 AAGTTCTGAGCACCAGCTCATCCAGACTGAATCCCCCAGGAGGAACCGTGACCTGGA 2329
QY 2656 CAGTATATGGTGTACATCCAGGTGCTGGGGGCCCTTGGGATTCCTGGTATTTATGG 2715
DB 2330 AAACATATACACAGTACATTAAGGCTTCTGGAGGGTACCTCTCTCTCTCACTGTGT 2389
QY 2716 CCCTTTTCATGTGAATGTAGGACGACCGCTTACAGACCTGGTGGTTGAGTTACTGGA 2775
DB 2390 TCCTCTCTCTGATGATGGCGGCTGCTTTCAGACAGTGGTGGGTCCTCGGT 2449
QY 2776 TCAAGCAAGGAAGCGGGAACACCTGTGACTCGAGGGAACGAGACC---TCGGTGAAGTG 2832
DB 2450 TGGACAAGGGCTCACGATGACTGTGGGCCCCAGGGAACAGGACCATGTGTGAGGTGCG 2509
QY 2833 ACAGATGAGACATCTCTATGTCAGTACTATGTCAGACATCTACGCCCTCTCCATGG 2892
DB 2510 GCGCGGTGTCGACAGACATCGGTGACGATGTGTACCAAGTGGGTGTACACTGCAAGCATGG 2569
QY 2893 CAGTCATGCTGATCCTGAAAGCCATTGAGGAGTTGTCTTGTCAAGGGCAGCTCGAG 2952
DB 2570 TGTTCATGCTGTTTGGCGTCAACAAGGCTTGTCTTCAACAAGACCACTGATGG 2629
QY 2953 CTTCTCCCGGTGATGACGAGCTTTTCCGAAGGATCCTTCCGAAGCCCTATGAAGTTTT 3012
DB 2630 CATCTCTCTCTGATGACACGGTGTGTGAAGATCTTAAAGAGCCCAATGAGTTCT 2689
QY 3013 TTGACAGACCCACAGGAGGATCTCAACAGGTTTTCGAAGACATGGAATGAGTTG 3072
DB 2690 TTGACAGCACTCCCACTGGCAGGGTAATGAACCGTTTTCGAAGGATATGAGCAGCTGG 2749
QY 3073 ACGTGGGTGCGGTTCAGGCGGAGATGTTTCATCCAGACGTTATCTCTGGTGTCTTCT 3132
DB 2750 ATGTGAGGCTGCGGTTTCAAGCAGAGAACTTCTCGACGAGTTTTTATGTTGGTGTGA 2809
QY 3133 GTGTGGGAATGATCGAGAGTCTTCCCGTGGTTCCTTGTGCGAGTGGGGCCCTTGTCA 3192
DB 2810 TTCTCGTATCTTGGCTGCTGTGTTTCTCTGCTGCTCTTTAGTCTGGCCAGCCTTGGT 2869
QY 3193 TCCTCTTTTCACTGCGACATTTGCTCCAGGGTCTCTGATTCGGGAGTGAAGCTGTGG 3252
DB 2870 TAGGGTCTCTTCTGTTACGCACTTTTCCACAGAGGAGTCCAGGAGTCAAGAAGGTGG 2929

QY 3253 ACAATATCAGCAGTCACTTTTCTCCTCCACATCAGTCCAGCATACAGGGCCTTGCCA 3312
DB 2930 AGAATGTACGGGTACCGTGTTCACCCACATCACTCTCCTCCATGCAGGGCCTTGGGCA 2989
QY 3313 CCATCCAGCCTACATAAAGGCGAGGAGTTTCTGACAGATACCAAGAGTGTGTGATG 3372
DB 2990 TCATTACGCTATGCAAGAAGAGAGCTGCATCACTAGTTTAAAGACGCTAAACGACG 3049
QY 3373 ARAACAAAGTCTCTTTTGTGTAGGTGCGATGCGGTGCTGCTGCTGCGGTGG 3432
DB 3050 AAAACTCCAGTCACTCTCTACTTTAACTGTCTCTCAGGTGTTTGGCGTGAGAAATG 3109
QY 3433 ACCTCATCAGCATCGCCTCATCACACACGCGGCTGATGATCTTCTTATGACACGGGC 3492
DB 3110 ATGTCTCATTAACATCTTACCTTTCATGTGGCCTTGTGGTGACCTGAGTTTCTCT 3169
QY 3493 AGATTCCCGCAGCCTATGCGGGTCTCGCCATCTCTTATGTCTCCAGTTAAACGGGGTGT 3552
DB 3170 CCATCAGTACTTTCATCCAAAGGCTGTCTATTGTCTATCATATCATCCAGCTGAGCGACTGC 3229
QY 3553 TCAGTTTACGGTCAGACTGGCATCTGAGACAGAGCTCGATTCACTCGGTGGAGAGA 3612
DB 3230 TCCAAGTGTGTGCGAAGCGGAACAGACAGCGAAGCCAAATTCACCTCCGTGGAGCTGC 3289
QY 3613 TCAATCACTACATTAAGACTCTGTCTTTGGAAGCACCTGCCAGAAATTAAGAACAGGCTC 3672
DB 3290 TCAGGAATACATTTGACACCTGTGCTGAATGCATCATCCCTCAAAATGGGGACCT 3349
QY 3673 CTTCCCTGACTGCGCCAGGAGGAGGTGACCTTTGAGACGACAGATGAGGTACC 3732
DB 3350 GTCCCAAGGACTGCCCCAGCTGTGGGAGATCACTTCAGAGACTATCATGATGATATACA 3409
QY 3733 GAGAAACCTCTCTTGTCTTAAAGAAAGTATCTTTCAGCATCAAACTTAAAGAGAGA 3792
DB 3410 GAGAACACACCCCTTGTCTCGACAGCCTGAATTTGAACATACAAAGTGGGCGAGACAG 3469
QY 3793 TTGGCATTTGGGCGGACAGGATCAGGAAGTCTCTGCTGGGATGGCCCTCTTCGCTC 3852
DB 3470 TCGGATTTGTGAAGAACAGGTTCCGGAAGATCATCGTTAGGAATGGCTTGTGTTCTC 3529
QY 3853 TGTGAGTATTTGAGGCTGCTCAAGATTTGATGAGTGAAGATCAGTGATTTGGCC 3912
DB 3530 TGTGAGGACGACCGCTGCGACAACTTTTATTGATGAGTGGATATCTGCTATCTCAGCT 3589
QY 3913 TTGCCAGCTCCGAAGAAACTCTCTATCTCTCAAGAGCGGTGCTGCTGAGTGGCA 3972
DB 3590 TGAAGACCTTCAGAACCAAGCTGACTGTGATCCACAGGATCTCTGCTCTTTGTAGGTA 3649
QY 3973 CTGTCAGATCAAAATTTGGACCCCTTCAACCCAGTACACTGAAGACCAAGATTTGGATCCC 4032
DB 3650 CAGTAAGGTACAATTTGGATCTCTTTGAGAGTCAACCGATGAGATGCTCTGCGAGTTT 3709
QY 4033 TGGAGGAGACACATGAAGAATGATTTGCTCAGCTACCTCTGAACACTTGAATCTGAAG 4092
DB 3710 TGGAGAGAACAATTCATGAGAGACACAATATGAACCTCCCAAGAAATATACAGCAGAAG 3769
QY 4093 TGATGAGAAATGGGGATACTTCTCAGTGGGGGAAGCGAGCTCTTGTGATAGTAGAG 4152
DB 3770 TCAGAAAATGGAGAAAATTTCTCAGTAGGGGAAGCTCAGCTGCTTTGTGTGCCCCGAG 3829
QY 4153 CCGTGTCCGCCACTGAAGATTTCTGATTTAGATGAAGCCACAGCTGCCATGACACAG 4212
DB 3830 CTCCTCTCGTAAATCAAGATCATTTCTCTTGTGATGAAGCCAGCGCTCTATGGATCCA 3889
QY 4213 AGACAGTATTTGATTCAAGAGACCATCCGAGAAGCATTTGCGAGACTGTACACTGCTGA 4272
DB 3890 AGACTGACACCTGGTTCAAGACACCATCAAGATGCCITCAAGGCTGCACCTGCTGA 3949
QY 4273 CCATGCCCATGCGCTGACACAGGTTCTTAGGCTCCGATAGGATTTAGGTGCTGCCGAGG 4332
DB 3950 CCATGCCCATGCGCTCAACACAGTCTCAACTGCGATACGCTCCTGTTGTTATGAAAATG 4009
QY 4333 GACAGGTGGTGGATTTGACACCCCATCGTCTCTT 4367

Db		!						4010	GGAAGGTGATGGATTTCACAAAGCCTGAAGTCCCT	4044
RESULT 9										
AAD14912										
ID									AAD14912 standard; cDNA; 4008 BP.	
XX										
XX									AAD14912;	
XX										
XX									01-NOV-2001 (first entry)	
DE									Human transporter-related protein #25 cDNA.	
XX										
KW									Human; transporter-related protein; metabolite transporter;	
KW									organic cation transporter; multi-drug resistance; MDR; gene therapy;	
KW									cellular transporter; sodium-glucose cotransporter; diagnosis; screening;	
KW									symptomatic; phenotypic manifestation; biological condition; ss.	
XX										
OS									Homo sapiens.	
XX										
FH									Key Location/Qualifiers	
FT									1..4008	
CD									/tag= a	
FT									/product= "Human transporter-related protein"	
FT									/transl_except= (pos:3025..3039, aa:Thr-Thr)	
FT									/transl_except= (pos:3370..3372, aa:Xaa)	
FT									/note= "Xaa can be any amino acid"	
XX										
PN									W0200157214-A2.	
XX										
XX									09-AUG-2001.	
PF									02-FEB-2001; 2001WO-US03646.	
XX										
PR									03-FEB-2000; 2000US-0179973.	
PR									14-FEB-2000; 2000US-0182422.	
XX									(LEXI-) LEXICON GENETICS INC.	
PA										
PI									Turner CA, Mathur B, Wang X, Abuin A, Friedrich G, Zambrowicz B;	
PI									Sands AT;	
DR									WPI; 2001-514599/56.	
XX									P-PSDB; AA08078.	
PT									Novel polynucleotides encoding novel human proteins with structural	
PT									similarity to cellular transporters for the diagnosis of disease and	
PT									use in gene therapy -	
XX									Disclosure; Page 73-74; 91pp; English.	
XX										
CC									The present sequence is a human transporter-related protein cDNA.	
CC									The human transporter-related protein share structural similarity with	
CC									mammalian metabolite or organic cation transporters, multi-drug	
CC									resistance (MDR) proteins, mammalian sodium-glucose cotransporters and	
CC									other cellular transporters. The transporter-related protein DNA may be	
CC									used for the detection of mutant sequences or inappropriately expressed	
CC									sequences for the diagnosis of disease. They may also be used to screen	
CC									for drugs effective in the treatment of the symptomatic or phenotypic	
CC									manifestations of perturbing the normal functions of the sequences of	
CC									invention in the body. They may also be used in gene therapy for treating	
XX									biological conditions.	
XX										
SQ									Sequence 4008 BP; 1018 A; 1005 C; 1022 G; 962 T; 1 other;	
Query Match 13.5%; Score 790.6; DB 22; Length 4008;										
Best Local Similarity 52.7%; Pred. No. 6.3e-181;										
Matches 2104; Conservative 0; Mismatches 1669; Indels 222; Gaps 9;										
QY									421 ACCCAGTGGAACATCGTGGGCTTTTTCCTGATGACTTTTTCGTGGCTTCCTCTGG 480	
Db										
									131 ACCCGGTGGATGATCGGGGCTACTTCCTCGGCATATTCCTGGCTCACGCCGGTGA 190	

QY 1561 TAAGAAACAACAGCAGCTCCTACATCAAGATAGAGATGAAAAATGCCACCTTGGCAT 1620
Db 1268 ACATACCCCAAGAGACCCAGATCTGTCTGTCTTTTAGCAAAATGCCACCTTGACAT 1327
QY 1621 GGGACTCTCCACTCCAGTATCCAGACTCGCCCAAGCTGACCCCAAAATGAAAAG 1680
Db 1328 GGG-----AGCATGAAGCCAGCAGGAAAAAGTA 1354
QY 1681 ACAAGAGGGCTTCCAGGGCAAGAAAGAGAGGTGAGGCAGCTGCAGCGCACTGAGCATC 1740
Db 1355 CCCAAGAAATTTGCAAGACCAAGAAAGGCAATTTATGCAAGAAACAGAGGTGACAG---- 1410
QY 1741 AGCGGTGTGGCAGACAGCAAGAGGCCACCTCTCTCTGGACAGTGAAGCGGCCAGTC 1800
Db 1411 -----GCATACAGTGAGAGAGTCCACC-----AGCCAAGGGAGCCACTG 1450
QY 1801 CGAAGAGAGAGGAGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGACACACTGC 1860
Db 1451 GCCAGAGGAGCAAGGTGACAGCTCAATTCGGT-----TCTGC 1489
QY 1861 ACAGCATCGATCTGGAGATCCAAAGAGGGTAAACTGTTGGAATCTGCGGCACTGGGAA 1920
Db 1490 ACAGCATAGCTTTGGTGAGAAAGGGGAGATCTTGGGAATATGTGGGAATGTGGAA 1549
QY 1921 GTGAAAAACCTCTCATTTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCA 1980
Db 1550 GTGAAAAGAGCTCCCTCTCTGACGCTCTCTAGGACAGATGACGCTGCAGAAAGGGGTG 1609
QY 1981 TTGCATCAGTGAACCTTCGCTTATGTGGCCAGCAGAGGCTGGATCTCAATGCTACTC 2040
Db 1610 TGGACGTCAATGGAACTTTGGCCCTAGCTTTTACAGAGGCGATGGATCTTTTCATGGAAATG 1669
QY 2041 TGAGACACAACATCCCTGTTTGGGAAGAAATATGATCAAGAAAGATACAACCTCTGCTGA 2100
Db 1670 TGAGAAACAACATACCTTTTGGGAAGAAATATGATCAACAAAGGTATACGACACAGTCC 1729
QY 2101 ACAGCTGCTGCTGAGGCTGACCTGGCCATTTCTCCAGCAGCGACCTGACGAGATG 2160
Db 1730 GGGTCTGTGGCTCCAGAAAGGACCTGAGCAACCTCCCTATGGAGACCTGACTGAGATTG 1789
QY 2161 GAGAGCGAGGACCACTTACGCGGTGGCAGCGCCAGAGGATCAGCTTGGCCGGGCT 2220
Db 1790 GGGAGCGGGGCTCAACCTCTCTGGGGGCGAGAGCAGAGGATAGCCCTGGCCCGGCTG 1849
QY 2221 TGTATAGTGACAGGAGCATCTACATCTCTGGACAGCCCTCAGTGCCTTAGATGCCATG 2280
Db 1850 TCTACTCCAGCCGTACGCTCTACCTCTGGACAGCCCTCTGCGCCGTGGAGCCCAAG 1909
QY 2281 TGGCAACCAATCTTCAATAGTGTCTATCCGGAACAATCTCAAGTCCAAAGACAGTCTGT 2340
Db 1910 TGGGAAGCACGCTCTTTGAGGAGTGCAATTAAGAAAGCGCTCAGGGGAAAGACAGTCTGC 1969
QY 2341 TTGTTACCCACAGTTACAGTACCTGTTGACTGTGATCAAGTGAATCTCAAGAAAGG 2400
Db 1970 TGGTGACCCACAGCTACAGTCTTTAGAGTCTTTAGAGTCTTTGATGAAGTATTTATTAGAAGATG 2029
QY 2401 GCTGTATACGGAAGAGCACCATGAGGAATGATGAATTTAAATGCTGACTATGCTA 2460
Db 2030 GAGAGATTTGTGAAAAGGGAACCCACAGAGTATATGAGGAGAGAGGGCGCTATGCAA 2089
QY 2461 CCATTTTAAATACCTTGTGCTGGGAGACACCGCCAGTGTGAGATCAATCAAAAAGG 2520
Db 2090 AACTGATTCAACAACCTGCGAGGATTCAGTTCAAGGATCCTGAACACCTTTACAATGCAG 2149
QY 2521 AAACAGTGGTTACAGAGAGATCAC-----AAGACAGGGTCTCAAAACAGGAT 2571
Db 2150 CAATGGTGAAGCCCTTCAAGAGAGACCCCTGCTGAGAGAGAGAGAGATGCTGTTTGGCTC 2209
QY 2572 CAGTAAAGAGGAAAGAGCAGTAAAGCCAGAGAA----- 2606
Db 2210 CAGGAAATGAGAAAGATGAGGAAAGATCTGAAACAGGCTCAGAAATTTGTAGACAAA 2269
QY 2607 -----GGGCAAGCTTTGTGACGTGGAAAGAGAGGGGAGGTTTCAGTGCCTGTGT 2655

Db 2270 AAGTTCTTGACACCACTCATCCAGACTGAATCCCCCAGGAAGAACCTGACCTGGA 2329
QY 2656 CAGTATATGGTGTCTACATCCAGGCTGTGGGGCCCTTGGCATTTCTGTGTTATATGG 2715
Db 2330 AAACATATCACACGTACATTAAGGCTTCTGGAGGTACTCTCTCTCTCTCTCTCTCT 2389
QY 2716 CCCTTTTTCATCTCAATGTAGGAGCAGCCGCTTTCAGCACCTGCTGTTGAGTTACTGGA 2775
Db 2390 TCCCTCTCTCTCTGATGTGGCAGCGTGCCTTTCAGCAACTGGTGGCTCTCTGCT 2449
QY 2776 TCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGAACAGACACTCGGTGAGTGACA 2835
Db 2450 TGGCAAGGCTCACGATGACCTGTGGGCCCCAGGGAACAGACCATGTGTGAGGTGCG 2509
QY 2836 GCA---TGAAGGCAATCTCTCATATGCACTACTATGCCAGCATCTACGCCCTCTCCATGG 2892
Db 2510 GCGCGTGTCTGGCAGACATCGGTGAGCATGTGTACCACTGGGTGTACACTGCAAGCATGG 2569
QY 2893 CAGTCATGCTGATCTGAAAGCCATTCAGAGGTGTCTTTGTCGAAGGACGCTGCGAG 2952
Db 2570 TGTTTCATGCTGGTGTGGCGTCCACAAAGGCTTCGCTTTCACCAAGACCACTGATGG 2629
QY 2953 CTTCTCTCCCGCTGCATGACGAGCTTTTCCGAAGGATCTTCGAAGCCCTATGAAGTTT 3012
Db 2630 CATCTCTCTCTGATGACAGCGTGTGTGATAGATCTTAAAGAGCCCAATGAGTTCT 2689
QY 3013 TTGACAGACCCCAAGGAGGATCTCAACAGTTTTCAAAGACATGATGAAGTTG 3072
Db 2690 TTGACAGACTCCCACTGGCAGGCTAATGAACGCTTTTCCAAAGGATATGACAGCTGG 2749
QY 3073 ACCTGCGGCTGCGCTTCCAGGCCAGATGTTTCATCCAGAGGTTATCCTGGTTCCTTCT 3132
Db 2750 ATGTGAGGCTGCGCTTTCACGACAGAACTTCTGACAGAGTTTATGCTGGTGTGTTA 2809
QY 3133 GTGTGGAATGATCGCAGAGGATCTTCCCGTGGTGTGGCAGTGGGCCCTCTGCA 3192
Db 2810 TTCTCGTGTCTTGGCTGCTGTGTCTCTGCTGCTTTAGTCGGGCCAGCTTCTGCTG 2869
QY 3193 TCCTCTTTTTCAGTCTGCAATGTTCTCCAGGGTCTGATTCGGGAGCTGAAGCGTCTGG 3252
Db 2870 TAGGCTCTCTCTCTGTTACGCAATTTTCCACAGAGAGTCCAGAGGCTCAAGAAGTGG 2929
QY 3253 ACAATATCAGCAGTACCTTCTCTCCACATCAGTCCAGCATACAGGCTTCCCA 3312
Db 2930 AGATGTCACCGGTACCTGCTGTCTCCCACTACCTCTCCATCGAGGGCTGGGCA 2989
QY 3313 CCATCCAGCCTTACAATAAAGGCGAGGTTTCTGACAGATACCAAGAGCTGCTGGATG 3372
Db 2990 TCATTCAGGCTATGGCAAGAGAGAGTGCATCACTAGTTTAAGACGCTAAACGACG 3049
QY 3373 ACAACCAAGTCTCTTTTGT 3432
Db 3050 AAAATCCAGTCACT 3109
QY 3433 ACCTCATCAGCATCGCCCTCATCACACACAGGGGCTGATGCTGTTTATGACCGGCG 3492
Db 3110 ATGCTCTCATGAACATCTTACCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3169
QY 3493 AGATTCCTCCAGCTTATGCGGGTCTCGCCATCTCTTATGCTGCTCCAGTTAAACGGGCTG 3552
Db 3170 CCATCAGTACTTCAACAAAGGCTGTCTATGTGTATCATATCATCCAGCTGAGCGGCTG 3229
QY 3553 TCCAGTTTACGTCAGCTGGCATCTGAGACAGAGCTGATTCACCTCGGTGGAGGAGGA 3612
Db 3230 TCCAGTGTGTGTGCGAAGCGGGAACAGAGACGCAAGCAAAATTCACCTCCGCTGAGCTGC 3289
QY 3613 TCAATCACTACATTAAGACTCTCTCTTGAAGCCTGCCCAATTTAAGAACAGGCTC 3672
Db 3290 TCAGGAAATACATTTTCGACCTGTGTCTCTGATGCACTCATCCCTCAAAAGTGGGACCT 3349
QY 3673 CTTCCCTGACTGGCCCCAGGAGGAGGTGACCTTTGAGAACGACGAGATGAGGTACC 3732

Qy	827	GTCCGTTGCACTGACTTGGGCATTGAAATTACCGAACCGGTGTCGCCTTGCGGGGGGGCCAT	886
Db	654	GAGTTTCTCTCCAGTTGGATCATCAACCAACGCGACGCCATCAGGTTTCCAAGCAGCTGT	713
Qy	887	CCTAACCATGGCATTTAAGAAGATCCTTAAGTTAAGAACATTTAAAGAGAAATCCCTGGG	946
Db	714	TTCTCTCTTTGGCTTTGAGAGCTCATCAATTTAAGTCTGTAATACACATCACCCTCAGG	773
Qy	947	TGAGCTCATCAACATTTGCTTCCAAGCATGGGCGAGAAATGTTTGAAGCAGCAGCGCTTGG	1006
Db	774	AGAGCCCATCAGCTTCTTCAACGGTGATGAACCTACCTGTTTGAAGGGGTGCTCTATGG	833
Qy	1007	CAGCTGCTGGCTGGAGGACCGTGTGGCCATCTTAGGCATGATTTATATGTAATAT	1066
Db	834	ACCCCTAGTACTGATCACTCGGCGATCGGTGTCATCTGCGACATTTCTTCCCTACTTCAT	893
Qy	1067	TCTGGGACCAACAGGCTTCTCGGGATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGAT	1126
Db	894	TATTTGGATACACTGCATTTATTGCCATCTTATGCTATCTCTGGTTTCCCACCTGGAGGT	953
Qy	1127	GTTTGCATACAGGCTCACAGCATATTTCAGGAGAAAAATGCGTGGCCGCGACGGATGAACG	1186
Db	954	ATTTCATCAAGAATGGCTGTGAAGGCTCAGCATCACACATCTCAGGTTCAGCGACCACGC	1013
Qy	1187	TGTCAGAGATGAATGAAGTTTCTTACTTACATTTAAATTTATCAAAATGTAATGCTGGGT	1246
Db	1014	CATCCGTGTGACCGTGAAGTTTCTCATTGCAATTAAGCTGATTAATGATGTACATGGGA	1073
Qy	1247	CAAAGCATTTTCTCAGAGTGTTCAAAAAATCCGCGAGGAGGCGTCGGATATTGAAAAA	1306
Db	1074	GAAACATTTGCAAAAAATCATTTGAAGACTAAGAAGGAAGAAAGGAAGCTATTGGAGAA	1133
Qy	1307	AGCGGGTACTTCCAGGGTATCACTGTGGGTGGCTCCCAATTTGTGGTGTGATGTCGAC	1366
Db	1134	GTGCGGGCTGTCCAGAGCCTGACAAGTATAACCTTGTTCATCATCCCCACAGTGGCCAC	1193
Qy	1367	CGTGGTGCACCTTCTCTGTTTCATATGACCCCTGGGCTTCGATCTGACAGCAGCACAGGCTTT	1426
Db	1194	AGCGGTCTGGTTCATCCACATCTCTTAAGCTGAAACTCACAGGCTCAATGGCCTT	1253
Qy	1427	CACATGGTGACAGTCTTCAATTTCCATGACTTTTGCTTTGAAAGTAAACCGTTTTCAGT	1486
Db	1254	CAGCATGCTGGCCCTCTTGAATCTCCTTCGGGTGTCAGTGTTCTTTGTGCCTATTGCACT	1313
Qy	1487	AAAGTCCCTCTCAGAGCCTCAGTGGCTTTGACAGATTTAAGAGTTGTTTCTAATGGA	1546
Db	1314	CAAAGGTCTCAGAAATTCCAAGTCTGCACTGATGAGTTTCAAGAAAGTTTTCCTCCAGGA	1373
Qy	1547	AGAGGTTTCATATGATAAAGAAACAAACAGCCAGTCCTTCACATCAAGATAGAGATGAAAA	1606
Db	1374	GAGCCCTGTTTCTATGTCTCAGACATTAAGACCCAGCAAGCTCTGGTCTTTGAGGA	1433
Qy	1607	TGCCACTTTGGCATNGGACTCTCCCACTCCCAAGTATCAGAACTCGGCCAAGCTGACCCC	1666
Db	1434	GGCCACTTGTATGCAACAGACACCTGTCCCGGGATC-----	1470
Qy	1667	CAAAATGAAAAGACAGAGGGCTTCCAGGGCAAGAAAGAGAGGTGAGGCAGCTGCA	1726
Db	1471	-----	1470
Qy	1727	GCAGCTGAGCATCAGCGGTGCTGGCAGAGCAAGAAAGCCACCTCCTCTCTGGACAGTGA	1786
Db	1471	-----GTCAATGGGCACTGGAGCTGGAGGAAACGGGCATCTCTCTCAGGGGATGAC	1523
Qy	1787	CGAGCGGCCGAGTCCGAGAGAGGAAGAAGCAACATCCACCTGGGCCACCTCGCGCTT	1846
Db	1524	CAGCCCTAGAGATGCCCTCTGGGCCAGAGGAAGGGGAACAGCCTGGGCCAGAG-----	1578
Qy	1847	ACAGGACACATCCACAGCATCGATCTGGAGATCAAGAGGGTAAACTGGTTGGAATCTG	1906
Db	1579	-----TTTCCACAGATCAACCTGGTGTGTCCAAGGGGATGATGTATGGGGTCTG	1628

QY	1907	CGGCATGTGGGAAGTGGAAAAACCTCTCTCTCATTTTCAGCCATTTTAGGCCAGATGACGCT	196
Db	1629	CGCGAACACAGCGGAGTGGTAAGACGACGCTTGTTTCAGCCCATCTCTGGAGGAGATGCACCT	1688
QY	1967	TCTAGAGGCGAGCATTGCATCACTAGTGAACCTTCGCTTATGTGGCCGACGCGCCCTGGAT	2026
Db	1689	GCTCGAGGCGTCGGTGGGGTGCAGGGAAGCGCTGGGCTATGTCCCCACAGAGCCCTGGAT	1748
QY	2027	CCTCAATGCTACTCTCAGAGACAACTCTGTTTGGGAAGGAATATGATCAAGAAAGATA	2086
Db	1749	CGTCAGCGGAACATCAGGGAGAACATCCTCATGGAGGCGCATATGCACAGGCCCGATA	1808
QY	2087	CAACTCTGTCTGAACAGCTGTGCTGAGGCGCTGACCTGGCCATTTCTCCACGACGCGA	2146
Db	1809	CCTCCAGGTGCTCCACTGCTGCTCCCTGAATCGGACCTGGAACCTTCTGCCCTTTGGAGA	1868
QY	2147	CCTGACGGAGATTGGAGCGGAGGCCAACCTGACGGGTGGCAGCGCCAGGAGTCAG	2206
Db	1869	CATGACAGAGATTGGAGCGGGGCGCTCAACCTCTCTGGGGGCGCAAAACAGAGSATCAG	1928
QY	2207	CCTTGCCCGGGCTTGTATAGTCACAGGAGCATCTACATCTCTGGAGACGCCCTCTAGTGC	2266
Db	1929	CCTGGCCCGCGCTCTATTCCGACCGCTCAGATCTACTGCTGAGACACCCCTGTCTGC	1988
QY	2267	CTTAGATGCCATGTGGGCAACACATCTTCAATAGTGTATCCGGAACATCTCAAGTC	2326
Db	1989	TGTGGACGCCACGTCGGGAAGCACATTTTGGAGGAGTGCAATTAAGAAGACACTCAGGG	2048
QY	2327	CAAGACAGTCTCTTTGTTTACCCACCAAGTTCACGTACCTGCTGGTGTGCTGAAGTGTAT	2386
Db	2049	GAAGACGGTGTCTGCTGCTGACCCACACGCTGCACTTAGAATTTTGTGGCCAGATCAT	2108
QY	2387	CTTCATGAAGAGGGCTGTATTACGGAAGAGCGCACCCATGAGGAACATGATGAATTTAAA	2446
Db	2109	TTTGTGGAAATGGGAAATCTGTGAATGGAACCTCACAGTGAGTTAATGCAGAAAA	2168
QY	2447	TGGTGACTATGTACCATTTTAAATACCTGTGTGGGAGAGACACCGCCAGTTCAGAT	2506
Db	2169	GGGGAATATGCCCACTTATCCAGAAGATGCACAAGGAAGCCACTTCG-----GACAT	2222
QY	2507	CAATTCAAAAAAGGAACACAGTGGTTCACAGAGAAGTCACAAAGACAAGGTCCTAAAC	2566
Db	2223	GTTGAGGACACAGCAAGATAGCAGAGAAGCCAAAGGTAGAAAGTCAGGCTCTGCCAC	2282
QY	2567	AGGATCAGTAAAGAGAAAAAGCAGTAAAGCCAGAGGAAGGCGCCTGTGACGCTGGA	2626
Db	2283	CTCCCTGGAAGAGTCTCTCAACGGAATGCTGTGCCGAGCATCAGCTCACACAGGAGA	2342
QY	2627	AGAGAAAGGCGAGGTTAGTGCCCTGTGTCAGTATATGTGTCTACATCAGGCTCTGTG	2686
Db	2343	GGAGATTGAAGAAGGCTCTCTGAGTTGGAGGGTCTACCACTACATCAGGCGACGCTG	2402
QY	2687	GGGCCCCGTCATCTCGTTATTATGCCCCCTTTTCATGCTGAATGAGGACGACCCG	2746
Db	2403	AGGTTACATGGTCTCTTGCAATAATTTCTTCTGTGGTGTGATCGTCTCTTAACGAT	2462
QY	2747	CTTCAGCACTGGTGGTGTGAGTTACTGGATCAAGGAAGGAAGCGGCAACCACTGTGAC	2806
Db	2463	CTTACGCTCTGTGCTGAGCTACTGGTTGGAGCAGGCTCGGGGACCAATAGCAGCCG	2522
QY	2807	TCGAGGGAACGAGACC---TCGGTGAAGTGAACGATGAAGGACAATCCTCATATGCAGTA	2863
Db	2523	AGAGAGCATGGAACCATGCCAGACCTGGCAACATTCAGACAAATCCTCAACTGTGCTT	2582
QY	2864	CTATGCCAGCATCTAGGCCCTCTCCATGGCAGTCACTGATCTCTGAAGGCCATTCGAGG	2923
Db	2583	CTACCAGCTGGTGTACGGGCTCAACGCCCTGCTCTCTCATCTGTGTGGGGGTCTGCTCTC	2642
QY	2924	AGTGTCTTTGTCAAGGGCAGCTGCGAGCTTCTCCCGGCTGCAATGACGAGCTTTCCG	2983
Db	2643	AGGGATTTTACCAGAGGTCACGAGGAAGCATCCACGGCCCTGCGACACAACAGCTTTCAA	2702
QY	2984	AAGGATCTCTGAAGCCCTTATGAAGTTTTTGTGACAGGACCCCAAGGAGGATTTCTCAA	3043

Db 2703 CAAGTTTTCGCTGCCCATGAGTTCTTTTGACACCATCCCATAGCGGCTTTGAA 2762
QY 3044 CAGTTTTCACAGACATGATGAAGTTGACGTGCGGCTCCGCTCCAGCCCGAGATGTT 3103
Db 2763 CTGCTTCGCGAGGAGCTTGAACAGCTGGACCAAGCTCTTCCCATCTTTTCAGAGCAGTT 2822
QY 3104 CATCEAGAACGTTATCCTGCTGTTCTCTCTGTGGGATGATCCAGAGTCTTCCCGTG 3163
Db 2823 CCTGGCTCTCCTTAATGGTGATGCGCGCTCCCTGTTGATGTTGTCAGTGTGCTCTCCATA 2882
QY 3164 GTTCTGTGTGGCAGTGGGCGCTGTCTATCCCTCTTTTCAGTCTGTCACATGTTCTCCAG 3223
Db 2883 TATCTGTTAATGGAGCCATATCATGTTATTTGCTTATTTATATGATGTTCAA 2942
QY 3224 GTTCTGATTCGGGAGCTGAAGCGTCTGGACATATCACAGATCATCCCTTTCCTCCCA 3283
Db 2943 GAAGGCCATCGGTGTGTTCAAGAGACTGGAGAACTATAGCCGCTCTCTTTTATTTCTCCCA 3002
QY 3284 CATCAGTCCAGATACAGGCGCTTCCACCATCCAGCCCTACAATAAAGGGAGGAGTT 3343
Db 3003 CATCTCTCAATCTCTCAAGCGCTGAGCTCCATCCATGCTATGGAATAAACTGAAGACTT 3062
QY 3344 TCTGCACAGATACAGGAGCTGCTGTGATGACAAACCAAGCTCTTTTGTGTTTACGTG 3403
Db 3063 CATCAGCCAGTTTAAGAGCTGACTGATGGCAGATACTACTGCTGTGTTTCTATC 3122
QY 3404 TGGGATCGGCTGGCTGGCTGTGCGGTGGACCTCATCAGCATCGCCCTCATCACACAC 3463
Db 3123 TTTCCACAGCATGGCATGAGCTTGGAGCTGGAGATCATGACCAACCTTGTGACCTTGGCTGT 3182
QY 3464 GGGGCTGATGATGTTCTTATGACCGGGCAGATTCCCGACCGCTATGCGGGTCTCGCAT 3523
Db 3183 TGGCTGTGCTGGCTTTTGGCATTTTCCACCCCTACTCTCTTAAAGTCAATGCGTGT 3242
QY 3524 CTCTTATGCTGCTCCAGTTAAACGGGCTGTTCAGTTTACGGTCAGACTGSCATCTGAGAC 3583
Db 3243 CAACATCGTGTGACCTGCGCTCCAGCTTCCAGGCCACTGCCGGATTGGCTTGGAGAC 3302
QY 3584 AGAAGTCGATTCACCTCGGTGGAGAGATCAATCACTACATTAAGACTGTGCTTGGGA 3643
Db 3303 AGAGGCACATTTACGGCTGTAGAGAGATGACTGCAATGATGTTGCTCTCGGA 3362
QY 3644 AGCAGCTGCGAGATTAAGAACAAAGCTCCCTCCCTGCTTGTCTCTAAAGAAAGT 3703
Db 3363 AGCTCTTTTACATGGAAGGACAAAGTTGTCCTCCAGGGGTGGCCACAGCATGGGAAAT 3422
QY 3704 GACCTTTGAGAACGAGATGAGGTACCGAGAAACCTCCCTCTTGTCTCTAAAGAAAGT 3763
Db 3423 CATATTTACAGATTATCATGAATACAGACACACACCCAGCTGCTTCACGGCAT 3482
QY 3764 ATCTTCAGCATCAACCTTAAGAGAAAGATTGGCATTTGGGCGGACAGGATCAGGGAA 3823
Db 3483 CAACCTGACATCCGCGGCGCACAGTGTGGGCACTGTGGGAAGACGGCTCTCGGAA 3542
QY 3824 GTCTCGCTGGGAGTGGCCCTCTCCGCTGCTGGAGTTATCTGGAGGCTGCATCAAGAT 3883
Db 3543 GTCTCTTGGCATGGCTCTCTCCGCTGCTGGAGCCCATGGGACGGCGGATTCTCAT 3602
QY 3884 TGATGAGTGAAGATCAGTATATTGGCTTGGCCAGCTCCCGAACCTCTCTATCAT 3943
Db 3603 TGACGCGTGGACATTTGACGATCGCTGGAGGACTTGGCGTCCAGCTCTCATGAT 3662
QY 3944 TCTCAAGAGCGGTGCTGTTTCAAGTGGCTGTCAGTGAATTAAGTAAATTTGACCCCTTCAACCA 4003
Db 3663 CCTCAAGATCCAGTCTGCTCTCAGGAACCATCAGATCAACCTTAGATCCCTTTGACCG 3722
QY 4004 GTACACTGAAGACAGATTTGGATGCGCTGGAGGACACATCAAGATGATTTCC 4063
Db 3723 TCACACTGACGAGATCTGGATGCGCTTGGAGGAGCATTTCTTCAACCAAGCCATCTC 3782
QY 4064 TCAGCTACTCTGAACCTTGAATCTGAAGTGGAGATGGGATTAACCTTCTCAGTGG 4123

Db 3783 AAAGTTCCCAAAAGCTGCATACAGATGTGTGTAACAGGTGGAACCTTCTCTGTGGG 3842
QY 4124 GGAACGGCAGCTCTGTGTATAGCTAGAGCCCTGCTCCGCCACTGTAAAGTCTGATTTT 4183
Db 3843 GGAGAGCGAGCTGCTCTCAITTCGAGGCTGTCTTCCGAACCTCAAGATCATCTTAT 3902
QY 4184 AGATGAAGCCACAGCTGCCATGGACAGACAGACACTTATGATTCAGAGACCATCCG 4243
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QY 4244 AGAAGCATTTTCAGACTGTACCATGCTGACCATTCGCCATTCGCCACCGTCTTAGG 4303
Db 3963 TGAAGCTTCCAGGCTCCAGCTGCTCGTATTGCCACCGTGTACCACTGTCTGAA 4022
QY 4304 CTCCATAGGATATTGTGCTGGCCAGGACAGCTGTGGAGTTTGACACCCCATCGT 4363
Db 4023 CTGTGACCATCTCTGTTATGGCAATGGGAAGTGTAGATTTGATCGCCCGGAGGT 4082
QY 4364 CTTCTGTCCAAACAGACTTCCCGATTTATGCCATGTTTGTCTGTCG 4411
Db 4083 ACTCGGAAGAAGCTGGTCTATTGTCGAGCCCTCATGGCCACAGC 4130

RESULT 11
AAD14910
ID AAD14910 standard; cDNA; 3660 BP.
XX
AC AAD14910;
XX
DT 01-NOV-2001 (first entry)
XX
DE Human transporter-related protein #23 cDNA.
XX
KW Human; transporter-related protein; metabolite transporter;
KW organic cation transporter; multi-drug resistance; MDR; gene therapy;
KW cellular transporter; sodium-glucose cotransporter; diagnosis; screening;
KW symptomatic; phenotypic manifestation; biological condition; ss.
XX Homo sapiens.
XX
FH Key
FT CDS
FT Location/Qualifiers
FT 1..3660
FT /tag= a
FT /product= "Human transporter-related protein"
FT /transl_except= (pos:3025..3039, aa:Thr-Thr)
FT /transl_except= (pos:3370..3372, aa:Xaa)
FT /note= "Xaa can be any amino acid"
XX
XX WO200157214-A2.
XX
PD 09-AUG-2001.
XX
PF 02-FEB-2001; 2001WO-US03646.
XX
PR 03-FEB-2000; 2000US-0179973.
PR 14-FEB-2000; 2000US-0182422.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Wang X, Abuin A, Friedrich G, Zambrowicz B;
PI Sands AT;
XX
XX WPI; 2001-514599/56.
DR P-PSDB; AAB08076.
XX
XX Novel polynucleotides encoding novel human proteins with structural
XX similarity to cellular transporters for the diagnosis of disease and
XX use in gene therapy -
PS Disclosure; Page 64-65; 91pp; English.
XX
XX The present sequence is a human transporter-related protein cDNA.
XX The human transporter-related protein share structural similarity with

CC mammalian metabolite or organic cation transporters, multi-drug
CC resistance (MDR) proteins, mammalian sodium-glucose cotransporters and
CC other cellular transporters. The transporter-related protein DNA may be
CC used for the detection of mutant sequences or inappropriately expressed
CC sequences for the diagnosis of disease. They may also be used to screen
CC for drugs effective in the treatment of the symptomatic or phenotypic
CC manifestations of perturbing the normal functions of the sequences of the
CC invention in the body. They may also be used in gene therapy for treating
CC biological conditions.

XX
SQ Sequence 3660 BP; 920 A; 915 C; 943 G; 881 T; 1 other;

Query Match 13.0%; Score 759.4; DB 22; Length 3660;

Best Local Similarity 52.9%; Pred. No. 2.2e-173;

Matches 1911; Conservative 0; Mismatches 1571; Indels 129; Gaps 8;

QY 421 ACCCGTGGATGATGCGGGCTACTCTCTCGCCACATTTTCTGGCTCAGCGCGGTGA 190
DB 131 ACCCGTGGATGATGCGGGCTACTCTCTCGCCACATTTTCTGGCTCAGCGCGGTGA 190
QY 481 CCCGTGTGCCACAAAGAGGGAGCTCTCAATGGAAGACGTGTGCTCTGTCTCAAGC 540
DB 191 TGGTGAAGGCTACCGGCAAG--GCTACCGGTAGACACCTGCCCCATTTGTGACAT 247
QY 541 ACGAGTCTCTGACGTGAATCGAGAAGACTAGAGAGACTGTGGCAAGAGAGCTGAATG 600
DB 248 ATGACTCATCTGACACCAATGCAAAAGATTTTCGAGTCTTTGGGATGAAGAGGTAGCAA 307
QY 601 AAGTTGGGCCACAGCGTCTCCCTCGGAGGGTGTGTGGATCTTCTCCGCGACAGCG 560
DB 308 GGGTGGGCTCTGAGAAGGCTCTCTGAGCCAGCTGTGTGGAATTTCCAGAGGACACGG 367
QY 661 TCATCTGTGCCATGTGTGCTGTGATCACGACGTGCTGCTCTAGTGACACAGCCT 720
DB 368 TGTGTGACATCTGTGCCACATCTGTGATCATATGACGACCATAGGCGCGACAG 427
QY 721 TCATGTTGAACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCACTACAGCT 780
DB 428 TTCTCATTTACCAAAATCTCCAGCAGACTGAGAGACCTCTGGGAAAGTCTGGTTGGCA 487
QY 781 TGTGTGTAGTGTGGGCTCTCTGACGGAATCGTGGGCTTGTGGCTGTGACTGA 840
DB 488 TTGGACTGTGCATAGCCCTTTTGGCCAGCGAGTTTACCAGAGCTCTCTTTGGGCGCT 547
QY 841 CTTGGGCTTGAATTTACGAAACGGTGTCCGCTTGGGGGGCCATCTCTAACCATGGCAT 900
DB 548 CTGGGCCATCACTACCGCAGGCGATCGGTTGAAGTGGCGCTCTCCACCTTGGTTT 507
QY 901 TTAAGAAGATCCTTAAGTTAAGAACATTAAGAGAAATCCCTGGGTGAGCTCATCAACA 960
DB 608 TTGAAAACCTAGTGTCTTCAAGACATTTGACCCACATCTCTGTTGGGAGGTGCTCAATA 667
QY 961 TTTGTCTCAACGATGGGAGAGAAATTTGAGGAGCAGCGCTTGGCAGCCTGTGGCTG 1020
DB 668 TACTGTCAAGTATAGCTATTCTTTGTTGAAGCTGCGCTTGTGTTGCTCTTTGGCAGCA 727
QY 1021 GAGGACCGCTTGTGCCATCTTAGGCATGATTAATATGTAATTTCTGGGACCAACAG 1080
DB 728 CCATCCGATCCTAATGCTCTTTGTGGCGGCTACGCGCTTTTCAATCTGGGGCCACAG 787
QY 1081 GCTTCTGGGATCAGCTGTTTTATCTCTTTTACCAGCAATGATGTTGATCAGCGC 1140
DB 788 CTTCTATCGGATATCAGTGTATGTCATATTCATACCCGTCAGATGTTTATGGCCAAAGC 847
QY 1141 TCACAGATATTTACGAGAGAAATCGGTGGCGGCCACCGATGAAGCTGTCCAGAGATGA 1200
DB 848 TCAATTCAGCTTTTCCGAAGGTACGAATTTTGGTGACAGACAAGCGAGTTCCAGACAATGA 907
QY 1201 ATGAAGTTCTTACTTACATTAATTTATCAAAATGTATGCTGCGGTCAAGCATTTTCTC 1260
DB 908 ATGAGTTTCTGACCTGCATCAGGCTGATCAAAATGTATGCTCTGGGAGAAATCTTTTACA 967
QY 1261 AGAGTGTTCAAAAAATCCGCGAGGAGGAGCGTGGATATTGGAAAAAAGCCGGTACTTCC 1320

DB 968 ACATATCCAAAGATATAAAGAGGAGGAAAGAAATTTACTGGAAAGAGCTGGATTTCTCC 1027
QY 1321 AGGTATCATCTGTGGTGTGGCTCCCATTTGTGTGGTGAATTCAGTGGTGGTACCTTCT 1380
DB 1028 AAGTGGAAACTGTGGCTGGCGCCCATCTGTGCCACATAGCATCTGTGCTGACATAT 1087
QY 1381 CTGTTTATATGACCTGTGGCTTCGATCTGACAGCAGCAGAGGCTTTCACAGTGGTGACAG 1440
DB 1088 CTGCGCACATCTCTGAGACGCAAACTCACCGACCCGTGGCATTTAGTGTGATGCCA 1147
QY 1441 TCTTCAATTCATGACTTTTGTCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAG 1500
DB 1148 TGTTAATGTAATGAAGTTTTCATTTGCCATCTTGGCTTCTCCATCAAGAAATGCGCTG 1207
QY 1501 AAGCCTCAGTGGCTGTGACAGATTTAAGAGTTTGTGTTCTTAATGGAAGAGGTTTCACATGA 1560
DB 1208 AAGCGAATGTCTCTTAAGAGAAATGAAGAAATTTCTATAGATAAAAGCCGCCATCTT 1267
QY 1561 TAAAGAACAAACAGCAGCTCTCACATCAAGATAGAGATGAAGATGAAGATGCAACCTTGGCAT 1620
DB 1268 ACATACCCAAACAGAGACCCAGATCTGTCTTGTCTTTAGCAAAATGCGCACCTTGACAT 1327
QY 1621 GGGACTCTCTCCACTCCAGTATCCAGAACTCGGCCCAAGCTGACCCCAATGAAGAAAG 1680
DB 1328 GGG-----AGCATGAAGCCAGCAGGAAAGTA 1354
QY 1681 ACAAGAGGCTTCCAGGGGCAAGAAAGAGAGTGAAGGAGCTGACGCGCACTGAGCATC 1740
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QY 1741 AGCGGTGTGGCAGAGCAGAGAGGACCTCTCTCTGGACAGTGAAGCGGCGCCAGTC 1800
DB 1411 -----GCATAGCTGAGAGGAGTCCACC-----AGCAAGGAGGAGCCACTG 1450
QY 1801 CCAGAGGAGAAAGGCAAGCAGCATCCACTGGGCCACCTGCGCTTACAGAGGACACATGC 1860
DB 1451 GCCCAGAGGAGCAAGTGAAGAGCTCAATTCG-----TTCGTC 1489
QY 1861 ACAGCATCATCTGGAGATCCAGAGGGTAAACTGGTGAATCTCGGGCAGTGTGGGAA 1920
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QY 1921 GTGAAAAACCTCTCTCATTTTCAGCCATTTTAGCCAGATGACGCTTCTAGAGGCGAGCA 1980
DB 1550 GTGGAAGAGCTCCCTCTCTGAGCTCTCTAGACAGATGACGCTGACAGAAAGGGTGG 1509
QY 1981 TTGCAATCAGTGGAACTTCTGCTTATGTGGCCAGCAGGCTTGATCTCTCAATGCTACTC 2040
DB 1610 TGGCACTCAATGGAACCTTTGGCCTACGTTTCACAGCAGGCACTGATCTTTTCATGGAATG 1669
QY 2041 TGAGACACAACATCTCTGTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGA 2100
DB 1670 TGAGAAAAACATCTCTTTGGGAAAAAGTATGATCAACCAAGGATATCAGCAGACAGTCC 1729
QY 2101 ACAGCTGTCTGCTGAGCCTGACCTGCGCATCTTCCAGCAGCAGCCTGACGAGATG 2160
DB 1730 GGTCTGTGGCTCCAGAGGACCTGAGCACTCCCTCTATGGAGACCTGACGTGAGATTG 1789
QY 2161 GAGAGGAGGAGCCACCTGAGCGTGGGAGCGCCAGCGAGGATCAGCCTTGGCCGGGCT 2220
DB 1790 GGGAGGGGGCTCAACCTCTCTGSGGGCAGAGGAGGATGATGCTGGCGCGCTG 1849
QY 2221 TGTATAGTACAGGAGCATCTACATCTCTGGAGACGCCCTCAGTCTAGTGTAGTGCCCATG 2280
DB 1850 TCTACTCCAGCGCTCAGCTCTACCTCTGTGAGCAGACCCCTGTGGCGCTGGAGCGCCAG 1909
QY 2281 TGGGAACACATCTTCAATAGTGTCTATCCGGAACATCTCAAGTCCAGACAGATTTCTGT 2340
DB 1910 TGGGAGACAGCTCTTTGAGGAGTGCATTTAAGAGACGCTCAGGGGAAAGACAGTCTGTC 1969
QY 2341 TTGTTACCCACAGTGTACAGTACCTGTTGACTGTGTGATGAAGTGTCTTCAATGAAGAGG 2400

Db 1970 TGGTGACCCACAGCTACAGTCTTGTAGAGTCTTGTGATGAAGTATTATTTATTAGAAGATG 2029
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QY 2521 AAACAGTGGTTCACAGAAGAAGTAC-----AAGACAGGGTCCCTAAACACAGAT 2571
Db 2150 CAATGGTGAAGCCTTCAAGAGAGAGCCCTGCTGAGAGAGAGGAAGATGCTGTTTGGCTC 2209
QY 2572 CACTAAGAGGAAAGCAGTAAGCCAGAGAGG----- 2609
Db 2210 CAGGAATGAGAAGATGAAGGAAAGAAATCTGAACAGAGCTCAGAAATTTAGACACAA 2269
QY 2610 -----CAGCTTGTGAGCTGGAAGAGAAAGGCGAGGTTTCAGTGCCCTGGT 2655
Db 2270 AAGTTCTGAGCAGCTATCCAGCTGAATCCCCAGGAGGAAACGTCGACCTGGA 2329
QY 2656 CAGTATATGCTGTACATCAGGCTGCTGGGGGCCCTTGGCATTCCTGGTTATTATGG 2715
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QY 2716 CCGTTTTCATGCTGAATGTAGGAGACACCGCTTACGACCTGCTGGTGTGAGTTACTGGA 2775
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QY 2776 TCAAGCAAGGAAAGCGGACACACCTGTGACTCGAGGAACGAGAC-----TCGGTGAGTG 2832
Db 2450 TGGACAAGGCTCAGGATGACATGTGGGCCCCAGGCAACAGACCATGTGTGAGTGC 2509
QY 2833 ACAGTATGAAGGACAACTCTCATATGACGACTATGCCAGCATCTAGCCCTCTCCATGG 2892
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QY 2893 CAGTATGCTGATCCTGAAAGCCATTCGAGGAGTTGTTTGTCAAGGGCAGCTGCGAG 2952
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QY 3013 TTGACACGACCCACAGGAGGATTTCTCAACAGGTTTCCAAAGACATGGATGAAGTTG 3072
Db 2690 TTGACACGACTCCACTGGCAGGCTAATGAACGGTTTTCGAAGGATATGGACGAGCTGG 2749
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Db 2750 ATGTAGGCTGCGGTTTCAGCAGAACTTTCTGACGAGATTTTATGGTGGTGTGTTA 2809
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Db 2810 TTTCTGTGATCTGGCTGTGTTTCTGCTCTCTTTAGTCGTGGCCAGCTTGTCTG 2869
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Db 2870 TAGGCTTCTTCTGTTACGATTTTCCACAGAGGAGTCCAGGAGCTCAAGAAGTGG 2929
QY 3253 ACATATCAGCAGTACCTTTCTCTCCACATACGATCCAGCATACAGGGCTTCCCA 3312
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QY 3433 ACCTCATCAGCATCCCTCTATCACCACCACGGGCTGATGATCTTCTTATGACGGGC 3492
Db 3110 ATGCTCTCATGAACATCCTTACCTTCACTGTGGCTTGTGTGACCTGAGTTTCTCT 3169
QY 3493 AGATTCCCCAGCCTATCGGGTCTCGCATCTCTTATGCTCTCCAGTTAACGGGCTGT 3552
Db 3170 CCATCAGTACTTATCCAAAGCCCTGTCATTGTCTATCATCATCCAGCTGACGGACTGC 3229
QY 3553 TCCAGTTTACGCTCAGACTTGCATCTGAGACAGAAGCTCGATTCACCTCGTGGAGAGA 3612
Db 3230 TCCAAGTGTGTGCGAACGGGAACAGACAGCAAGCCAAATTACCTCCGTGGAGCTGC 3289
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QY 3913 TTGCGGACCTCCGAAGCAAACTCTATCATCTCTCAAGAGCCGCTGTGTTCACTGGCA 3972
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QY 3973 CTGTCCAGATCA 3983
Db 3650 CAGTAAGATAA 3660

RESULT 12

AAD36023
ID AAD36023 standard; cDNA; 4074 BP.

XX AAD36023;

DT 09-AUG-2002 (first entry)

XX Human adenosine triphosphate-binding cassette protein cDNA #1.

DE Human; adenosine triphosphate-binding cassette; chemoprotectant; ATP;
XX ABC protein; gene therapy; breast proliferative fibrocystic disease;
KW breast adenocarcinoma; drug resistance; breast disorder; transgenic;
KW vaccine; gene; ABCP; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..3996
FT /*tag= a
FT /product= "Human ABC protein"

XX WO200224742-A2.

XX 28-MAR-2002.

XX 20-SEP-2001; 2001WO-US29455.

XX 22-SEP-2000; 2000US-0668628.

XX (INCY-) INCYTE GENOMICS INC.

2160 GGAGAGCAGGAGCCAACTGAGCGGTGGCGAGCCGAGAGGATCAGCCTTCCCGGGCC 2219
1729 GGAGAGCGGGCCTCAACTCTCTGGGGGGGAGAAACAGAGGATCAGCCTGCGCCGGCC 1788
2220 TTGTATAGTACAGAGGAGATCATCTCTGGACGACCCCTCAGTGCCTTAGATGCCCAT 2279
1789 GTCTATTCCGACCGTCAGATCTACCTGCTGGACGACCCCTCTCTGCTGTGGACGCCAC 1848
2280 GTGGCAACCAATCTTCAATAGTGTATCCGGAACATCTCAAGTCCAAAGACATTTG 2339
1849 GTGGGAAGACATTTTGGAGAGTGCATTAAGAAAGACACTCAGGGGAAGACGGTCTGTC 1908
2340 TTGTGTACCCACCACTTACAGTACCTGCTGACTGTGATGAAGTCACTTTCATGAAGAG 2399
1909 CTGGTACCCACCACTGCTGACTTGAATTTTGTGGCCAGATCATTTTGTGGAAAT 1968
2400 GGCTGTATTACGGAAGAGGCCATCCATGAGGAACCTGATGAATTTAAATTTGGTACTGCT 2459
1969 GGGAAATCTGTGAAATGGAACCTCACAGTGAAGTTAATGACAGAAAAGGGGAAATATGCC 2028
2460 ACCATTTTAAATACCTGTTGCTGGGAGAGACACCGCCAGTGTAGATCAATTTCAAAAAG 2519
2029 CAACCTATCCAGAGATGCACAAGGAAGCCACTTCCGACATGTTTCAGGACACAGCAAG 2088
2520 GAAACCACTGTTTACAGAAGAGTCAACAAGAACAGGTCCTTAAACAGGATCACTAAAG 2579
2089 ATAGCAGAGAACCAAGGTAGAAAGTCAGGCTTGGGCCACCTCCCTGGAAGAGTCTCTC 2148
2580 AAGGAAAAGCAGTAAAGCCAGAGGAGGAGCTTGTGCTGAGGAGAAAGGGGAG 2639
2149 AAGGAAATGCTGT-----GCCGAGCATCAGCTCACAGGAGGAGGAGATGAAGAA 2202
2640 GGTTCAGTCCCTGCTGATATATGTTCTATATCCAGAGTGTCTGAGGAGGAGGAGGAGG 2699
2203 GGCTCCTTGTGAGTGTGAGGAGTGTACACCACTACATCCAGGAGCTGAGGAGTGTGTC 2262
2700 TTCTGCTGTTATATGAGGCTTTTCTGATGCTGAATGTAGCAGCAGCCCTTACAGACCTGG 2759
2263 TCTTGCATAAATTTCTTCTGTTGCTGATGCTCTTCTTAAACGATCTTCAAGCTTCGG 2322
2760 TGGTTGAGTTACTGATCAAGAAAGGAGGAGGAGCTTGTGCTGAGGAGGAGGAGGAG 2819
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2820 ACTCGGTGAGT---GACAGATGAGGAGCAATCTCTATATGCACTACTATGCCAGATC 2876
2383 ACCATGGCAGACCTGGGCAACATTCAGACAAATCTCAACTGTCTCTTACAGCTGTGTG 2442
2877 TAGCCCTCTCCATGGCAGTCACTGATCTCTGAAAGCCATTCGAGGAGTGTCTTTGTC 2936
2443 TAGGGCTCAAGCCCTGCTCTCATCTGTGTGGGGTCTGCTCTCAGGATTTTCACC 2502
2937 AAGGCGAGCTCGAGCTTCTCCCGGTGCTGATGACGAGCTTTTCCGAGGATCTCTGGA 2996
2503 AAGGTCAGGAGGAGGATCCAGGCTCCGACCAAGCTCTTCAACAAGGTTTTCGC 2562
2997 AGCCCTATGAAGTTTGTGACAGACCCACAGGAGGATTTCTCAACAGGTTTTCAAA 3056
2563 TGCCCCATGAGTTTCTTTGACACCAATCCCAATAGGCGGCTTTTGAATGCTTCGAGG 2622
3057 GACATGATGAGTGTAGCTGGCTGCTGCTTCCAGGCGGAGATCTTCAACAGACGTT 3116
2623 GACTTGGAAAGCTGGAGCAGCTCTTGGCCATCTTTTTCAGAGCAGTCTCTGGTCTGTC 2682
3117 ATCTGTTGTTCTTCTGTGGGATGATCGCAGGAGTCTTCCCGTGGTCTCTGTGGCA 3176
2683 TTAATGGTATCGCGCTCTGTGATTTCTAGTGTCTCTCCATATATCTCTGTTAATG 2742
3177 GTGGGCCCCCTTGTATACCTCTTTTGTGCTGTGACATGTCTCAGGAGTGTCTGATTCGG 3236
2743 GGAGCCATAATCATGGTTATTTGTTTCAATTTATATATGATGTTTCAAGAGGCCATCGT 2802
3237 GAGCTGAGGCTGTGGCAATATACCGCAGTCACTTTCTCTCCCATCAGTCCAGC 3296

2803 GTGTTCAAGAGACTGGAGACTATAGCCGGTCTCTTTATTTCCCATCTCTCAATTCT 2862
3297 ATACAGGGCCTTCCACCATTCCAGCCTTACAATAAAGGCGAGGAGTTTCTGCACAGATAC 3356
2863 CTGCAAGGCTGAGCTCCATCCATGCTATATGGAATAACTGAAGACTTTCATCAGCCAGTTT 2922
3357 CAGGAGCTCTGGATGACAAACCAAGCTCTCTTTTGTGTTAGTGTGGGATGCGGTGG 3416
2923 AAGAGGCTGACTGATGCGCAGAAATAACTCTGCTGTTGTTTCTTCTTCCACACGATGG 2982
3417 CTGGCTGTGCGCTGACCTCTCATCAGATCGCCCTCATCACCAACGAGGGGCTGATGATC 3476
2983 ATGGGATTCAGGCTGGAGATCATGACCAACCTTGTGACCTTGGCTGTTGCCCTTGTGCTG 3042
3477 GTTCTTATCACGGGAGATTTCCCGAGCCTATCGGGTCTCGCCATCTCTTATGCTGTC 3536
3043 GCTTTTGGCATTTCTCCACCCCTACTCTCTTTAAAGTCATGCTGTCAACATCGTCTG 3102
3537 CAGTTAACGGGCTGTTCCAGTTTACGTCAGACTGGCATCTGAGACAGAGCTCGATTC 3596
3103 CAGCTGGCTCCAGCTTCCAGGCCACTGGCCGATTTGGCTTGGAGACAGAGGCACAGTTC 3162
3597 ACCTGGTGGAGAGGATCAATCACTACATTAAGACTCTGCTTGAAGACACCTGCCAGA 3656
3163 ACGGCTGTAGAGAGATCTGACATGATGAAGTGTGCTCGGAAGCTCTCTTTACAC 3222
3657 ATTAAGAACAAAGCTCCCTCCCTGACTGGCCCCAGGAGGAGAGTGTGACCTTTGAGAAC 3716
3223 ATGGAAGGCACAAGTTGTCCAGGGGTGGCCACAGCATGGGAAATCATATTTTCAGAT 3282
3717 GCAGAGATCAGGTACCGAGAAAACCTCTCTTGTCTCTTAAAGAAAGTATCTTACAGATC 3776
3283 TATCATATGAATAACAGAGACAAACACACCCACCGCTCTCACGGCATCAACCTGACCATC 3342
3777 AAACCTAAAGAAAGATTTGCGATTTGGGCGGACAGGATCAGGAGTCTCTCGCTGGGG 3836
3343 CCGGGCCAGAGTGTGGGATCTGTGGAGAGACGGGCTCTGGGAAGTCTCTCTTGGGC 3402
3837 ATGGCCCTCTCCGCTGTGTGGAGTTATCTGGAGGCTGCATCAAGATTTGATGAGTGA 3896
3403 ATGGCTCTCTCCGCTGTGGAGCCCATGCGAGCGGATTTCTCATTTAGCGCGTGGAC 3462
3897 ATCAGTGTATTTGGCTTCCGACCTCCGAGCAAACTCTCTATCATTTCTCAAGAGCG 3956
3463 ATTTGAGCATCGGCTGGAGGACTTGGCGTCCAGCTCTCTCAGTGTATCCCTCAAGATCCA 3522
3957 GTGCTGTTTCACTGGCAGTCTCAGATCAAAATTTGGACCCCTTCAACAGTACACTGAAGAC 4016
3523 GTGCTGCTCTCAGGAACCATCAGATTCACCTAGATCCCTTTGACCGTCACTGACCAG 3582
4017 CAGATTTGGATGCCCTGGAGAGGACACATGAAAGAATGTATTTGCTCAGTACCTCTG 4076
3583 CAGATCTGGATGCCCTTTGGAGAGGACATCTCTGACCAAGGCCATCTCAAAGTTTCCCAA 3642
4077 AAACCTGAATCTGAAGTGTGAGAGATGGGATAACTCTCAGTGGGGAACGGCAGCTC 4136
3643 AAGCTGCATACAGATGTGGTGGAAAACGGTGGAAACTTCTCTGTGGGAGAGGAGCTG 3702
4137 TTGTGCATAGCTAGAGCCTGCTCCGCCACTGTAAAGATTTCTGATTTTATAGATGAAGCCACA 4196
3703 CTCTGATTTGCCAGGGCTGTGCTTCGCACTCCAGATCATCTCTTATTCATGAAGCCACA 3762
4197 GCTGCATGGACAGACAGACACTTTATTTCAAGAGACCATCCGAGAAGCATTTTGA 4256
3763 GCCTCCATTCAGATGGAGACAGACACCTGATCCAGGCAACATCCGTGAAGCTTCCAG 3822
4257 GACTGTACCATGCTGACCATTTGCCATCGCCTGCACAGGTTTCTAGGTCCTCGATGATT 4316
3823 GGCTGACCGCTGCTGCTCATTTGCCACCGTGTCAACACTGTGTAACCTGTGACCGCATC 3882
4317 ATGGTGTCTGGCCAGGACAGGTTGGAGTTTTCACACCCCTCTCTCTCTGTCACAC 4376

Db 3883 CTGGTTATGGCAATGGGAAGTGGTAGAATTTGATCGCGGAGTACTGCGAAGAAG 3942
QY 4377 GACAGTTCGGGATCTATGCAATGTTGCTGCTGC 4411
Db 3943 CTTGGGTCTATGTTCCGAGCCCTCATGGCCACAGC 3977

RESULT 13
AAD14911
ID AAD14911 standard; cDNA; 3753 BP.
XX
AC AAD14911;
XX
DT 01-NOV-2001 (first entry)
DE Human transporter-related protein #24 cDNA.
XX
KW Human; transporter-related protein; metabolite transporter;
KW organic cation transporter; multi-drug resistance; MDR; gene therapy;
KW cellular transporter; sodium-glucose cotransporter; diagnosis; screening;
KW symptomatic; phenotypic manifestation; biological condition; ss.
XX
OS Homo sapiens.
XX

Key Location/Qualifiers
CDS 1..3753
FT /*tag= a
FT /product= "Human transporter-related protein"
FT /transl_except= (pos:3025..3039, aa:Thr-Thr)
FT /transl_except= (pos:3370..3372, aa:Xaa)
FT /note= "Xaa can be any amino acid"
XX
XX WO200157214-A2.
XX
XX 09-AUG-2001.
XX
XX 02-FEB-2001; 2001WO-US03646.
XX
XX 03-FEB-2000; 2000US-0179973.
XX 14-FEB-2000; 2000US-0182422.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Turner CA, Mathur B, Wang X, Abuin A, Friedrich G, Zambrowicz B;
PI Sands AT;
XX
XX WPI: 2001-514599/56.
XX P-PSDB; AAE08077.
XX
XX Novel polynucleotides encoding novel human proteins with structural
PT similarity to cellular transporters for the diagnosis of disease and
PT use in gene therapy
XX
XX Disclosure; Page 68-70; 91pp; English.
XX
XX The present sequence is a human transporter-related protein cDNA.
CC The human transporter-related protein share structural similarity with
CC mammalian metabolite or organic cation transporters, multi-drug
CC resistance (MDR) proteins, mammalian sodium-glucose cotransporters and
CC other cellular transporters. The transporter-related protein DNA may be
CC used for the detection of mutant sequences or inappropriately expressed
CC sequences for the diagnosis of disease. They may also be used to screen
CC for drugs effective in the treatment of the symptomatic or phenotypic
CC manifestations of perturbing the normal functions of the sequences of the
CC invention in the body. They may also be used in gene therapy for treating
CC biological conditions.
XX
XX Sequence 3753 BP; 949 A; 937 C; 965 G; 901 T; 1 other;
SQ

Query Match 12.9%; Score 753.2; DB 22; Length 3753;
Best Local Similarity 52.9%; Pred. No. 7.1e-172;
Matches 1900; Conservative 0; Mismatches 1563; Indels 129; Gaps 8;

QY 421 ACCCAGTGGACAATGCTGGGCTTTTCTCTGTATGACTTTTTCGTGGCTTTCTTCTCTGG 480
Db 131 ACCCGTGGATGTCGGGCTACTCTCTTCGCCACATTTTCTTGGCTCAGCCGGTGA 190
QY 481 CCCGTGTGGCCACAAGAAGGGGAGCTCTCAATGGAAAGAGTGTGTCTCTGTCCAAGC 540
Db 191 TGGTGAAGGCTACCGGCAAG--GCTGACCGTAGACACCTGCCCCCTGTCGACAT 247
QY 541 ACAGTCTTCTGACGTGAACTGCAGAAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATG 600
Db 248 ATGATCATCTGACACCAATGCCAAAGATTTCGAGTCTTTGGGATGAAGAGGTAGCAA 307
QY 601 AAGTTGGCCAGAGCGCTGCTTCCCTGCGAAGGTTGTGTGATCTTTCGCCACACAGGC 660
Db 308 GGGTGGTCTGAGAGGCCCTCTCTGAGCCACGTGTGTGAAATTCAGAGGACACGG 367
QY 561 TCATCTGTCTGATCGTGTGCTGATGATCATGACGAGTGGCTTTCAGTGACACAGCT 720
Db 368 TGTGTGATGGACATCGTGCCCAACATCTCTGTCATCATGCGAGCCATAGGGCCGACAG 427
QY 721 TCATGGTGAACACCTCTTGGAGTATACCCAGGCAACAGAGCTTAACCTGCAGTACAGCT 780
Db 428 TCTCATTCACCAATCTCCAGCAGACTGAGAGGACCTCTGGGAAAGTCTGGGTTGCA 487
QY 781 TGTGTGTAGTCTGGGCTCTCTCTGACGGAATCGTGGCTTCTTGGTCGCTTGCACTGA 840
Db 488 TTGGACTGTGCATAGCCCTTTTTCGCCAGGAGTTTACCAAGTCTCTTTTGGGCCCTTG 547
QY 841 CTTGGGATTAATTAACCGAGTGTCTGCTTTCGGGGGGCCATCTTAACCATGGCAT 900
Db 548 CTTGGGCTCACTACCTACCGCACGCCATCCGTTGAAGTGGCGCTCTCCACCTTGGTTT 607
QY 901 TTAAGAGATCCITTAAGTTAAAGAACATTAAGAGAAATCCCTGGGTGAGCTCATCAACA 960
Db 608 TTGAAGACCTAGTGTCTCTCAAGACATTTGACCCACATCTCTGTGGCGAGGTGCTCAATA 667
QY 961 TTTGCTCCAAACGATGGGCGAGAGAAATGTTGAGCGAGACAGCGCTTGGCAGCTGTGGCTG 1020
Db 668 TACTGTCAAGTGATAGTATTTCTTTTGTGAAGTGGCTTGTCTTGTCTTGGCAGCA 727
QY 1021 GAGGACCGGTTGTGGCCATCTTAGGCATGATTTATAATGTAATTTCTGGGACCAACAG 1080
Db 728 CCATCCCGATGCTTAATGGTCTTTTGTGGCGGTACGGCTTTTTCATCTGGGCGCCACAG 787
QY 1081 GCTTCTCCGGATCAGCTGTTTATCTCTTTTACCCAGCAATGATGTTTCCATCAGCGC 1140
Db 788 CTCTCATCGGATATCAGTGTATGTCATATTCATCCCGTCCAGATGTTTATGGCAAG 847
QY 1141 TCACAGCATATTTACGAGAAATTCGTCGCCGCCAGGATGAACGTGTCCAGAAAGATGA 1200
Db 848 TCAATTCAGCTTTCCGAAGGTGAGCAATTTTGGTGACAGACAAGCGAGTTCAGACAATGA 907
QY 1201 ATGAAGTCTTACTTACATTAATTTATCAAAATGATGCTGGGTCAAGCATTTTCTC 1260
Db 908 ATGAGTTCTTGACCTGTCATGAGCTGATCAAAATGATGCTGGGAGAAATCTTTTACCA 967
QY 1261 AGAGTGTTCAAAATAATCCGCGAGGAGGCTCGGATTTGGAAAAAGCCGGTACTTCC 1320
Db 968 ACATATCAAGATATAAGAAAGGAGGAAGAAATTAATCTGGAAGAAAGCTGGATTTGTCC 1027
QY 1321 AGGATATCAGTGTGGGTGTGGCTCCCATTTGGTGTGATTCGCCAGGTGTGGACCTTCT 1380
Db 1028 AAAGTGAATACTGTCCCTGCCCCCATCGTGTCCACCATAGCCATCGTGTGACATTAT 1087
QY 1381 CTGTTTATATGACCTCGGCTTCGATCTGACAGACAGCAGGCTTTCACAGTGTGACAG 1440
Db 1088 CTTGCCACATCTCTCTGAGACGCAAACTCACCGCACCGCTGGCATTTAGTGTGATGCA 1147
QY 1441 TCTTCAATTCATGACTTTTGTGCTTTGAAAGTAAACACCGTTTTCAGTAAAGCTCCCTCAG 1500
Db 1148 TGTTTAAATGAAGTGTTCATTTCCATTTGCGCTTCTCCATCAAGAAATGGCTG 1207
QY 1501 AAGCCTCAGTGGTGTGACAGATTTAAGAGTTTGTGTTTCTAATGAAGAGGTTTCACATGA 1560

Db	2210	CAGGAATATGAAAGATGAAGGAAGAATCTGAACAGGCTCAGAAATTTGTAGACACAA	2269
Qy	2610	-----CAGCTTTGTCAGCTGGAAAGAAAGAGGCGAGGTTTCAGTGCCTGGT	2655
Db	2270	AAGTCTTCGAGCACCAGCTCATCCAGACTGAATCCCTCCAGGAAGAACCGTGACCTGGA	2329
Qy	2656	CAGTATATGGTGTCTACATCCAGGTGCTGGGGGCCCTTGGCACTCTCGTTATTATPGG	2715
Db	2330	AAACATATACACAGTACATTAAGGCTTCTGGAGGTAAGTCTCTCTTCATCTGCTGT	2389
Qy	2716	CCCTTTTCATGCTGAATGTAGGCAGACAGCCCTTCAGACACCTGGTGTGAGTTACTTGGA	2775
Db	2390	TCCTCTCTCTCTGATGATGGCAGCGCTCCCTTCAGAACTTTGGTGTGGCTTCTGGT	2449
Qy	2776	TCAAGCAAGGAAGCGGAACACACTGTGACTCGAGGGAACGAGACC--TCGGTGAAGTG	2832
Db	2450	TGGACAAGGCTCACGGATGACCTGTGGGCCCCAGGGCAACAGGACCATGTCTGAGTCTG	2509
Qy	2833	ACAGCATGAAGGACAACTCTCATATGCTAGTACTATGCGCAGCATCTACGCCCTCTCCATP	2892
Db	2510	GCAGCGTGTGGCAGACATCGGTTCAGCACTGTACCAAGTGTGAGTGTGCTGCTCAAGCA	2569
Qy	2893	CAGTCATGCTGATCCTGAAGCCATTCGAGGAGTTGCTTTGTTCAAGGGCAGCTGCGAG	2952
Db	2570	TGTTTCATGCTGGTGTGGCGTACCAAGGCTCTGCTCTACCAAGACCAACACTGATGG	2629
Qy	2953	CTTCTCTCCGGCTGCATGACGAGCTTTTCCGAAGGATCTCTCGAAGCCCTATGAAGTTT	3012
Db	2630	CATCCTCTCTCTGATGACACGGTGTGTGATAAGATCTTAAAGAGCCCAATGAGTTTCT	2689
Qy	3013	TTGACACGACCCCCACAGGAGGATTTCTCAACAGSTTTTCCAAAGACATGGATGAAGTTG	3072
Db	2690	TTGACACGACTCCACTGGCAGGCTAATGAACCGTTTTTCCAAAGATATGAGCAGCTGG	2749
Qy	3073	ACGTGGGCTGGGTTCCAGGCGGAGATTTCTATCCAGAGCTTATCTCGTGTGTTCTTCT	3132
Db	2750	ATGTGAGGTCGGGTTTTCAGCAGAGAACTTTCTCAGCAGTTTTTATGTTGGTGTGTTA	2809
Qy	3133	GTGTGGAAATGATCGCAGGAGCTTCCCGTGGTCTCTGTGTCAGTGGGGCCCTTGTC	3192
Db	2810	TTCTCTGATCTTGGCTGTGTGTTTCTGTGCTCTTCTTGTAGCTGGCCAGCCTTGC	2869
Qy	3193	TCCTCTTTTCAGTCCCTGCACATGTCTCCAGGGTCTCTGATTCGGGAGCTGAAGGCTCG	3252
Db	2870	TAGGCTCTTCTATCTCTGTTACGCATTTTCCACAGAGGAGTCCAGSAGCTCAAGAAGTGG	2929
Qy	3253	ACAATATCAGGATCAGCTTTCTCTCTCCACATCAGCTCCAGCATACAGGGCCTTGCCA	3312
Db	2930	AGAATGTACGCGGTGACCCCTGGTTACCCACATCACCCTCTCCATGCAAGGCGCTGGCA	2989
Qy	3313	CCATCCACGCTACAAATAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTGCTGGATG	3372
Db	2990	TCATTACGGCTATGCAAGAGGAGAGCTGCATCACCTAGTTTAAAGACGCTAAACGACG	3049
Qy	3373	ACAACCAAGCTCCTTTTTTTTTTTTACGTGCGATCGGTGGCTGGCTGTGCGGCTGG	3432
Db	3050	AAAACCTCAGTCACTCCCTCTACTTTAACTGTGCTCTCAGGTGGTTTTCGCTGAGAA	3109
Qy	3433	ACCTCATCAGCATCGCCCTCATCACCCACCGGGCTGATGATCGTTCTTATGCAACGGG	3492
Db	3110	ATGTCTCTATGAACATPCTTACTCTTCACTGTGGCCTCTGTTGGTACCCTGAGTTTCT	3169
Qy	3493	AGATTCGCCAGGCTATGGGGTCTCGGCATCTCTTATGCTGTCCAGTTAAACGGGCTGT	3552
Db	3170	CCATGACTACTTCAATCCAAAGGCTGTCTATGTCTATACATCATCCAGCTGAGCGGACT	3229
Qy	3553	TCAGGTTTACGGTTCAGACTGGCATCTGAGACAGAAGCTCGATTCACTTCGGTGGAGAG	3612
Db	3230	TCCAAAGTGTGTGGCAACGGGAACAGAGACGAAGCCAAATTCACCTCCGTGGAGCTG	3289
Qy	3613	TCATCACTACATATTAAGATCTGTCTCTGGGAAGACCTTGCACGAATTTAAGAACAAAG	3672
Db	3290	TCAGGAATATCAATTTTCGACCTGTGTCTCTGAAATGACATCACTCCCTCAAGTGGG	3349

Db 1000 GGTGGCTGAGCTACTGTTGGAGCAGGCTCGGGGACCAATAGCAGCGCAGAGAGCAATG 1059
QY 2818 AGACC---TCGGGTGAGTGACAGCATGAAGACAACTCTCATATGACGTACTATGCCAGCA 2874
Db 1060 GAACCATGGCAGACCTGGGCAACATTCGACAACTCTCAACTGTCTTCTACAGCTGG 1119
QY 2875 TCTACGCCCTCTCCATGGCAGCTATGCTGATCTGTAAGGCCATTCGAGGAGTTGCTTTG 2934
Db 1120 TGTACGGGCTCAAGCGCTCTCTCTCATCTGCTGGGGTCTGCTCTCAGGGATTTCA 1179
QY 2935 TCAAGGCGCAGCTGCGAGACTTCTCCCGGCTGCAATGACGAGCTTTTCCGAAGGATCTTC 2994
Db 1180 CCAAGGTCACGAGGAGGCACTCCAGCGCTTCGCAACAAGCTCTTCAACAAGGTTTTC 1239
QY 2995 GAAGCCCTATGAAGTTTTCGACAGCAGCCCGCAGAGGAGGATTTCTCAACAGGTTTTC 3054
Db 1240 GCTGCCCATGAGTTCTTTTGACACCAATCCCAATAGGCGGCTTTTGAACGTCTTCGAG 1299
QY 3055 AAGACATGATGAAGTTGACGTGCGGCTCGGCTTCCAGGCGGAGATGTTATCCAGAAGC 3114
Db 1300 GGGACTTGGAAACAGCTGACAGCTCTTGCCCATCTTTTCAGAGCAGTCTCTGGTCTGT 1359
QY 3115 TTATCTGTGTCTCTGTGTGGGAATGATCGCAGGAGTCTTCCCGGTGTTCTGTGG 3174
Db 1360 CCTTAATGTGTATCGCGCTCTCTGTGATTCAGTGTCTGTCTCCATATATCTGTTAA 1419
QY 3175 CAGTGGGCCCCCTGTCATCTCTTTTCAGTCTGCAATGTCCTCAGGCTCTGATTC 3234
Db 1420 TGGAGCCATAATCATGTTTATTGCTTCATTTATATATGATGTTCAAGAAAGGCCATCG 1479
QY 3235 GGGAGCTGAAGCGCTTGGACAATATACGCAGTCACCTTCTCTCCACATCACGTCCA 3294
Db 1480 GTGTGTTCAAGACACTGGAGAACTATAGCGGTCTCTCTTATCTCCCATCTCTCAAT 1539
QY 3295 GCATACAGGCGCTTGCCACCATCCAGCCCTACAAATAAGGCGAGGAGTTCTTGACAGAT 3354
Db 1540 CTCTGAAGCGCTGAGCTCCATCTCATGTCTATGAAAAAAGTGAAGACTTCATCAGCCAGT 1599
QY 3355 ACCAGGAGCTGCTGGATGACAAACAGCTCTTTTCTTTTGTGTACGTGCGGATGGGT 3414
Db 1600 TTAAGAGCTGACTGATGCGCGAGAACTACCTGCTGTGTTTCTATCTTCCACAGAT 1659
QY 3415 GCGTGTCTGCGGTGGAGCTCATCAGCATCGCCCTCATCACACCGCGGCTGATGA 3474
Db 1660 GGATGCAATGAGCTGGAGATCATGCCAACTTGTGACCTTGGCTGTGGCCCTGTTCG 1719
QY 3475 TCGTCTTATGACGGGAGATTCGCCACCGCTATGCGGGTCTGCGCATCTCTTATGCTG 3534
Db 1720 TGGCTTTTGGCAATTCCTCCACCGCTTACTCTTTAAAGTCAATGGCTGTCAACATCTGC 1779
QY 3535 TCCAGTTAACGGGCTGTTCCAGTTTACGTCAGCTGAGATGGCATCGACAGAGAAGCTCGAT 3594
Db 1780 TGACGTGGCGTCCAGCTTCCAGCGCCACTGCCCGGATTTGGCTTGGAGACAGAGGCACAGT 1839
QY 3595 TCACCTCGGTGGAGAGGATCAATCACTACATTAAGACTCTGTCTTGGAAAGCACTGCCA 3654
Db 1840 TCACGCTGTAGAGAGGATACTCAGTACATGAGATGTGTCTCGAAGCTCTTTAC 1899
QY 3655 GAATTAAGAACAGGCTCCCTCCCTGCTGAGTGGCCCGCAGGAGGAGGTGACCTTTGAGA 3714
Db 1900 ACATGAAGGCACAAAGTTGTCCCGAGGGGTGGCCACAGCATGGGAAATCATATTTTCAG 1959
QY 3715 ACCGAGATGAGGTACCGAGAAACCTCCCTCTTGTCTTAAGAAAGTATCTTTCACGA 3774
Db 1960 ATTATCACATGAATACAGAGAACACACACCCACCCTGCTTTCAGGCATCAACCTGACCA 2019
QY 3775 TCAAACTTAAGAGAGATTTGGGCGGACAGCATCAGGGAAGTCTCGCTGG 3834
Db 2020 TCCCGGCCACGAGTGTGGGATCTGTGGGAAGGAGCGGCTCTGGGAAGCTCTCTTTG 2079
QY 3835 GGATGCCCTCTTCCGTCTGGTGGAGTTATCTGGAGGCTGCATCAGATTTGAGGTGA 3894
Db 2080 GCATGCTCTCTTCCGCTGGTGGAGCCCATGCGAGCGGATTCATTTGACGCGCTG 2139

QY 3895 GAATCAGTGATATTGGCCTTGGCCGACCTCCGAGCAAACTCTCTATCATTTCTCAAGAGC 3954
Db 2140 ACATTTGAGCATGGCCTGGAGGACTTGGCTCCAAGCTCTCAGTGTATCCCTCAAGATC 2199
QY 3955 CGGTCTGCTTCAAGTGGCAGTGTGACATCAAAATTTGGACCCCTTCAACCACTACACTGAAG 4014
Db 2200 CAGTGTCTCTCAGGAACCATCAGATTCAACCTAGATCCCTTTGACCTGCACACTGACC 2259
QY 4015 ACCAGATTGGGATGCCCTTGGAGAGGACACATCAAGAAATGTATTGCTCAGCTACCTC 4074
Db 2260 AGCAGATCTGGATGCCCTTGGAGAGGACATTCCTGACCAAGGCCATCTCAAAGTTCCCA 2319
QY 4075 TGAACATTGAATCTGAAGTGTGAGAGATGGGGATAACTTCTCAGTGGGGGAAACGCGCAG 4134
Db 2320 AAAAGCTGCATACAGATGTGTGGAACCGGTGGAACCTTCTCTGTGGGGAGAGGCGC 2379
QY 4135 TCTTGTGATAGTAGAGCCCTGCTCCGCACTGTAAGATTCTGATTTAGATGAGGCCA 4194
Db 2380 TGCTCTGATTGCCAGGCTGTGCTTCGAACTCCAAAGATCATCCTTATCGATGAAGCCA 2439
QY 4195 CAGCTGCCATGGACACAGACAGACACTTATTGATTCAAGAGACCATCCGAGAGCAATTTG 4254
Db 2440 CAGCTCCATTGACATGGAGACAGACACCCCTGATCCAGGCGACATCCGCTGAAGCTTCC 2499
QY 4255 CAGACTGTACCATGCTGACCATTTGCCCATCGCCTGCACACAGGTTCTAGGCTCCGATAGA 4314
Db 2500 AGGCTGACCGCTGCTGCTCATTTGCCACCGCTGTCCACACTGTGCTGAACTGTGACCCGA 2559
QY 4315 TTATGTTGCTGCGCCAGGACAGGTTGGAGTTTGCACACCCCATCGTCTCTCTCCA 4374
Db 2560 TCTTGGTTATGGGAATGGGAAGGTGGTAGAATTTGATCGCGCGGAGTACTGCGGAAGA 2619
QY 4375 ACAGAGTTCCTGATTCTATGCCATTTTGTGCTGTC 4411
Db 2620 AGCCTGGGTCTATTGTCAGCGCCCTCATGGCCACAGC 2656

RESULT 15

ABV26879
ID ABV26879 standard; cdna; 3055 BP.
XX AC ABV26879;
XX AC
XX AC
DT 16-SEP-2002 (first entry)
XX XX
DE Human prostate expression marker cdna 26870.
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
OS Homo sapiens.
XX OS
XX WO200160860-A2.
XX PD 23-AUG-2001.
XX XX
PF 20-FEB-2001; 2001WO-US05171.
XX XX
PR 17-FEB-2000; 2000US-18319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX Novel isolated nucleic acid molecule associated with cancerous state of

prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer

Claim 1; Page 5435-5436; 11750pp; English.

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

(e) selecting a composition for inhibiting prostate cancer in a patient;

(f) assessing the prostate cell carcinogenic potential of a compound;

(g) determining whether prostate cancer has metastasized in a patient;

(h) assessing the aggressiveness or indolence of prostate cancer in a patient;

(I) is also useful as a pharmacodynamic or pharmacogenomic marker.

Sequence 3055 BP; 731 A; 765 C; 845 G; 712 T; 2 other;

Query Match 12.5%; Score 727; DB 23; Length 3055;

Best Local Similarity 55.8%; Pred. No. 1.4e-165;

Matches 1428; Conservative 0; Mismatches 1120; Indels 9; Gaps 2;

1858 TCCACAGATCGATCGGATCCAGAGGTAACCTGGTGGATCTCGGCGCATGTGG 1917
 186 TCCACAGATCAACCTGGTGGTCCAGGGATGATGTTAGGGTCTCGGCGCACACGG 165
 1918 GAAGTGGAAAAACCTCTCTCAATTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGCA 1977
 166 GGATGGTAAGAGACGCTGTTCTAGCCATCTCGGAGGATGACCTTGTCTCGAGGGCT 225
 1978 GCAATGCAATCAGTGAACCTTCGCTTATGTGGCCAGCAGCCCTGGATCTCAATGCTA 2037
 226 CGGTGGGGTGCAGGGAAGCCCTGGCTATGCTCCCGCAGCAGCCCTGGATCGTCAGCGGA 285
 2038 CTCACAGAGACACATCTGTTGGAGGATATGATGAGAGATGATGATGATGATGATGATG 2097
 286 ACATCAGGAGAACATCTCTGAGGAGCGCATATGACAAAGCCGATACCTTCCAGGTGC 345
 2098 TGAACAGCTGTGCTGAGCCGTGACCTGGCCATTTCTCCAGCAGCAGCTGACCGAGA 2157
 346 TCCACTGTCTCCTGATCGGACCTGGAACTTCTGCCCTTTGGAGACATGACAGAGA 405
 2158 TTGGAGAGGAGGAGCCAACTGAGCGGTGGGCGAGGAGATGACCTTGGCCCGGG 2217
 406 TTGGAGAGCGGGCCCTCAACCTCTCTGGGGGCGAGAAACAGAGGATGACGCTTGGCCCGG 465
 2218 CTTCTATAGTACAGGAGCATCTACATCTCGGAGCAGCCCTCAGTCCCTTAGATGCC 2277
 466 CGCTATCTCCGAGCGTACAGATCTACCTGCTGGAGCAGCCCTGCTGCTGCTGGAGCGCC 525
 2278 ATGTGGGCAACACATCTTCAATAGTGTATCGGGAACATCTCAAGTCCAGAGAGTTC 2337
 526 ACGTGGGGAAGCACATTTTGGAGAGTGCATTAAGAGACACTCAGGGGAGAGCGGTGC 585
 2338 TGTGTTTACCCACAGATGACAGTACCTGTTGATGATGATGATGATGATGATGATGATG 2397
 586 TCCTGGTGACCCACAGCTGAGTACTTGAATTTTGTGGCCAGATCATTTTGTGGAAA 645
 2398 AGGCTGTATTACGGAAGAGCCACCATGAGGACTGATGAATTAATGGTACTATG 2457
 646 ATGGAAATCTGTGAATGGAATCTACAGTGTAGTATGATGATGATGATGATGATGATG 705
 2458 CTACCATTTTAAATACCTGTTGCTGGGAGAGACACCCAGTGTGAGATCAATCAAAA 2517
 706 CCCAACTTATCCAGAGATGACAGAGGAGCCACTTCG-----GACATGTTGAGGACA 759
 2518 AGGAACCAAGTGGTTACAGAGAGAGTACAGAGAGAGGGTCTTAAAAACAGGATCAGTAA 2577

760 CAGCAAGATAGCAGAGAGCAAGCCAAAGGTAGAAAGTCAGGCTCTGGCCACCTCCCTGCAAG 819
 2578 AGAGAGAAAGACAGTAAGAACCCAGAGAGGAGGAGCTTGTGACGTGGAAGAGAGAAAGGGC 2637
 820 AGTCTCTCAACGGAATAGCTGTGCCGAGCATCAGCTCACACAGGAGGAGAGATGGAAG 879
 2638 AGGGTTCAGTCCCTGCTAGTATATGTTCTACATCCAGGCTGTGGGGGCCCCCTTGG 2697
 880 AAGGCTCCTTGTGAGTGGAGGGTCTACACACATCATCCAGGAGCTGGAGGTTACATGG 939
 2698 CATTCCTGGTTATTTATGAGGCTTTTCATGCTGAATGTAGCAGCAGCCCTTTCAGCACCT 2757
 940 TCTCTTGCATAATTTCTTCTTGTGCTGATCGTCTTCTTAAAGATCTTCAGCTTCT 999
 2758 GGTGGTGTAGTACTGATCAACAGGAAAGCGGAAACCACTGTGACTGAGGGAACG 2817
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 2818 AGACC---TCGGTGTAGTACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCA 2874
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AF146074

LOCUS AF146074 5881 bp mRNA linear PRI 10-AUG-1999

DEFINITION Homo sapiens ABC protein mRNA, complete cds.

ACCESSION AF146074

VERSION AF146074.1 GI:5006890

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 5881)

AUTHORS McAleer, M.A., Breen, M., White, N.L. and Matthews, N.

TITLE pABC11 (also known as MOAT-C and MRP5), a member of the ABC family of proteins, has anion transporter activity but does not confer multidrug resistance when overexpressed in human embryonic kidney 293 cells

J. Biol. Chem. 274 (33), 23541-23548 (1999)

MEDLINE 99367488

PUBMED 10438534

REFERENCE 2 (bases 1 to 5881)

AUTHORS McAleer, M.A., Breen, M., White, N. and Matthews, N.

TITLE Direct Submission

JOURNAL Submitted (27-APR-1999) Yamanouchi Research Institute, Armstrong Road, Oxford OX4 4SX, UK

FEATURES

source

1. 5881

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ORIGIN

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Db	2845	GATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGAACGAGACCTCGGTGAGTGA	2904
QY	2834	CAGCATGAAGGACATCTTCATATGAGTACTATGCCAGCATCTACGCCCTCTCCATGCC	2893
Db	2905	CAGCATGAAGGACATCTTCATATGAGTACTATGCCAGCATCTACGCCCTCTCCATGCC	2964
QY	2894	AGTCATGCTGATCTCTGAAAGCCATTCCGAGAGTTGCTTTTGTCAAAGGCAACGCTCGCAGC	2953
Db	2965	AGTCATGCTGATCTCTGAAAGCCATTCCGAGAGTTGCTTTTGTCAAAGGCAACGCTCGCAGC	3024
QY	2954	TTCTCCCGGGCTGCATGACGAGCTTTTCGGAAGGATCTTCGAAGGCCCTATGAAGTTTTT	3013
Db	3025	TTCTCCCGGGCTGCATGACGAGCTTTTCGGAAGGATCTTCGAAGGCCCTATGAAGTTTTT	3084
QY	3014	TCACAGACCCCCACAGGAGGATCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGA	3073
Db	3085	TCACAGACCCCCACAGGAGGATCTCAACAGGTTTTCCAAAGACATGGATGAAGTTGA	3144
QY	3074	CGTGGCGGTGCGCTTCCAGGCGGAGATGTTTCATCCAGAACGTTATCTCGTGTCTTCCTG	3133
Db	3145	CGTGGCGGTGCGCTTCCAGGCGGAGATGTTTCATCCAGAACGTTATCTCGTGTCTTCCTG	3204
QY	3134	TGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCCTTCTGCAT	3193

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Db 3205 TGTGGGATGATCGCAGAGTCTCCCGTGGTCTCTGTGGCAGTGGGGCCCTTGTCAT 3264
QY 3194 CCTCTTTTCAGTCTCGACATGTTCTCCAGGGTCTGATTCGGAGCTGAAGCGCTCTGGA 3253
Db 3265 CCTCTTTTCAGTCTCGACATGTTCTCCAGGGTCTGATTCGGAGCTGAAGCGCTCTGGA 3324
QY 3254 CAATATCAGGAGTACCTTTCTCTCCACATCAGTCCAGCATACAGGGCCTTGCCAC 3313
Db 3325 CAATATCAGCAGTACCTTTCTCTCCACATCAGTCCAGCATACAGGGCCTTGCCAC 3384
QY 3314 CATCCAGCCTACAAATAAGGGCAGGAGTTTCTGCACAGATACAGGAGCTGCTGGATGA 3373
Db 3385 CATCCAGCCTACAAATAAGGGCAGGAGTTTCTGCACAGATACAGGAGCTGCTGGATGA 3444
QY 3374 CAACCAAGCTCCTTTTTTTTGTAGTGTGCGATCGGCTGGCTGTGCGGCTGGA 3433
Db 3445 CAACCAAGCTCCTTTTTTTTGTAGTGTGCGATCGGCTGGCTGTGCGGCTGGA 3504
QY 3434 CCTCATCAGATCGCCCTCATCACCACACCGGGCTGATGATCGTTCTTATGACGGGCA 3493
Db 3505 CCTCATCAGATCGCCCTCATCACCACACCGGGCTGATGATCGTTCTTATGACGGGCA 3564
QY 3494 GATTCCCGCAGCCTATCGGGTCTCGCCATCTCTTATGCTGTCAGTTAAACGGGCTGTT 3553
Db 3565 GATTCCCGCAGCCTATCGGGTCTCGCCATCTCTTATGCTGTCAGTTAAACGGGCTGTT 3624
QY 3554 CCAGTTTACGGTCAAGCTGGCATCTGAGACAGAAAGCTCGATTCACCTCGGTGGAGAGAT 3613
Db 3625 CCAGTTTACGGTCAAGCTGGCATCTGAGACAGAAAGCTCGATTCACCTCGGTGGAGAGAT 3684
QY 3614 CAATCACTACATTAAGACTCTGCTTGGAAAGCACTGCCAGAAATTAAGAAACAAGGCTCC 3673
Db 3685 CAATCACTACATTAAGACTCTGCTTGGAAAGCACTGCCAGAAATTAAGAAACAAGGCTCC 3744
QY 3674 CTCCCTGACTGCCCCAGAGGAGAGTGCACCTTTGAGAACCCAGAGATGAGTACCG 3733
Db 3745 CTCCCTGACTGCCCCAGAGGAGAGTGCACCTTTGAGAACCCAGAGATGAGTACCG 3804
QY 3734 AGAAACCTCCCTCTGCTCTGCTTAAAGAAAGTATCCTTCACGATCAAACTAAAGAGAGAT 3793
Db 3805 AGAAACCTCCCTCTGCTCTGCTTAAAGAAAGTATCCTTCACGATCAAACTAAAGAGAGAT 3864
QY 3794 TGGATTTGGGGGGACAGATCAGGAGTCTCTCGTGGGGATGGCCCTCTCCGTC 3853
Db 3865 TGGCATTTGGGGGGACAGATCAGGAGTCTCTCGTGGGGATGGCCCTCTCCGTC 3924
QY 3854 GGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGATCAGTGATTTGGCCT 3913
Db 3925 GGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGATCAGTGATTTGGCCT 3984
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Db 3985 TGCCGACCTCCGAGCAAACTCTCTATCTCTCAAGAGCCGCTGCTGTTAGTGGCAC 4044
QY 3974 TGTGAGATCAAAATTTGGACCCCTTCACCCAGTACACTGAAGACCAGATTTGGGATGCCCT 4033
Db 4045 TGTGAGATCAAAATTTGGACCCCTTCACCCAGTACACTGAAGACCAGATTTGGGATGCCCT 4104
QY 4034 GGAGAGACACATGAAGAAATCTATTGCTCAGCTACCTCTGAACCTTGAATCTGAAGT 4093
Db 4105 GGAGAGACACATGAAGAAATCTATTGCTCAGCTACCTCTGAACCTTGAATCTGAAGT 4164
QY 4094 GATGGAGAATGGGATAACTTCTCAGTGGGGAAACGGCAGCTCTGTGTCATAGCTAGAGC 4153
Db 4165 GATGGAGAATGGGATAACTTCTCAGTGGGGAAACGGCAGCTCTGTGTCATAGCTAGAGC 4224
QY 4154 CCTGCTCCGCCACGTGAAGATCTGATTTAGATGAAGCCACAGCTGCCATGGACACAGA 4213
Db 4225 CCTGCTCCGCCACGTGAAGATCTGATTTAGATGAAGCCACAGCTGCCATGGACACAGA 4284
QY 4214 GACAGACTTATTGATTAAGAGACCATCCGAGAGCAATTTGCACACTGTACCATGCTGAC 4273
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Db 4285 GACAGACTTATTGATTCAAGAGACCATCCGAGAGCATTTTGCAGACTGTACCATGCTGAC 4344
QY 4274 CATTCGCCCATCGCTGACACAGGTTCTTAGGCTCCGATAGGATTTATGTTGCTGGCCGAGG 4333
Db 4345 CATTCGCCCATCGCTGACACAGGTTCTTAGGCTCCGATAGGATTTATGTTGCTGGCCGAGG 4404
QY 4334 ACAGTGTGGAGTTTGACACCCCATCGGTCCTCTGTCACAGCAGATTCGCCGATTCFA 4393
Db 4405 ACAGTGTGGAGTTTGACACCCCATCGGTCCTCTGTCACAGCAGATTCGCCGATTCFA 4464
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Db 4465 TGCCATGTTTGTGCTGCAGAGAACAGGTCGCTGTCAGAGGCTGACTCCTCCCTCTTGA 4524
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Db 4585 CCTCTACCGAAACCTTGCCTTCTCGATTTTATCTTTCCGACAGCAGATTCGGATTCGC 4644
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Db 4645 TTGCTGTTTTCACCTTTTAGGGAGAGTCATATTTTGATTTATGTTATTTATTCATATTCAT 4704
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Db 4705 GTAAACAAATTTAGTTTTTGTCTTAATTTGACACTCTAAAGGTTTCAGGGAACCGTTAT 4764
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Db 5125 GGCTGGAGACCATCAGAGCGGGCTGAGTTCTCAGGGTCTCGCTCTGCTCTGCTGGTCT 5184
QY 5113 CACTTACTGTTTCTGTAGGAGCAGCGGGGCGGAGCCAGCCGCTTTTCTACTCCCTC 5172
Db 5185 CACTTACTGTTTCTGTAGGAGCAGCGGGGCGGAGCCAGCCGCTTTTCTACTCCCTC 5244
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DB 601 CGTGTGCTGATGATCAGCAGCTGGCTTGGCTTCAGTGGACCGAGCTTTCATGGTGAACA 660
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DB 841 TAAGTTAAAGAACATTAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGCTCCAACA 900
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DB 1081 CAGAGAAATCGTGGCGCCAGGATGACGTTGTCAGAGATGAATGAAGTCTTAC 1140
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DB 1141 TTACATTAATTTATCAAAATGATGCTGGGTCAAAAGCATTTTCTCAGAGTGTTCAAA 1200
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DB 1201 AATCCGCGAGGAGGCGTCGGATATTGGAAAAAGCCGGTACTTCCAGGATACACTGT 1260
QY 1334 GGGTGTGGCTCCCATGTTGGTGTGATGTCAGCGGTGGTACCTCTCTGTTATATGAC 1393
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DB 1561 CTCAGTATCCAGAACTCGCCCAAGCTGACCCCAAAATGAAAAAGAGAGGCTTC 1620
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DB 1861 TCTCATTTTCAGCCATTTTAGGCCAGATGACCTTCTAGAGGCGAGCATTCGAATCAGTGG 1920
QY 1984 AACCTTCGCTTATGTGGCCAGCAGCGCTGGATCTCAATGCTACTCTCTGAGAGACAACAT 2053
DB 1921 AACCTTCGCTTATGTGGCCAGCAGCGCTGGATCTCAATGCTACTCTCTGAGAGACAACAT 1980
QY 2054 CCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGCTGCTGAACAGCTGCTGCCT 2113
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 QY 1942 CAGCATTTTGGGCGCAGATGACGCTTCTAGAGGCGCAGCTTGCATCAGTGGAACTTCG 2001
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LOCUS AR099619 4847 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6077936.
ACCESSION AR099619
VERSION AR099619.1 GI:12809385
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4847)
AUTHORS Shyjan,A.
TITLE Multidrug resistance-associated polypeptide
JOURNAL Patent: US 6077936-A 1 20-JUN-2000;
FEATURES
location/Qualifiers
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BASE COUNT 1226 a 1178 c 1263 g 1180 t
ORIGIN

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LOCUS AR091520 4781 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from patent US 5994130.
ACCESSION AR091520
VERSION AR091520.1 GI:10018275
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4781)
AUTHORS Shyjan,A.
TITLE Multidrug resistance-associated polypeptide
JOURNAL Patent: US 5994130-A 1 30-NOV-1999;
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Location/Qualifiers
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Source /organism="unknown"
BASE COUNT 1217 a 1161 c 1232 g 1165 t 6 others
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LOCUS AR136853 4781 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 1 from patent US 6162616.
ACCESSION AR136853
VERSION AR136853.1 GI:14478103
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 4781)
Shyjan, A.

TITLE Multidrug resistance-associated polypeptide
JOURNAL Patent: US 6162616-A 1 19-DEC-2000;
FEATURES Location/Qualifiers
source 1. 4781
BASE COUNT 1217 a 1161 c 1232 g 1165 t 6 others
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AUTHORS Suzuki, T., Nishio, K., Sasaki, H., Kurokawa, H., Saito-Ohara, F.,
Ikeuchi, T., Tanabe, S., Terada, M. and Saijo, N.
TITLE CDNA cloning of a short type of multidrug resistance protein
homologue, SMRP, from a human lung cancer cell line
JOURNAL Biochem. Biophys. Res. Commun. 238 (3), 790-794 (1997)
MEDLINE 97472289
REFERENCE 2 (bases 1 to 4939)
AUTHORS Suzuki, T.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-1997) Toshihiro Suzuki, National Cancer Center
Research Institute, Pharmacology Division; Tsukiji 5-1-1, Chuo-ku,
Tokyo 104, Japan (E-mail:tsuzuki@ncc.res.ncc.go.jp,
Tel:03-3542-2511, Fax:03-3542-1886)
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QY	1209	CTTACTTACATTAATTTATCAAAATGATGCTGGGTCAAAAGATTTTCTCAGAGCTGT	1268		
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VERSION AB019003.1
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ORGANISM Mus musculus cdna to mRNA.
REFERENCE 1 (sites)
AUTHORS Suzuki,T., Sasaki,H., Kuh,H.J., Agui,M., Tatsumi,Y., Tanabe,S., Terada,M., Saijo,N. and Nishio,K.
TITLE Detailed structural analysis on both human MRP5 and mouse mrp5 transcripts
JOURNAL Gene 242 (1-2), 167-173 (2000)
MEDLINE 20184734
REFERENCE 2 (bases 1 to 5400)
AUTHORS Suzuki,T., Kuh,H. and Nishio,K.
TITLE Direct Submission
JOURNAL Submitted (20-OCT-1998) Toshihiro Suzuki, National Cancer Center Research Institute, Pharmacology Division, Tsukiji 5-1-1, Chuo-ku, Tokyo 104-0045, Japan (E-mail:tsuzuki@ncc.ncc.go.jp, Tel:81-3-3542-2511(ex.4451), Fax:81-3-3542-1886)
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 *TITLE A FAMILY OF ORGANIC ANION TRANSPORTERS, NUCLEIC ACIDS ENCODING

JOURNAL THEM, CELLS COMPRISING THEM AND METHODS FOR USING THEM
 Patent: WO 97/31111-A 62 28-AUG-1997;
 COMMENT INTRIGENE BV (NL)
 FEATURES Other publication AU 1736697 19970910.
 Location/Qualifiers
 source 1..2167
 /organism="unidentified"
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 BASE COUNT 494 a 511 c 626 t 25 others
 ORIGIN
 Query Match 33.2%; Score 1936.4; DB 6; Length 2167;
 Best Local Similarity 96.7%; Pred. No. 0;
 Matches 2069; Conservative 9; Mismatches 47; Indels 14; Gaps 10:
 QY 3692 GGAGGGAGAGTGTACCTTTTGAGAACGACAGATGAGTACCGAGAAAAACCTCCCTCTTGT 3751
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ACCESSION	A64695		
VERSION	A64695.1	GI:4530760	
KEYWORDS			
SOURCE	unidentified.		
ORGANISM	unidentified.		
REFERENCE	1 (bases 1 to 1761)		
AUTHORS	Oude,E.R., Paulusma,C.C., Bosma,P.J., Borst,P., Evers,R., Kool and Marcel.		
TITLE	A FAMILY OF ORGANIC ANION TRANSPORTERS, NUCLEIC ACIDS ENCODING THEM, CELLS COMPRISING THEM AND METHODS FOR USING THEM		
JOURNAL	Patent; WO 9731111-A 61 28-AUG-1997;		
COMMENT	INTROGENE BV (NL).		
FEATURES	Other publication AU 1736697 19970910.		
source	Location/Qualifiers		
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Best Local Similarity	99.6%;	Pred. No. 0;	
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Db	1380	ATACAGGAGCTGCTGGATGACAACCAAGCTCCTTTTTTTTGTATTTACGTGTGCGATGCG	1439
Qy	3413	GTGGCTGGCTGTCCGGCTGGACCTCATCAGCATGCCCTCATCACCAACCGGGGCTGAT	3472
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 LOCUS
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 159070 bp DNA linear
 HTG 17-AUG-2002
 unordered pieces.

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 DEFINITION Homo sapiens clone RP11-449K6, *** SEQUENCING IN PROGRESS ***, l3
 linear HTG 17-AUG-2002
 159070 bp DNA
 AC131160
 Homo sapiens clone RP11-449K6, *** SEQUENCING IN PROGRESS ***, l3
 unnumbered pieces.
 AC131160
 AC131160.1 GI:22296663
 HTG; HTGS_PHASEL.
 human.
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 (bases 1 to 159070)
 Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.

TITLE	Direct Submission
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 159070)
AUTHORS	Worley, K.C.
TITLE	Direct Submission
JOURNAL	Submitted (17-AUG-2002)


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AC068644
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human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaralungu,H.C., Are,J.R., Ayelle,M., Banks,T.,
Barbaria,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brivea,M., Brown,E., Brown,M., Bryant,N.P.,
Burch,C., Burch,P., Burrett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
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Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
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Douchwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
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Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Hernandez,J., Hernandez,O., Hodgson,A., Hoques,M., Holloway,C.,
Hollins,B., Homs1,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Loulsegh,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Massey,E., McLeod,M.P., Meador,M.,
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Moore,S., Morgan,M., Moorish,T., Morris,S., Moser,M., Neal,D.,
Neelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N.,
Nickerson,E., Nwokwenkwo,S., Ogih,M., Okwuonu,G., Oragunye,N.,
Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L.,
Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M.,
Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S.,
Scott,G., Shen,H., Shoshitari,N., Sisson,I., Sodergren,E.,
Sonaikar,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A.,
Taber,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C.,
Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L.,
Vera,V., Villalón,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S.,
Warren,R., Washington,C., Watlington,S., Williams,G.,
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Wu,Y.F., Zhou,J., Zorrilla,S., Naylor,S.L., Weinstock,G. and
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
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REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 178688)
Worley,K.C.
Direct Submission
Submitted (06-MAY-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 178688)
Worley,K.C.
Direct Submission
Submitted (21-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 178688)
Worley,K.C.
Direct Submission
Submitted (14-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Aug 14, 2002 this sequence version replaced gi:21490042.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the
entire insert of this clone. Overlapping regions of clones are only
sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.

ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL: <http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annot>
ation.html

FEATURES

source

Location/Qualifiers
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:04:25 ; Search time 4307.47 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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REFERENCE 1 (bases 1 to 1977)
AUTHORS Allikmets,R., Gerrard,B., Hutchinson,A. and Dean,M.
TITLE Characterization of the human ABC superfamily: isolation and mapping of 21 new genes using the expressed sequence tags database
JOURNAL Hum. Mol. Genet. 5 (10), 1649-1655 (1996)
MEDLINE 97049974
PUBMED 8894702
REFERENCE 2 (bases 1 to 1977)
AUTHORS Allikmets,R., Gerrard,B. and Dean,M.
TITLE Direct Submission
JOURNAL Submitted (12-AUG-1996) Human Genetics Section, National Cancer Institute, NCI-FCRDC, Frederick, MD 21702, USA
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ACCESSION BQ941613

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TITLE NIH-MGC http://mgc.nci.nih.gov/
JOURNAL 1 (bases 1 to 920)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DP/Genar
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2596 row: m column: 06
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GACACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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QY 3070 AGGGTTCTTGGTATGCTGGCAGCCATGGCCATGACGGGTGCATCCAGGCTGCCCG 3129
Db 360 AGGGTTCTTGGTATGCTGGCAGCCATGGCCATGACGGGTGCATCCAGGCTGCCCG 419
QY 3130 TGTGTTGACACCGGACTGCTGCACAACAAGATACGCTGCACACAGTCTCTTTTGACAC 3189

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Db 420 TGTGTTGACACCGGACTGCTGCACAACAAGATACGCTGCACACAGTCTCTTTTGACAC 479
QY 3190 CACACCATAGCGCCGATCCTGAATGCTTCTCCAAAGACATCTATGTGTTGATGAGGT 3249
Db 480 CACACCATAGCGCCGATCCTGAATGCTTCTCCAAAGACATCTATGTGTTGATGAGGT 539
QY 3250 TCTGGCCCTGTATCTCTCATGCTGCTCAATTCCTTTCACGCGCATCTCCACCTTGT 3309
Db 540 TCTGGCCCTGTATCTCTCATGCTGCTCAATTCCTTTCACGCGCATCTCCACCTTGT 599
QY 3310 GGTATCATATGCCACGCGCGCTTTCACCTGTGTGTCATCTGCCCTGGTGTGCTCTA 3369
Db 600 GGTATCATATGCCACGCGCGCTTTCACCTGTGTGTCATCTGCCCTGGTGTGCTCTA 659
QY 3370 CACCTTAGTCAGCGCTTCTATGAGCCACATCAGCGCAACTGAAGCGGCTGGAAATCAGT 3429
Db 660 CACCTTAGTCAGCGCTTCTATGAGCCACATCAGCGCAACTGAAGCGGCTGGAAATCAGT 719
QY 3430 CAGCGCTACCTATCTACTCCACTTTTCGGAGACAGTACTGTCGACGTGTCATCCG 3489
Db 720 CAGCGCTACCTATCTACTCCACTTTTCGGAGACAGTACTGTCGACGTGTCATCCG 779
QY 3490 GGCTACACCGCGACGCGGATTTTGAGATCATCATGATAGTGGAGTGCAGTCCG 3549
Db 780 GGCTACACCGCGACGCGGATTTTGAGATCATCATGATAGTGGAGTGCAGTCCG 839
QY 3550 GAGAAGCTGTACCCCTACATCTCCAACC-GTGGCTCAGCATCGGAGTGGAGTTCG 3608
Db 840 GAGAAGCTGTACCCCTACATCTCCAACC-GTGGCTCAGCATCGGAGTGGAGTTCG 899
QY 3609 TGGGGAA 3615
Db 900 TGGGGGA 906
RESULT 3
BM924812
LOCUS
DEFINITION BM924812 1098 bp mRNA linear EST 12-MAR-2002
5', mRNA sequence.
ACCESSION BM924812
VERSION BM924812.1 GI:19375191
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM12809 row: j column: 19
High quality sequence stop: 656.
FEATURES
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Location/Qualifiers
1..1098
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/db_xref="taxon:9606"
/clone_lib="IMAGE:5761266"
/lab_host="DH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo

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female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

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BASE COUNT      178 a   365 c   293 g   262 t
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Query Match      16.6%; Score 843.6; DB 14; Length 1098;
Best Local Similarity 94.9%; Pred. No. 1.1e-177;
Matches 905; Conservative 0; Mismatches 44; Indels 5; Gaps 3;

Qy 1 CCCATGACGCCCTGTCGGTTCGGGGAGCTCGGCTCCAAAGTTCTGGGACTCCAACT 60
Db 25 CCCATGACGCCCTGTCGGTTCGGGGAGCTCGGCTCCAAAGTTCTGGGACTCCAACT 84
Qy 61 GTCTGTGCACACAGAAAACCGGACCTCACTCCCTGCTTCCAGAACTCCCTGCTGGCTG 120
Db 85 GTCTGTGCACACAGAAAACCGGACCTCACTCCCTGCTTCCAGAACTCCCTGCTGGCTG 144
Qy 121 GGTGCCCTGCATCTACTGTGGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 145 GGTGCCCTGCATCTACTGTGGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 204
Qy 181 TTGTGCGGCTACATCAATCTCTCCACCTGCTCAAGCTCAAGATGGTCGGGTGCTCT 240
Db 205 TTGTGCGGCTACATCAATCTCTCCACCTGCTCAAGCTCAAGATGGTCGGGTGCTCT 264
Qy 241 GCTGTGGTGGCTCTCTGGGGGACCTTTTCTACTCTCTCTCTCTCTCTCTCTCTCTCT 300
Db 265 GCTGTGGTGGCTCTCTGGGGGACCTTTTCTACTCTCTCTCTCTCTCTCTCTCTCTCT 324
Qy 301 GGCCCTGCCCCCTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 360
Db 325 GGCCCTGCCCCCTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 384
Qy 361 CACCTGCTGATACAGTATGAGCGGCTGACGGGCTACAGTCTTCGGGGGTCCTCATTTAT 420
Db 385 CACCTGCTGATACAGTATGAGCGGCTGACGGGCTACAGTCTTCGGGGGTCCTCATTTAT 444
Qy 421 CTCTGTTGTTCTGTGTGGTCTGCGCATGCTCCATCTCCGCTCCCAAGATCCTTTTAGC 480
Db 445 CTCTGTTGTTCTGTGTGGTCTGCGCATGCTCCATCTCCGCTCCCAAGATCCTTTTAGC 504
Qy 481 CAAGCAGAGGGTGAGATCTCAGACCCCTTCCGCTTCCACCATCTTACATCCACTTTGC 540
Db 505 CAAGCAGAGGGTGAGATCTCAGACCCCTTCCGCTTCCACCATCTTACATCCACTTTGC 564
Qy 541 CCTGGTACTCTCTGCTCATCTTGGGCTGTTTCCAGGAGAAACCTCCATTTTTCGCGC 600
Db 565 CCTGGTACTCTCTGCTCATCTTGGGCTGTTTCCAGGAGAAACCTCCATTTTTCGCGC 624
Qy 601 AAGAATGTGACCCCTAACCCCTACCTGAGACCGGCTGGCTTCTCTCCCGCCTGTT 660
Db 625 AAGAATGTGACCCCTAACCCCTACCTGAGACCGGCTGGCTTCTCTCCCGCCTGTT 684
Qy 661 TTTCTGGTGGTTTCAAAAGATGGCCATCTATGGCTACCGGCTATCCCTGGAGGAGGA 720
Db 685 TTTCTGGGTTTCAAAAGATGGCCATCTATGGCTACCGGCTATCCCTGGAGGAGGA 744
Qy 721 CCTCTGTTCCCTTAAAGGAGGACAGATCCAGATGGTGGTGCAGAGCTGTGGAGGC 780
Db 745 CCTCTGTTCCCTTAAAGGAGGAGGACAGATCCAGATGGTGGGACCAAGCTGTGGAGGC 804
Qy 781 ATGAGAGACAGAGAAAGCAGCGGACGACACAAAGCTTCACGACCACTGGGAAAAA 840
Db 805 TTGGAAGAGCAGAGAAAGCAGCGGACGACCAAGCTTCAGCAGAACCTGGGGGAAAAA 864
Qy 841 TGCCCTCCGGCAGGACGAGGTGCTGCTGGGTG -CCCGGCCCCAGGCCCGGAAGCCC -TC 897

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Db 865 GCCTCCCGCAGGAGGAGGCTGCTGCTGGGGGCCCGGCGCCAGGCCCCGGAAGCCCTCC 924
Qy 898 CTTCTGTAAGGCCCTGCTGCTGGCCACCTT--CGGCTCCAGCTTCTCATCATGTC 949
Db 925 TTCTCTGAAAGGCTTCTGCTGGGACCTTTTCGGGTCCAGTTCTCTCATTAAGGCG 978

RESULT 4
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LOCUS      BQ227366               860 bp      mRNA      linear      EST 02-MAY-2002
DEFINITION AGENCOURT_7574821 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6060072
5', mRNA sequence.
ACCESSION  BQ227366
VERSION    BQ227366.1 GI:20408766
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 860)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgaabs-remail.nih.gov
            Tissue Procurement: DCTD/DFP/Gazdar
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LIAM13327 row: m column: 01
            High quality sequence stop: 577.
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                        /db_xref="taxon:9606"
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                        /tissue_type="large cell carcinoma"
                        /lab_host="DH10B (phage-resistant)"
                        /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: Not I;
                        Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                        Average insert size 1.8 kb. Library constructed by Life
                        Technologies."
BASE COUNT      146 a   288 c   215 g   211 t
ORIGIN
Query Match      16.2%; Score 821.2; DB 14; Length 860;
Best Local Similarity 98.7%; Pred. No. 1e-172;
Matches 849; Conservative 0; Mismatches 8; Indels 3; Gaps 2;

Qy 148 CTGCGCTGCTACTTGTCTTACCTCGCGCACCATGTGCTGGCTACATCATCTCTCCA 207
Db 1 CCTGCCCTGCTACTTGTCTTACCTCGCGCACCATGTGCTGGCTACATCATCTCTCCA 60
Qy 208 CCTGTCCAAGCTCAAGATGGTCTGCTGGGTGCTGCTGGGTGCTGCTGGGTGCTGCT 267
Db 61 CCTGTCCAAGCTCAAGATGGTCTGCTGGGTGCTGCTGGGTGCTGCTGGGTGCTGCT 120
Qy 268 TTTTCTACTCTTCATGCGCTGGTCCATGCGCGGCCCTGCCCCCTGTTTCTTTGTGAC 327
Db 121 TTTTCTACTCTTCATGCGCTGGTCCATGCGCGGCCCTGCCCCCTGTTTCTTTGTGAC 180
Qy 328 CCCCTGTGTGGTGGGTCACCATGCTGCTGCGCACCTGCTGATACAGATGACGCGCT 387
Db 181 CCCCTGTGTGGTGGGTCACCATGCTGCTGCGCACCTGCTGATACAGATGACGCGCT 240
Qy 388 GCAGGGCTACAGTCTTCGGGGGCTCCTCATTTATCTTCTGTTTCTGTTGTTGTTGCTG 447
Db 241 GCAGGGCTACAGTCTTCGGGGGCTCCTCATTTATCTTCTGTTTCTGTTGTTGTTGCTG 300

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QY 448 CATCGTCCCATTCGGCTCCCAAGATCCCTTTTAGCCAAAGCAGAGGCTGAGATCTCAGACCC 507
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QY 508 CTTCGGCTTACACACCTTCTACATCCTTTGCGCTGGTACTCTCTGCTCCCTCATCTTGGC 567
Db 361 CTTCGGCTTACACACCTTCTACATCCTTTGCGCTGGTACTCTCTGCTCCCTCATCTTGGC 420
QY 568 CTGCTTTCAGGAGAAACCTCCATTTTCTCCGAAAGAAATGCGACCTTAACCCCTACCC 627
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QY 628 TGAGACAGCGTGGTCTCTCCCGCTCTTTTCTGCTGGTTCACAAAGATGGCCAT 687
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QY 868 GGTGCGCGCGCCAGCGCCGGAAGCCCTCTCTCTGAGG--CCCTGCTGGCCACCTTCG 926
Db 721 GGTGCGCGCGCCAGCGCCGGAAGCCCTCTCTCTGAGG--CCCTGCTGGCCACCTTCG 780
QY 927 GCTCAGCTTCTCTCAGTGTCTGCTTCAAGC--TTATCCAGGACCTGCTCTCTCTCAT 984
Db 781 GCTCAGCTTCTCTCAGTGTCTGCTTCAAGC--TTATCCAGGACCTGCTCTCTCTCAT 840
QY 985 CAATCCACAGCTGCTCAGCA 1004
Db 841 CAATCCACAGCTGCTCAGCA 860

RESULT 5
LOCUS B1196662
DEFINITION 602755456F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4891237 5',
mRNA sequence.
ACCESSION B1196662
VERSION B1196662.1 GI:14651682
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 849)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: rcgaps-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMI769 row: o column: 14
High quality sequence stop: 799.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:4891237"
/clone_lib="NIH_MGC_19"

FEATURES
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/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: brain; Vector: pOTB7; Site: 1: XhoI; Site_2:
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cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 175 a 241 c 243 g 190 t
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Query Match 15.8%; Score 800.8; DB 13; Length 849;
Best Local Similarity 98.8%; Pred. No. 3.7e-168;
Matches 836; Conservative 0; Mismatches 7; Indels 3; Gaps 3;
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QY 2769 CCGGAGGACCTGGGTCCATCAGAGAAGGTGCAGGTGCAGAGCGGAGGAGGATGGG 2828
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QY 2829 CACTGACCCAGGAGGAGAAAGCAGCCATGCGACTGTGGAGCTCAGTGTCTGGGATT 2888
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QY 2949 GTGCGGTGCAATGGAGCCAAATGTGGCTCAGTGTGGACAAATCATGCCATGGCAG 3008
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Db 302 ACAGTAGACAGACACACTTCCCTGAGGCTGGGCGTCTATGCTGCTTTAGGAATCTGC 361
QY 3069 AAGGGTCTTGGTGATGCTGGCAGCCATGGCCATGGCAGGGGTGGCATCAGGCTGCC 3128
Db 362 AAGGGTCTTGGTGATGCTGGCAGCCATGGCCATGGCAGGGGTGGCATCAGGCTGCC 421
QY 3129 GTGTGTGACACGAGCACTGCTGCACAAAGATACCTCGCCACAGTCCCTTCTTTGACA 3188
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QY 3189 CCACACCATCAGGCGGATCCTGAACTGCTTCCCAAGGACATCTATGCTGTGATGAGG 3248
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Db 542 TTCTGCGCCTGTCTCATCTGCTCAATTCCTTCTTCAAGGCCATCTCCACTCTTG 601
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QY 3547 CCAGAGAA 3554
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Db 841 CCAGAGAA 848

RESULT 6
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LOCUS
DEFINITION BI761935 959 bp mRNA linear EST 25-SEP-2001
603048767F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5188984 5',
mRNA sequence.
ACCESSION BI761935
VERSION BI761935.1 GI:15753513
KEYWORDS EST.
SOURCE human.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 959)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11472 row: e column: 17
High quality sequence stop: 832.
Location/Qualifiers
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/clone="IMAGE:5188984"
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/lab_host="PH10B"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
BASE COUNT 159 a 325 c 254 g 221 t
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Query Match 15.4%; Score 784.4; DB 13; Length 959;
Best Local Similarity 94.5%; Pred. No. 1.8e-164;
Matches 835; Conservative 0; Mismatches 46; Indels 3; Gaps 2;

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QY 61 GTCTGTGCACACAGAAACCCGAGCTCACTCGCTGGTTCAGAACTCCCTGCTGGCGCTG 120
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QY 121 GGTGCGCTGTACATCTGCTGGGTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
|||||
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QY 181 TTGTGCTGGGTACATCATCTCTCCACCTGTCCAAAGTCAAGATGGTCTCTGGGTGTCCT 240
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QY 301 GGCCCTCGCCCTGTTTCTTGTACCCCTTGTGGTGGGGGTACCATGCTGCTGGC 360
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QY 361 CACCTGTGTATACAGTATGAGCGGCTGAGGGCGGTACAGTCTTCGGGGGTCTCAATTAT 420
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QY 421 CTCTGCTGCTGTGTGGTCTGGCCATCGTCCCAATTCGCTCCAAAGATCTTTTATAGC 480
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QY 481 CAAGCAGAGGGTGTAGATCTCAGACCCCTTCGCGCTTCACACCTTCTACATCCACATTTGC 540
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Db 545 CAAGCAGAGGGTGTAGATCTCAGACCCCTTCGCGCTTCACACCTTCTACATCCACATTTGC 604
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QY 541 CCTGTACTCTCTGCCCTCATCTTGGCCTGTTCAGGGAGAAACCTTCCATTTTCTCCGC 600
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QY 660 TTTTCTGTGGTGTCAAAAGATGGCCATCTATGGCTACCGGCATCCCTGGAGGAGAAGG 719
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QY 720 ACCTCTGTCTCTAAAGGAGGAGACAGATCCAGATGGTGTGAGCAGCTGCTGGAGG 779
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QY 780 CATGGAGAAACAGGAGAAAGCAGCGGCACACACAAAGCTTCAGCAGCAGCTGGGAAAA 839
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QY 840 ATGCTCGCGGAGGAGCAGGCTGTGCTGGGTGCCGCCCGCCAGG 883
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RESULT 7
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ACCESSION BQ936868
VERSION BQ936868.1 GI:22352251
KEYWORDS EST.
SOURCE human.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 969)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2662 row: k column: 12
High quality sequence stop: 565.
Location/Qualifiers

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/notes="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dt priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 241 a 245 c 261 g 220 t
ORIGIN
Query Match 15.3%; Score 779.2; DB 14; Length 969;
Best Local Similarity 98.3%; Pred. No. 2.6e-163;
Matches 798; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

QY 4267 GGCSCGGGAGAACTCAGCGTGGSCCA-GAGGCAGCTCGTGTGCTGGCCGAGCCCTGC 4325
DB 812 GCGCGGGGAGAACTCAGCGTGGGCGAGGAGGAGCTGTGTGCTGGCCGAGGCTTGC 753
QY 4326 TCCGCAAGAGCCGATCCTGTTTATAGCAGGCGCCACAGCTGCATCGACCTGGAGACTG 4385
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DB 692 ACACCTTCATCCAGGTACCATCCGACCCAGCTTTGATGACTGCTGCTGACCATCG 633
QY 4446 CACACCGGCTTAACACTATCATGACTATACACAGGCTGCTGGTGGCAAGAGGACTAG 4505
DB 632 CACACCGGCTTAACACTATCATGACTATACACAGGCTGCTGGTGGCAAGAGGACTAG 573
QY 4506 TAGCTGAATTTGATTTCCAGCCAACTCATTCAGCTAGAGGACTCTTCTAGGGATGG 4565
DB 572 TAGCTGAATTTGATTTCCAGCCAACTCATTCAGCTAGAGGACTCTTCTAGGGATGG 513
QY 4566 CCAGAGATGCTGAGCTGCTTAAATATATATCTGAGATTTCTCTGCGCTTCTGCTGGT 4625
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QY 4626 TTTTCATCAGGAAGAAATGACACCAATATGTCGAGAGTGCATTTGATGAGCAAACT 4685
DB 452 TTTTCATCAGGAAGAAATGACACCAATATGTCGAGAGTGCATTTGATGAGCAAACT 393
QY 4686 GGGGCGACCTTAAGATTTTGCACCTGCTAAAGTGCCTTACAGGTAAGTGTGCTGAATGCT 4745
DB 392 GGGGCGACCTTAAGATTTTGCACCTGCTAAAGTGCCTTACAGGTAAGTGTGCTGAATGCT 333
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QY 4926 CTAAGTTTCGTTCTGTTTTTAAATAAGCTTTTTCTCTCGAAGAGAGAGAGCT 4985
DB 152 CTAAGTTTCGTTCTGTTTTTAAATAAGCTTTTTCTCTCGAAGAGAGAGAGCT 93
QY 4986 GCTGGGTGAGGCCACCCCTAGGAACTCAGTCTGCTGCTGGGTGCTGGCTGAATCCAT 5045
DB 92 GCTGGGTGAGGCCACCCCTAGGAACTCAGTCTGCTGCTGGGTGCTGGCTGAATCCAT 33

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QY 5046 TAAAAATGGAGTACTGATGAATAAAATACTAC 5077
DB 32 TAAAAATGGAGTCTGCTGATGAATAAAATACTAC 1

RESULT 8
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LOCUS AGENCOURT_8058516 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6206756
DEFINITION 5', mRNA sequence.
ACCESSION BQ687464
VERSION BQ687464.1 GI:21812780
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 888)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-re@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2361 row: 1 column: 21
High quality sequence stop: 707.
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/lab_host="DH10B (phage-resistant)"
/notes="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dt priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 178 a 263 c 260 g 186 t 1 others
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Query Match 15.2%; Score 773; DB 14; Length 888;
Best Local Similarity 95.6%; Pred. No. 6.2e-162;
Matches 839; Conservative 0; Mismatches 31; Indels 8; Gaps 4;

QY 3777 AGAGGTCAGGAGTACTCCAAAGACAGACAGAGCGCCCTGGTGGTGGAGGCGAGC 3836
DB 1 AGAGGTCAGGAGTACTCCAAAGACAGACAGAGCGCCCTGGTGGTGGAGGCGAGC 60
QY 3837 GCCTCTCCGAGGTTGGCCCGCCACCTGGGAGGTTCCGGAATATTCTGTGCGCT 3896
DB 61 GCCTCTCCGAGGTTGGCCCGCCACCTGGGAGGTTCCGGAATATTCTGTGCGCT 120
QY 3897 ACCGCGCGGCTAGACCTGTGTGCTGAGAGACCTGAGTCTGCATGTGACGGTGGCGAGA 3956
DB 121 ACCGCGCGGCTAGACCTGTGTGCTGAGAGACCTGAGTCTGCATGTGACGGTGGCGAGA 180
QY 3957 AGGTGGGATCTGTGGCGGCACTGGGCTGGCAAGTCTTCCATGACCCCTTTGCCGTGCC 4016
DB 181 AGGTGGGATCTGTGGCGGCACTGGGCTGGCAAGTCTTCCATGACCCCTTTGCCGTGCC 240
QY 4017 GCATCTGAGGCGCGCAAGGTTGAAATCCGCAATTGATGGCTCAATGTGGCAGACATCG 4076

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Db	241	GCATCTGGAGCGGCAAGAGGTGAATCCGATGATGGCTCAATGTGGCAGACATCG	300
QY	4077	GCCTCATGACCTGGGCTCTCAGCTGACCATCATCCGAGGAGCCCATCTTCTCGG	4136
Db	301	GCCTCATGACCTGGGCTCTCAGCTGACCATCATCCGAGGAGCCCATCTTCTCGG	360
QY	4137	GGACCTGGGATGAACCTGGAGCCCTTCGGCAGCTACTCAGAGGAGACATTTGGTGGG	4196
Db	361	GGACCTGGGATGAACCTGGAGCCCTTCGGCAGCTACTCAGAGGAGGACATTTGGTGGG	420
QY	4197	CTTTGGAGCTGCCACCTGCACACGTTTGTGAGCTCCAGCGCGCAGGCTTCC	4256
Db	421	TTTTGGAGCTGCCACCTGCACACGTTTGTGAGCTCCAGCGCGCAGGCTTCC	480
QY	4257	ACTGCTCAGAGCGGGGAGAACTCTCAGCTGGGCGCAGAGGAGCTCGTGTGCTGGCC	4316
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QY	4317	GAGCCCTGCTCGCAAGAGCGCATCTCTGTTTATAGCAGGCGCACAGCTGCCAC	4376
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QY	4377	TGGAGACTGACAACTCATCAGGCTACCATCCGACCCAGCTTGTATACCTGCTGTC	4436
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QY	4437	TGACCATCGCACACCGGCTTAACACTATCATGCACTACACAGGCTCTGCTGGACA	4496
Db	661	TGACCATCGCACACCGGCTTAACACTATCATGCACTACACAGGCTCTGCTGGACA	720
QY	4497	AAGGAGTAGTAGTGAATTTGATTTCCAGGCACTCATTCAGCTAGAGGATCTT	4554
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QY	4555	CTACGGATGGCCAGAGATGCTGG--ACTTGCTTAAATATATCTCTGAGA--TTTCT	4609
Db	780	TACCGAATGGCCAGAGATGCTGGAGCTTGGCTTAAATATTTTTCCTGAGATTTCC	839
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LOCUS			
DEFINITION AGNCOURT_8171427 NIH_MGC_110 Homo sapiens CDNA clone IMAGE:6252004			
5', mRNA sequence.			
ACCESSION BQ690370			
VERSION BQ690370.1 GI:21815686			
KEYWORDS EST.			
SOURCE human.			
ORGANISM Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
1 (bases 1 to 898)			
NIH-MGC http://mgc.nci.nih.gov/.			
National Institutes of Health, Mammalian Gene Collection (MGC)			
Unpublished (1999)			
Contact: Robert Strausberg, Ph.D.			
Email: cgapbs-r@mail.nih.gov			
Tissue Procurement: ATCC			
CDNA Library Preparation: Rubin Laboratory			
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
DNA Sequencing by: Agencourt Bioscience Corporation			
Clone distribution: MGC clone distribution information can be			
found through the I.M.A.G.E. Consortium/LLNL at:			
http://image.llnl.gov			
Plate: LLCM2397 row: j column: 05			
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High quality sequence stop: 708.			
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		/note="Organ: pancreas; Vector: pDB7; Site: 1: XhoI;	
		Site: 2: EcoRI; cDNA made by oligo-dT priming.	
		Directionally cloned into EcoRI/XhoI sites using the	
		following 5' adaptor: GGCAGGAG(G). Library constructed by	
		Ling Hong in the laboratory of Gerald M. Rubin (University	
		of California, Berkeley) using ZAP-cDNA synthesis kit	
		(Stratagene) and Superscript II RT (Life Technologies).	
		Note: this is a NIH_MGC Library."	
BASE COUNT	176 a	264 c	268 g
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Best Local Similarity 98.8%; Pred. No. 1.9e-147;			
Matches 724; Conservative 0; Mismatches 8; Indels 1; Gaps 1;			
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QY	3897	ACCGCGCGGCGCTTAGACCTGGTCTGAGAGACCTGAGTGTGCATGTGCACGGTGGCGAGA	3956
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QY	4017	GCATCTGGAGGCGCAAGGTTGAATCCGCATTTGATGGCTCAATGTGCACACATCG	4076
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QY	4077	GCCTCATGACCTGGCGCTCTCAGCTGACCATCATCCGCGAGGAGCCCATCTGTTCTCGG	4136
Db	301	GCCTCATGACCTGGCGCTCTCAGCTGACCATCATCCGCGAGGAGCCCATCTGTTCTCGG	360
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Db	361	GGACCTGGCGATGAACCTGGACCCCTTCGCGAGCTACTCAGAGGAGGAGACATTTGGTGGG	420
QY	4197	CTTTGGAGCTGTCCCATCTGCACACGTTTGTGAGCTCCCGAGGCGAGGCTGGACTTCC	4256
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QY	4257	AGTGTCTAGAGGCGGGGAGAAATCTCAGCGTGGGCCAGAGGAGCTCGTGTGCTGGGCC	4316
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Db	601	TGGAGACTGACAACTCATCAGGCTACCATCCGCGACCCAGTTTGTATACCTGCACTTCC	660
QY	4437	TGACCATCGCACACCGGCTTAACACTATCATGAGTGTGCATGTGCACGCTGTC	4495
Db	661	TGACCATCGCACACCGGCTTAACACTATCATGAGTGTGCATGTGCACGCTGTC	720
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Db	721	CAAAGGAGTAGTAG	733

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RESULT 10
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ACCESSION
BI907445
VERSION
BI907445.1 GI:16170278
KEYWORDS
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SOURCE
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ORGANISM
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 776)
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11534 row: g column: 09
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and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."
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107 a 276 c 195 g 198 t
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Best Local Similarity 99.3%; Pred. No. 1,3e-143;
Matches 694; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY 121 GGTGCCCTGCATCTACTGTGGGTGCGCCCTGCGCTGCTACTTGTCTACCTGGGACCA 180
DB 198 GGTGCCCTGCATCTACTGTGGGTGCGCCCTGCGCTGCTACTTGTCTACCTGGGACCA 257
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QY 301 GGCCCTGCCCCCTGTTTCTTTGTCACCCCTTGTGGTGGGGGTCCACATGCTGCTGGC 360
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QY 361 CACCTGCTGTATACAGTATGAGCGGTGAGGCGGTACAGTCTTCGGGGGTCTCTCATTA 420
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VERSION
BO944733.1 GI:22360211
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ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 956)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/BTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2660 row: e column: 07
High quality sequence stop: 591.
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Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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224 a 276 c 234 g 216 t

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ORIGIN

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 Matches 701; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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QY 4087 CTTGGCTCTCAGCTGACCATCATCCCGCAGGACCCCATCTCTTCTCGGGACCCCTGCG 4146
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QY 4147 CATGAACCTGGACCCCTTCGGCAGCTACTCAGAGGAGCATTTGGTGGCTTTGGAGCT 4206
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QY 4207 GTCCACCTGCACACGTTTGTGAGCTCCCGCAGGACCCCATCTCTTCTCGGGACCCCTGCG 4266
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QY 4267 GCGCGGGAGAACTCAGCTGGCGCAGAGGAGCTCGTGTGCTGGCCGCGGAGCCCTGCT 4326
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 717)
 REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

Location/Qualifiers
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 TAG_TISSUE=Chondrosarcoma
 TAG_SEQ=CGTCAAGGCT"
 BASE COUNT 195 a 148 c 171 g 201 t 2 others
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Query Match 13.5%; Score 686; DB 14; Length 717;
 Best Local Similarity 99.7%; Pred. No. 1.7e-142;
 Matches 686; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 4451 CGGCTTAAACACTATCATGACTACACAGGCTCCTGGTCTCGACAAAGGAGTAGTAGCT 4510
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VERSION BG750831.1			
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REFERENCE 1 (bases 1 to 680)			
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.			
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL Unpublished (1999)			
COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-i@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCMI680 row: p column: 11 High quality sequence stop: 677. Location/Qualifiers 1. 680 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4844026" /clone_lib="NIH_MGC_43" /tissue_type="normal pigmented retinal epithelium" /lab_host="DH10B (phage-resistant)" /note="Organ: eye; Vector: pORB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: This is a NIH_MGC library. "			
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California, Berkeley) using ZAP-cDNA synthesis kit
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cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
BASE COUNT 249 a 258 c 340 g 200 t
ORIGIN
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Best Local Similarity 95.8%; Pred. No. 2.1e-137;
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QY 4344 TGGTTTTACAGAGCGCCACAGCTGCGATCGACCTGGAGCTGACACCTCATCCAGCTA 4403
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VERSION BI524575.1 GI:15349367
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 793)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Cloned through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."
BASE COUNT 183 a 208 c 220 g 182 t
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Best Local Similarity 95.8%; Pred. No. 2.1e-137;
Matches 757; Conservative 0; Mismatches 23; Indels 10; Gaps 7;
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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Title: US-09-647-140A-5

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Searched: 356696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 713392

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1749.4	34.4	1977	10 US-09-967-768A-190	Sequence 190, App
4	1408.6	27.7	1448	10 US-09-925-299-157	Sequence 157, App
5	1094.8	21.6	5300	10 US-09-880-107-3373	Sequence 3373, App
6	1034	20.4	4918	10 US-09-917-800A-1578	Sequence 1578, App
7	1030.2	20.3	5728	10 US-09-917-800A-479	Sequence 479, App
8	982	19.3	1019	10 US-09-925-297-247	Sequence 247, App
9	407	8.0	418	10 US-09-998-598-2049	Sequence 2049, App
10	407	8.0	419	10 US-09-998-598-175	Sequence 175, App
11	386	7.6	1936	10 US-09-880-107-3832	Sequence 3832, App
12	354	7.0	4551	9 US-09-938-842A-1674	Sequence 1674, App
13	335.2	6.6	418	9 US-10-042-125A-32	Sequence 32, Appl
14	326	6.4	4872	9 US-09-938-842A-436	Sequence 436, App
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16	297.2	5.9	4545	9 US-09-938-842A-55	Sequence 55, Appl
17	280	5.5	496	10 US-09-864-761-51	Sequence 51, Appl
18	279.4	5.5	3786	9 US-10-012-896-1006	Sequence 1006, Ap
19	279.4	5.5	4395	9 US-10-012-896-1007	Sequence 1007, Ap

20	279.4	5.5	6140	9 US-10-012-896-536	Sequence 536, App
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ALIGNMENTS

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US-09-954-456-804
; Sequence 804, Application US/09954456
; Patent No. US20020115057A1

; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
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; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 804

; LENGTH: 1977
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: n=a,t,g or c
US-09-954-456-804

;; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

;; FILE REFERENCE: 44921-5028-WO

;; CURRENT APPLICATION NUMBER: US/09/880,107

;; CURRENT FILING DATE: 2001-06-14

;; PRIOR APPLICATION NUMBER: US 60/211,379

;; PRIOR FILING DATE: 2000-06-14

;; PRIOR APPLICATION NUMBER: US 60/237,054

;; PRIOR FILING DATE: 2000-10-02

;; NUMBER OF SEQ ID NOS: 3950

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;; ORGANISM: Homo sapiens

;; FEATURE:

;; OTHER INFORMATION: Genbank Accession No. U520020142981A1 U66674

;; NAME/KEY: unsure

;; LOCATION: (1)..(1968)

;; OTHER INFORMATION: n = a o r g o r t

US-09-880-107-3407

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QY 4267 GGGCGGGAGATCTCAGCTGGCGCAGAGGAGCTGCTGCTGGCGCCGAGCCCTGGT 4326

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DB 1376 AGCTGAATTTGATTTCTCCAGCCACCTCATTTGAGCTAGAGGACTGCTTCTACGGGATGGC 1435

QY 4567 CAGAGATGCTGGACTTGGCTTAAATATATTTCTGAGATTTCTCTGCGCTTTCTGCTGCTGCTGCTGCT 4626

DB 1436 CAGAGATGCTGGACTTGGCTTAAATATAT--CTGAGATTTCTCTGCGCTTTCTGCTGCTGCTGCTGCT 1493

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DB 1614 TTAGATCAGGAATGATCCCAAGTGGTGAATGACACGCTTAAGTTCACAGCTAGTTGA 1673

QY 4806 GCGAGTTAGACTAGTCCCGGCTCTCCCGATTCGCAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCA 4865

DB 1674 GCGAGTTAGACTAGTCCCGGCTCTCCCGATTCGCAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCA 1733

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Db 1794 CTAAGTTTCGTTCTCTGTTTTTAAATAAAGCTTTTCCCCCTGGAACAGAGACGCT 1853
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Db 1914 TAAAAATGGGAGTACTGATCAATAAATACTACA 1946

RESULT 3
US-09-967-768A-190
; Sequence 190, Application US/09967768A
; Patent No. US20020150877A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-72
; CURRENT APPLICATION NUMBER: US/09/967.768A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/60/236,109
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,034
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,111
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 190
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1977)
; OTHER INFORMATION: n-a,t,g or c
US-09-967-768A-190

Query Match 34.4%; Score 1749.4; DB 10; Length 1977;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 1889; Conservative 0; Mismatches 49; Indels 15; Gaps 10;

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Db 181 GTCATCATGGCCAGCAGCAGCGGATCTTACTTGTGGGTNANNNGCCCTGCTGTGCTC 240
QY 3368 -TACACCTTAGTGAGCGCTTCTATGACGACACATCAGGCAACTGAGCGGCTGGAATC 3426
Db 241 TTACACCTTAGTGAGCGCTTCTATGACGACACATCAGGCAACTGAGCGGCTGGAATC 300
QY 3427 AGTCAGCGGCTACCTATCTACTCCCACTTTTCGGAGACAGTACTGCTGTCAGTGTGAT 3486
Db 301 AGTCAGCGG-TCACCTATCTACTCCCACTTTTCGGAGACAGTACTGCTGTCAGTGTGAT 359
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Db 360 CCGGGCTTACACCGCAGCGCGGATTTTGATGATCATCAGTGATATAGGTGGATGCCAA 419
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Db 1196 CCAGAGAGCGCATCTGCTGTTTGTAGAGGCGCAGAGTGGCTGCTGAGAGCTGA 1255
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QY 4567 CAGAGATGCTGAGCTTGTCTAAATATATTTCTGAGATTTCTCTGCGCTTCTCGGTT 4626
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QY 4627 TTCATCAGGAAGAAATGACACCAATATGTCCGAGAAATGAGCTTGTATAGCAACACTG 4686
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Qy	4923	TTTCTAAAGTTTCGTTTCTGTTTTTAAATAAAAAAGCTTTTTTCCCTCGGAACAGACACA	4982
Db	1262	TTTCTAAAGTTTCGTTTCTGTTTTTAAATAAAAAAGCTTTTTTCCCTCGGAACAGACACA	1321
Qy	4983	GCTGCTGGGTGAGGCCACCCCTAGGAACTCAGTCTCTACTCTGGGTGCTGCCTGAATC	5042
Db	1322	GCTGCTGGGTGAGGCCACCCCTAGGAACTCAGTCTCTACTCTGGGTGCTGCCTGAATC	1381
Qy	5043	CATTAAAAAATGGGAGTACTGATGAAATAAAACTACA	5078
Db	1382	CATTAAAAAATGGGAGTACTGATGAAATAAAACTACA	1417

RESULT 5
 US-09-880-107-3373
 ; Sequence 3373, Application US/09880107
 ; Patent No. US20020142981A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Horne, Darci T.
 ; APPLICANT: Vockley, Joseph G.
 ; APPLICANT: Scherf, Uwe
 ; APPLICANT: Gene Logic, Inc.
 ; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
 ; FILE REFERENCE: 44921-5028-WO
 ; CURRENT APPLICATION NUMBER: US/09/880,107
 ; CURRENT FILING DATE: 2001-06-14
 ; PRIOR APPLICATION NUMBER: US 60/211,379
 ; PRIOR FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: US 60/237,054
 ; PRIOR FILING DATE: 2000-10-02
 ; NUMBER OF SEQ ID NOS: 3950
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3373
 ; LENGTH: 5300
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U49248
 US-09-880-107-3373

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Db	1500	GTTCGGGTGATCGTCTGTAAATCCCAATTATGCGATACTGTCTCCACCAAGAGTAAGACC	1559
QY	1430	TTCCAGGTAAAGCAATGAATTTGAAGGACTCGCGCATCAAGCTGATGATGAGATCCTG	1489
Db	1560	ATTCAGGTCAAAAATATGAAGAATAAAGACAACGTTTAAAGATCATGAATGAGATTCTT	1619
QY	1490	AACGCGATCAAGGTCTCAAGCTGTACGCCCTGGGAGGCCAGCTTTCCTGAAGCAGGTGGAG	1549
Db	1620	AGTGAATCAAGATCCTGAAATATTTTGCCTGGGAACCTTCATTTCAGAGACCAAGTACAA	1679
QY	1550	GGCATCAGGCGAGGTGAGCTCCAGCTGCTGCGCACGGCGGCTACCTCCACACCACAACC	1609
Db	1680	AACCTCCGGAAGAAGAGCTCAAGAACCTGTGCGCTTTTGTGACCTTTCAGTCAACTACAGTGTAGTA	1739
QY	1610	ACCTTCACCTGGATGTGAGGCCCTTCTGTGACCCCTGATCAACCTCTGGGTGTAGCTG	1669
Db	1740	ATAATCGCTTTCAGTTTAACTCCAGTCTCGTATCTGTGCTCAGATTTCTGTTTATGTC	1799
QY	1670	TACGTGGACCCAAACAATGTCTGGAGCCGAGAGGCCCTTTGTGTGTGCTCTGTTT	1729
Db	1800	CTGGTGATAGCAACAATATTTTGGATGSCACAAAAGGCTTCACCTCCATTACCCCTTC	1859
QY	1730	AATATCTTAAGACTTCCCCCTCAACACTGCTGCCCGAGTTAATCAGAACCTGACTCAGGCC	1789
Db	1860	AATATCTCGCTTTCCTCTGAGATGCTTCCCTCATGATGATCTCCCTCAATGCTCCAGGCC	1919
QY	1790	AGTGTGCTCTGAACGGATCCAGCAATTCCTGAGGCCAAGAGGAATGTGACCCCAAGAGT	1849
Db	1920	AGTGTTCACAGAGCGGCTAGAGAAGTACTTGGAGGGGATGACTTTGACACATC---T	1976
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Db	2037	TGGGAACATGATTCGGAAGCCACAGTCCGAGATGTCAACTGGACATTTATGCGAGCCAA	2096
QY	1970	CTGGTGGCGGTGTGGGGCTGTGGCTGTGGGAAGTCTCCCTGGTGTCTGCCCTGCTG	2029
Db	2097	CTTGTGGCTGTATAGGCCCTGTGGCTCTGGGAAATCTCTTGATATCAGCCATGCTG	2156
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Qy 2630 GCACCTGCTGATTGAAGACACACTCAGCAACACACAGGATCTCAGACACAAATGATCCAGTC 2689
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Qy 3098 GCCATGGCAGGGGTGGATCCAGGCTGCCGTGCTGTGACCAAGGCACTGCTGCACAAC 3157
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RESULT 6
US -09-917-800A-1578
; Sequence 1578, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917.800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1578
; LENGTH: 4918
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; US -09-917-800A-1578
; US2002002

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Query Match	20.4%	Score 1034;	DB 10;	Length 4918;
Best Local Similarity	55.8%;	Pred. No. 5.5e-250;		
Matches 2067;	Conservative 0;	Mismatches 1615;	Indels 24;	Gaps 4;
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Db 1001	AAATCGTGGTTAG	CAAGTCTCTCTTCAAAACCTTCC	ACGTAGTCATCCTGAAATCATTT 1060	
Qy 950	TGCTTCAAGCTTAT	CCAGGACCTGCTCTCTTCAATCAATCA	CACAGCTGCTCAGCATCTGT 1009	
Db 1061	ATACTGAAATTA	ATACATGACCTTTGGTGTTTCTGAATCCT	CACTGCTGAAAGTTGCTG 1120	
Qy 1010	ATCAGGTTTATCT	CCAACCCCATGGCCCCCTTC	TGGTGGGCTTCCTGGTGGCTGGGCTG 1069	
Db 1121	ATCGGTTTCGTG	AAGAGCTCTAACTCATACGTGTGGTT	TGGCTATATCTGTGCAATCTGA 1180	
Qy 1070	ATGTTTCCTGTCT	CCATGATCGTCGTGATCTTACAACACTATT	ACCACCTACATCTTT 1129	
Db 1181	ATGTTGCTGTGAC	TCTCATCAATCTTTTCGCCCTCAGTCTT	ACTTTCAACATGTGTTT 1240	
Qy 1130	GTGACTGGGGTGA	AGTTTCGTACTGGGATCATGGGTGTCATC	TACAGGAAGCTCTGCTT 1189	
Db 1241	GTGTTGGGAATG	TGGTACGGACACCGTCATGCTTCGATAT	ATAGAAGGCATTTGACC 1300	
Qy 1190	ATCAACCACTCAG	TCAAAACGTCCGTCCACTGTGGGGAAAAT	TGTCAACCTCATGTCACTG 1249	
Db 1301	CTATCTACTTGG	CTAGGAAGCAGTACACCATTTGGAGAGACGG	TGAACCTTGATGTCTGTA 1360	
Qy 1250	GATGCCACGCCCT	TTCATGGACCTTGGCCCCCTTCCTCAATCT	GCTGTGGTGTGAGCAGCCCTG 1309	

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Db 2438 GATCCCTGTGGCTGTGGATGCTCATGTGGGAAACACATTTTCAACAAGTTGTGGGC 2497
Qy 2390 CCAGAGCGCTGCTGCGAGGCAAGACGCGAGTGTGGTCAACCGACCGCATTTAGCTTCCTG 2449
Db 2498 CCCACGGCCTGTTGGCTGGCAAGACGAGATCTTTGTATCTACATGCTTCCTTT 2557
Qy 2450 CCCAGACAGACTTTCATCATTTGTCTAGCTGTATGACAGGTCTCTGAGATGGCCCGTAC 2509
Db 2558 CCCCAAGTGATGATGATTGTCTGGGAAGGACCATCTTATAGAAAGATCTCTAT 2617
Qy 2510 CCAGCCCTGCTGACGCGCAAGCGCTCTTTGTCACACTTTCTCTGCAACTATCCGCCCGAT 2569
Db 2618 CGTGACCTGTGGGCAAGAGGAGTGTTCG- - - - -TAGGAACCTGGAAGACCTTCATG 2671
Qy 2570 GAGACCAAGGCGACCTGGAGGACAGCTGGACCGGTTGGAGGTCGAGAGATGAAGAG 2629
Db 2672 AAGCATTCAGGCGCTGAAGGAGAGGCCACAGTCAATAATGACAGTGAAGCGGAAGACGAC 2731
Qy 2630 GCATGCTGTATTGAAGACACACTCAGCAACACACCGGATCTGACAGACAATGATCCAGTC 2689
Db 2732 GATGATGGCTGATTCACCATCGAGGAATCCCTGAGGATGAGCTTCTTGCCCATG 2791
Qy 2690 ACCTATGTGTCAGAGACGATTTATGAGACAGTGTAGTGCCTCTGCTCAGATGGGAG 2749
Db 2792 AGAAGAGAAAATAGTCTTTCGCGGTACACTGAGCGCGACGCTTAGTCTCCAGCGCGACGT 2851
Qy 2750 GGACAGGTCGCGCTGTATACCCGAGGACCTGGGTCTCAGAGAAGGTGAGGTGACA 2809
Db 2852 GGAAGTCCCTCAAAAATCTCTGAAGATTAAAAATGTGAATGTCTTGAAGGAGAAGAA 2911
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Db 2912 AAAGAAGTGAAGGACAAAATAATTAAGAAGAAATTTGGAAACCGGAAGGTCAAG 2971
Qy 2870 CTCAGTGTGTTCTGGGATTAATGCAAGCGCTGGGGCTCTGTACACGCTGCCCATCTGT 2929
Db 2972 TTCTCCATCTACCTGAAGTATCTACAGGCACTAGGGTGTGGTCCATCTTTTCATCATC 3031
Qy 2930 CTCCTGTATGTGGTCAAGTGGCGCTGCCATTTGGAGCAATGTGTGGCTCAGTGCCTG 2989
Db 3032 CTTTCTACGGATGAATAATTTGTGCTTTTATCGGCTCTAACCTCTGGCTGAGTGCCTGG 3091
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Db 3092 ACCAGTGACTCTGCAACTTGAATGGGACCAACAATTCGTCTTCATAGGAGCATGAGA 3151
Qy 3038 CTGGGCTCTATGCTGCTTTAGGAATTTCTGCAAGGTTCTTTGGTGTGATGCTGGCAGCATG 3097
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Qy 3098 GCCATGGCAGGGTGGCATCCAGGCTGCCGCTGTGTGACACAGGCACTGCTGCACAAC 3157
Db 3212 TGGAGCATATGCTTGCAGAAATGCAATCAAAAGCTTTGACGGGCGAGCTGTTAACCAAC 3271
Qy 3158 AAGATAGCTTCGCCACAGTCTCTTTTGACACACACCACTCAGCGCGCATCTCTGAACCTGC 3217
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Qy 3338 ACTGTGGTCTGCTGCCCTGGCTGCTCTACACCTTACTGAGCGCTTCTATGAGACC 3397
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Qy 3758 TCTAATCATGCTGGCTGTGGAGAGGGTCAAGGAGTACTCCAAAGACAGACAGAGAGCGCCC 3817
Db 3872 ACCAATTTGTGGCACTTGAGCGAATAAGTGAATACATAAATGTAGAAATAGAGCGCCC 3931
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Db 3989 AACAACTATCAAGTGGCGTATCGCGCGAGCTGGATCTGGTCTGAAAGGAGTCACTTGT 4048
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Db 4049 ACATCAAGAGCGGAGAGAGGTGCGGCTAGTGGGAGGAGCTGGGCTGGGAAATCATCC 4108
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Db 4109 CTCAAAACGTGCTCTTCAGAACTTTAGAGTCTGCGGGGGCCAGATCATCTATGATGG 4168
Qy 4058 CTCATGTGGAGACATCGGCTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4117
Db 4169 ATAGATGTGCTCTTCATTTGAGTCTGCGGGGGCCAGATCATCTATGATGG 4228
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Db 4229 GACCCCATTTGCTCTCGGGGAGTCTGAGGATGAATCTCGACCTTTCAACAAATATTCA 4288
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Db 4289 GATGAGGAGTTTGGAGGCGCTGGAGTTGGCTCACCTCAGATCTCTTGTGCTGCGCTTA 4348
Qy 4238 CCGGAGGCTTGGACTTCCAGTGTCTCAGAGGCGGGGAGAAATCTCAGCTGTGGCGCAGAG 4297
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Db 4469 GCCAGGCTGAGTGTGATCTCGAGACGATAGCTTATTCAGACACCATCTCGAAAGAG 4528
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Db 4529 TTTCCCAAGTGCAGGCTCATCACCATCGCTCACAGGCTGACACCATCATGAGCAGTAC 4588
Qy 4478 AGGCTCTGCTGGCAAGAGGAGTAGTGTGAATTTGATTTCTCCAGCCCACTCATTT 4537
Db 4589 AAGATAATGGTCTTAGACAACGGGAAGATTGTCTGAGTATGGCAGTCTCTCAAGAACTGCTG 4648

QY	4538	GCAGCTAGAGGCATCTTCTACGGGATGCCAGAGATGCTGGACTTG	4583
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Db	4649	TCCACAGAGGTTCTTCTATCTGATGGCCAGGAAGCCGGCATTG	4694

RESULT 7

US-09-917-800A-479
: Sequence 479, Application US/09917800A
: Patent No. US20020119462A1
: GENERAL INFORMATION:
: APPLICANT: Mendrick, Donna
: APPLICANT: Porter, Mark
: APPLICANT: Johnson, Kory
: APPLICANT: Castle, Arthur
: APPLICANT: Elashoff, Michael
: APPLICANT: Gene Logic, Inc.
: TITLE OF INVENTION: Molecular Toxicology Modeling
: FILE REFERENCE: 44921-5038-US
: CURRENT APPLICATION NUMBER: US/09/917,800A
: CURRENT FILING DATE: 2001-07-31
: PRIOR APPLICATION NUMBER: US 60/222,040
: PRIOR FILING DATE: 2000-07-31
: PRIOR APPLICATION NUMBER: US 60/222,880
: PRIOR FILING DATE: 2000-11-02
: PRIOR APPLICATION NUMBER: US 60/290,029
: PRIOR FILING DATE: 2001-05-11
: PRIOR APPLICATION NUMBER: US 60/290,645
: PRIOR FILING DATE: 2001-05-15
: PRIOR APPLICATION NUMBER: US 60/292,336
: PRIOR FILING DATE: 2001-05-22
: PRIOR APPLICATION NUMBER: US 60/295,798
: PRIOR FILING DATE: 2001-06-06
: PRIOR APPLICATION NUMBER: US 60/297,457
: PRIOR FILING DATE: 2001-06-13
: PRIOR APPLICATION NUMBER: US 60/298,884
: PRIOR FILING DATE: 2001-06-19
: PRIOR APPLICATION NUMBER: US 60/303,459
: PRIOR FILING DATE: 2001-07-09
: NUMBER OF SEQ ID NOS: 1740
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 479
: LENGTH: 5728
: TYPE: DNA
: ORGANISM: Rattus norvegicus
: FEATURE:
: OTHER INFORMATION: Genbank Accession No. US20020119462A1
US-09-917-800A-479

[illegible]

D	b	1480	GCACGGCTCACAGCTCCATGCTCAGAACTGTGAGAAACCACTCAAGTCCCACGGCTGGGAG	1539
Q	y	1526	CCCAGCTTCCTGAAGCAGGTGSGAGGCATCAGCAGGCTGAGCTCCAGCTGCTCGCGCAGC	1585
D	b	1540	TGTGCCTTCCTGGAGCGACTCCTTGTCATATCCGGGGCCAGGAGCTAGGTGCCCTGAAGACC	1599
Q	y	1586	CGCGCCTACTCCACACACACACACCTTCACCTGATGTGCGAGCCCTTCCTTGGTGACC	1645
D	b	1600	TCCGCCTTCCTCTCTCTGTCTCTCGTGTCTCTCCAGTGTACATTTCTCTGCTGGCG	1659
Q	y	1646	CTGATCACCTCTGGGTGTACGTGTACGTGGACCCCAACCAATGCTGGACGCCGAGAAG	1705
D	b	1660	CTGGTTGTGTTGCTGTCCACACCTTGGTGCGAGAGCAACGCCATGGATGCGGAGAAG	1719
Q	y	1706	GCCTTTGTGCTGTGCTTGTGTTAATATCTTAAGACTTCCCTCAACATGCTGCCCCAG	1765
D	b	1720	GCCTTTGTGACGCTACGCTGTCTAGCAATCTTAACAAAGCCACGCCCTTCCTCCCTTC	1779
Q	y	1766	TTAATCAGCAACTGACTCAGGCCAGTGTCTCTGAAACGGATCAGCAATTCCTTGAGC	1825
D	b	1780	TTCTGTGCATGCTCTGTTTCAAGCTCGGGTGTCTTTGACGCGCTAGCTGTCTTCCTGTG	1839
Q	y	1826	CAAGAGAACTTGACCCCCAGAGTGTGGAAGAAAGACC-----ATCTCCCCAGGCTAT	1879
D	b	1840	CTGGAGAAGTAGACCCCAATGGCATGGTCTTGAGTCCCTCCAGATGCTCTCTCGAAGAT	1899
Q	y	1880	GCCATCACCATACACAGTGGCACTTCACTGGGCCAGGACCTGCCCCCACTCTGCAAC	1939
D	b	1900	CGAATTTCTATACAAATGGCACTTCGCTTGGTCCCAGGAGAGCCGCTTGCCTGCAC	1959
Q	y	1940	AGCCTAGACATCCAGTCCGAAAGGGCACTTGGTGGCCGTGGTGGGCGCTGTGGGCTGT	1999
D	b	1960	GGGATCAACCTCACCGTGGCCAGGGCTCTCTGCTGGCTGTGTGGTCCAGTGGGGGCT	2019
Q	y	2000	GGGAAGTCTCTCGTGTCTGCCCTGCTGGAGAGATGGAGAGCTAGAAAGCAAGTG	2059
D	b	2020	GGAAAGTCTCTCGTGTCTGCCCTGCTGGGAGCTTTGAAAGTAGAAGGGTCTGTG	2079
Q	y	2060	CACATGAAGGGCTCGTGCGCTATGTGCCCAAGCAGCATGGATCCAGAACTGCACCTCT	2119
D	b	2080	AGCATGAGGGTTCCGTGGCTTACGTGCTCAGGAGGCTTGGTCCAGATACCTCTGTG	2139
Q	y	2120	CAGGAAGAGCTGCTTTGGCAAGCCCTGAACCCCAAGCGCTACACAGACACTCTGGAG	2179
D	b	2140	GTGGAGAATGTGCTTTCAGCAGAGCTGGATCTGCCATGGTTGCAGGAAGTTCTAGAA	2199
Q	y	2180	GCTCTGCTCTGCTAGCTAGCTCGAGATGCTGCTGTGGGGATCAGACAGAGATTGGA	2239
D	b	2200	GCCTGTGCTTGGGTCTGATGTGGCCAGCTTCCTTCAGGAGTTTCAACCCCACTAGG	2259
Q	y	2240	GAGAAGGCATTAACCTCTCTGGGGCCAGCGGACGCGGTGAGTCTGGCTCGAGCTGTT	2299
D	b	2260	GAGCAGGCATGAATTTCTTCTGGGGCCAGAAAGACGCGCTGAGCTTGGCTCGGCGCTG	2319
Q	y	2300	TACAGTGATCGGATATTTTCTGCTGATGACCCACACTGTCCGCGGTGACTCTCATGTG	2359
D	b	2320	TACAGAAGGCTGCTGTACTCTGATGATGACCCCTTACAGCCCTGAGAGCCCTGATGTC	2379
Q	y	2360	GCCAAGCACATTTTGACACGCTCATCGGCCAGAAAGCGTGTCTGGCAGGCAAGACGGA	2419
D	b	2380	AGCCAGGAAGTCTTCAACAGGTCATTGGCCCCAGTGGACTTCTCCAAGTTACGACTCG	2439
Q	y	2420	GTGCTGTGACGCACGGCATTAGCTTCTGCCCCACAGACAGACTTCATCATTTGTGCTAGCT	2479
D	b	2440	ATCCTTGTAAACACACAGCTCATGCTCTGCCCCCAAGCTGACCAGATCTGGTGTGCCC	2499
Q	y	2480	GATGACAGGTGTCTGAGATGGGCCGCTTACCCAGCCCTGCTGCGAGCGCAACGGCTCTTT	2539
D	b	2500	AATGGGACCATCGAGAGATGGGCTCTTACCAAGACCTTCTGCTAGGAACGGAGCCCTG	2559
Q	y	2540	GCCAACTTTCTTGCACATATGCCCCGATCAGAGCAACGAGGCACTCGGAGACAGCTGG	2599
D	b	2560	GT-----GGTCTTCTGG	2572

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DB	2573	ATG	AGCCG	CAGACAG	CCCTG	CAGG	CAAGGAGAAGGAGAAG	-----CACATGCTGCAGC	2624	
QY	2660	CAC	ACG	GAATCTG	ACACAC	AATGATCC	AGTCACCTATGTG	GTCCAGAAAGCAGTTATGAGA	2719	
DB	2625	CAC	CA	GTGATGACCTTTG	GAGGCTTTCTG	AGAGTGGGACG	CCACGCGCAG	-----	2675	
QY	2720	CAG	CTGAGTGC	CCCTGCTCCT	CAGATGGG	AGGACAGGGTC	GCCTGTACCCCGGAGGCAC	2779		
DB	2676	-ACC	AGAGAGG	CCCCAGAC	CCAGCTG	AGCAGCCCTGTG	AAAGGCGAGTACTTCAG	AGGGCAG	2734	
QY	2780	CTGGG	TCCATCAG	AGAAAGTGC	AGGTGAC	AGAGGGGAAAGG	CAGATGGG	CACATGACCCAG	2839	
DB	2735	AGATGG	-	-----	AGCCTTCTCT	GGATGACGTTG	AGGTCACCTGG	ACTGTGACACGAGA	2784	
QY	2840	GAGG	AGAAAGC	AGCCATTCG	CACTGTGG	AGCTCAGTGTG	TTCTGGGATTTATGCC	AAGGCC	2899	
DB	2785	GAGG	ACAGTGTG	AGATGAGG	CGGTGAAG	AGCGCCACATAC	CTGAGCTACCTG	CGGGCG	2844	
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DB	2845	GTGGG	CACACCCCTCTG	CACCTTAC	ACCCTGTTCCTCT	CTGCCAGCA	AGTGGCGTCC	2904		
QY	2960	ATTG	AGC	CAATGTGTG	GCTCAGTGCCTG	GACAAATGATGC	CATGGCAGACAGT	AGACAG	3019	
DB	2905	TTCTG	CCAAAGGCTACT	GGTGA	GCCTCTGGG	CGCAGCACCCGGTCTG	TGATGGGAAGCAG	2964		
QY	3020	AACA	CACTTCCCTG	AGGCTGGG	CTCTATGCTGCTTTT	AGGAATTTCTG	CAAGGGTCTTTG	3079		
DB	2965	ATG	CAATCAG	CCCTCGGTG	CTCCATCTTTG	GACTCTTTGGCTGTCTG	CAAGCCATCGGA	3024		
QY	3080	GTG	ATGCTGG	CAGCCATG	GCCTAGCG	GGGTGGCATCC	AGGCTGCGCTGTGTTGCAC	3139		
DB	3025	CTGTTTG	GCCTCCATG	GGCTGCGGTGTTCT	CTGGTGGAGCCG	AGCTTCATG	CGCTTTTTC	3084		
QY	3140	CAGG	CACTGTG	CACAAAG	ATACGCTCGC	CACTCTTTTG	ACACCAACCACTCA	3199		
DB	3085	CGG	AGCTTCTCTG	GAGGTGG	CTCGCTCTCCCA	TGCTTTTG	AGCGCACACCACTG	3144		
QY	3200	GGCC	CACTCCG	ACTGCTTCT	CCAAGGACATCTATG	CTGTGATG	AGGTCTCGCCCT	3259		
DB	3145	GGAA	CACTGCTGA	ACCGTTTTT	TCCAAGGAGACG	GACATAGTGG	ATGTGGACATCC	3204		
QY	3260	GTCA	TCTCTCATG	CTGCTCA	ATTCTCTTCA	ACGCACTCC	CACTTCTGTGGT	CATCATG	3319	
DB	3205	AAGAT	GAGGACCCCTG	CTGACCTATGC	CTTTGG	ACTCTGG	AGGTGGCCTGG	CAGTGTG	3264	
QY	3320	GCC	AGCAGCGCG	CTCTTCA	CTGTGCTATC	CTGCCCCCTGG	CTGTCTATAC	CCCTTAGT	3379	
DB	3265	ATG	CCACACCACTG	GGTATTG	TGGCCATCCTAC	CTCTATGCT	CTTTATGCTGG	TTT	3324	
QY	3380	CAG	CGCTTCTATG	CAGCCACATC	ACGCACTGA	AGCGGCTGG	AATCAGT	CAGCCGCTCA	3439	
DB	3325	CAG	AGCTCTAC	GTGGCCACATGTTG	CAGCTG	AGACGCTGG	AGTGGCG	CAGTTACTCC	3384	
QY	3440	CCT	ATCTACTCCC	ACTTTTCG	GAGACAGTACTG	GTGCTG	CTCATCCG	GGCCCTACAAC	3499	
DB	3385	TCAG	TGCTTCCCATCTG	GCTGAG	ACCTTCC	AGGCGAGT	TCAGTGGT	CAGGGCCTTCAG	3444	
QY	3500	CGC	AGCGGG	ATTTGAG	ATCATCAGT	GTATTAAG	GTGGATG	CCAACCAAG	AGCTGC	3559
DB	3445	GCCC	AGGGGCCCTT	CACAGCTC	ACGACGATG	CCCTCATGG	ATGAGACCA	GAGATCAGT	3504	
QY	3560	TAC	CCCTTACATCATCT	CCAACCG	TGGTGG	ATCAGCAT	CGAGTGG	AGTTCTG	TGGGAACTGC	3619
DB	3505	TTCC	CGAGGCTGGT	GTGAC	AGGTGGCTGG	CTGCCAACCT	GGAGCTCT	TGGGAA	TGC	3564
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Db 661 AGGGCATCAGGAGGTGAGCTCCAGCTGTGCGCAGCGGGGCTACCTCCACACACAA 720
QY 1608 CCACCTTACCTGGATGTGTCAGCCCTCTCTGCTGACCCCTGATCACCCTCTGGGTGACG 1667
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QY 1668 TGTACGTGACCCAAACAATGTGTCGGACCGCGAGAGGCTTGTGTCTGTCTCTCTGT 1727
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QY 1728 TTAATATCTTAAGACTTCCCTCAACATGCTGCCCGCCAGTTATCAGCAACCTGACTCAGG 1787
Db 841 TTAATATCTTAAGACTTCCCTCAACATGCTGCCCGCCAGTTATCAGCAACCTGACTCAGG 900
QY 1788 CCAGTGTGCTCTGAAACGGATCCAGCAATCTCTGAGCCAGAGGAACCTTGACCCCGAGA 1847
Db 901 CCAGTGTGCTCTGAAACGGATCCAGCAATCTCTGAGCCAGAGGAACCTTGACCCCGAGA 960
QY 1848 GTGTGGAAGAAGACCACTCTCCAGGCTATGCCATCACCATACACAGTGGCACCCTTCA 1907
Db 961 GTGTGGAAGAAGA-CATCTTCCAGGCTATGC--ATACCATACACAGTGGNACCTTTA 1017
QY 1908 CC 1909
Db 1018 CC 1019

RESULT 9
US-09-998-598-2049/c
; Sequence 2049, Application US/09998598
; Patent No. US20020150922A1
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Meagher, Madelein Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.561
; CURRENT APPLICATION NUMBER: US/09/998,598
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 2049
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-998-598-2049

Query Match 8.2%; Score 418; DB 10; Length 418;
Best Local Similarity 100.0%; Pred. No. 1.4e-95;
Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4566 CCAGAGATGCTGGACTTGGCTTAAATAATATTCCTGAGATTTCCCTCGGCTTTCTCTGGT 4625
Db 418 CCAGAGATGCTGGACTTGGCTTAAATAATATTCCTGAGATTTCCCTCGGCTTTCTCTGGT 359
QY 4626 TTTTCATCAGGAAGAAATGACACCAATATGTCGCGAGATGGACTGTATGACCAAACT 4685
Db 358 TTTTCATCAGGAAGAAATGACACCAATATGTCGCGAGATGGACTGTATGACCAAACT 299
QY 4686 GGGGGACCTTAAGATTTGACCTGTAAAGTGCCTTACAGGGTAACTGTCTGAATGCT 4745
Db 298 GGGGGACCTTAAGATTTGACCTGTAAAGTGCCTTACAGGGTAACTGTCTGAATGCT 239
QY 4746 TTAGATGAGGAATGATCCCAAGTGGTGAATGACACGCCCTAAGGTACACAGCTAGTTTGA 4805
Db 238 TTAGATGAGGAATGATCCCAAGTGGTGAATGACACGCCCTAAGGTACACAGCTAGTTTGA 179

QY 4806 GCCAGTTAGACTAGTCCCGGTCTCCGATTCCCAACTAGTGTATTGTCACACTGCAC 4865
Db 178 GCCAGTTAGACTAGTCCCGGTCTCCGATTCCCAACTAGTGTATTGTCACACTGCAC 119
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Db 118 TGTATTTCAATAAAGATTTATGAATGACCTCTGCTCCCTCTGATTTTTCATATTTT 59
QY 4926 CTAAGTTTCTGTTCTGTTTAAATAAAGCTTTTCTCTCTGGAACAGACAG 4983
Db 58 CTAAGTTTCTGTTCTGTTTAAATAAAGCTTTTCTCTCTGGAACAGACAG 1

RESULT 10
US-09-998-598-175
; Sequence 175, Application US/09998598
; Patent No. US20020150922A1
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Meagher, Madelein Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.561
; CURRENT APPLICATION NUMBER: US/09/998,598
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 175
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-998-598-175

Query Match 8.0%; Score 407; DB 10; Length 419;
Best Local Similarity 99.8%; Pred. No. 8.2e-93;
Matches 418; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 4566 CCAGAGATGCTGGACTTGGCTTAAATAATATTCCTGAGATTTCCCTCGGCTTTCTCTGGT 4625
Db 1 CCAGAGATGCTGGACTTGGCTTAAATAATATTCCTGAGATTTCCCTCGGCTTTCTCTGGT 60
QY 4626 TTTTCATCAGGAAGAAATGACACCAATATGTCGCGAGATGGACTGTATGACCAAACT 4685
Db 61 TTTTCATCAGGAAGAAATGACACCAATATGTCGCGAGATGGACTGTATGACCAAACT 120
QY 4686 GGGGGACCTTAAGATTTGACCTGTAAAGTGCCTTACA-GGGTAACTGTGCTGAATGC 4744
Db 121 GGGGGACCTTAAGATTTGACCTGTAAAGTGCCTTACAGGGTAACTGTGCTGAATGC 180
QY 4745 TTTAGATGAGGAATGATCCCAAGTGGTGAATGACACGCCCTAAGGTACAGCTAGTTTG 4804
Db 181 TTTAGATGAGGAATGATCCCAAGTGGTGAATGACACGCCCTAAGGTACAGCTAGTTTG 240
QY 4805 AGCCAGTTAGACTAGTCCCGGTCTCCGATTCCCAACTGACTGTATTGTCACACTGCA 4864
Db 241 AGCCAGTTAGACTAGTCCCGGTCTCCGATTCCCAACTGACTGTATTGTCACACTGCA 300
QY 4865 CTGTTTTCAATAAAGATTTATGAATGACCTCTGCTCCCTCTGATTTTTCATATTTT 4924
Db 301 CTGTTTTCAATAAAGATTTATGAATGACCTCTGCTCCCTCTGATTTTTCATATTTT 360
QY 4925 TCTAAAGTTTCTGTTCTGTTTAAATAAAGCTTTTCTCTCTGGAACAGACAG 4983
Db 361 TCTAAAGTTTCTGTTCTGTTTAAATAAAGCTTTTCTCTCTGGAACAGACAG 419

RESULT 11
US-09-980-107-3832
; Sequence 3832, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:

; APPLICANT: Horne, Darci T.
 ; APPLICANT: Vockley, Joseph G.
 ; APPLICANT: Scherf, Uwe
 ; APPLICANT: Gene Logic, Inc.
 ; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
 ; FILE REFERENCE: 44921-5028-WO
 ; CURRENT APPLICATION NUMBER: US/09/880,107
 ; CURRENT FILING DATE: 2001-06-14
 ; PRIOR APPLICATION NUMBER: US 60/211,379
 ; PRIOR FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: US 60/237,054
 ; PRIOR FILING DATE: 2000-10-02
 ; NUMBER OF SEQ ID NOS: 3950
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3832
 ; LENGTH: 1936
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X95715
 ; US-09-880-107-3832

Query Match 7.6%; Score 386; DB 10; Length 1936;
 Best Local Similarity 60.3%; Pred. No. 3.8e-87;
 Matches 638; Conservative 0; Mismatches 420; Indels 0; Gaps 0;

Qy	3556	CTGCTACCCCTACATATCTCCAAACGGTGGCTGAGCATCGGAGTGGAGTTCTGTTGGGAA	3615
Db	445	CTGTTCTCTCTACGCTGGGTTTTCAGTGGCTTGGCGCAATGTGGAGTCTCTGGGAA	504
Qy	3616	CTGGTGGTCTCTTCTGCTGACATTTTGGCGTCATCGGGAGGAGCCCTGAACCCGGG	3675
Db	505	TGGCTGTGTGTTCCAGCTGCGACGTGTGCTGTGCTGAGCAAAACCCACCTCATGTCTGG	564
Qy	3676	GCTGGTGGGCTTCTTGTGCTACTCTTGCAGGTGACATTTTCTGTAAGTGGATGAT	3735
Db	565	CTCTGGGCTTCTCTCTCTGCTGCTCCAGTGCACCCAGACACTGCAGTGGTTGT	624
Qy	3736	ACGAATGATGACATTTGGAATCTACATCGTGGCTGTGGAGAGGTGCAAGGAGTACTC	3795
Db	625	TCGCAACTGGACACACCTAGAGAACAGCATCGTCTAGTGGAGGGATGCGAGGACTATGC	684
Qy	3796	CAACAGACAGACAGCGCCCTGGTGGTGGAGGAGCGCCCTCCGAAAGTGTGGCC	3855
Db	685	CTGACCCCAAGAGGCTCTCTGGAGGCTGCCACATGTGACACTCAACCCCTGGCC	744
Qy	3856	CCACGTGGGAGGTGGAGTTCCGGAATTTCTGTGCGTACCGCGCGGCTTAGACCT	3915
Db	745	TCAGGGCGGCAGATCAGTTCCGGACTTTGGCTAAGATACCGACTGAGCTCCGCT	804
Qy	3916	GGTCTGAGAGACCTGAGTCTGCATGTGCACGGTGGCGAGAGGTGGGATGCTGGGCGG	3975
Db	805	GGTGTGACGGGCTGTCTTCAAGATCCAGGAGAGAGGTGGGCATCGTTGGCAG	864
Qy	3976	CACGTGGGCTGGCAAGTCTCCATGACCTTTGCTCTCCGATCTCGAGCGGCAAA	4035
Db	865	GACCGGGCAGGAGTCTCTCCCTGGCAGTGGCTCTGGGCTCCAGGAGGAGCTGA	924
Qy	4036	GGGTGAATCCGATTTGATGGCTCAATGTGGCAGACATCGGCTCCATGACCTCGCGTC	4095
Db	925	GGGTGGATCTGGATCGACGGGTCCCATTTGCCACGTGGGCTGCACACATCGCGCTC	984
Qy	4096	TCAGCTGACCATCATCCCGAGAGACCCCATCTCTGTTCTGGGAGACCTCGCATACACT	4155
Db	985	CAGGATCAGATCATCCCGAGGAGCCCATCTCTCTCCCTGGCTCTCTGGGATGAACCT	1044
Qy	4156	GGACCCCTCGGAGCTACTCAGAGGAGACATTTGTTGGCTTTGGAGCTGTCCACCT	4215
Db	1045	CGACCTCTGCAGAGACACTCGGAGAGGTATCTGGGAGCCCTCGAGAGGCTGACCT	1104
Qy	4216	GCACACCTTTGTAGCTCCCGAGCGGAGGCTGACCTTCCAGTGTCCAGAGGCGGGA	4275
Db	1105	CANAGCCCTTGGTGGCTTGGCTTGGCCCGCCAGCTGCAGTACAAAGTGTCTGACCGAGCGGA	1164

RESULT 12
 US-09-938-842A-1674
 ; Sequence 1674, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: SPRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SCRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 1674
 ; LENGTH: 4551
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; US-09-938-842A-1674

Query Match 7.0%; Score 354; DB 9; Length 4551;
 Best Local Similarity 45.9%; Pred. No. 6.9e-79;
 Matches 1671; Conservative 0; Mismatches 1865; Indels 108; Gaps 9;

Qy	893	CCCTCTCTCTGAAAGGCCCTCTGCGCCACCTTCGGCTCCAGCTTCCTCATCAGTCCGTCG	952
Db	934	CACCTATCCGTACGACTCTACTCCGATGTTCTTGGAGGAGAGATCCTCTTACCCTGATT	993
Qy	953	TTCAAGCTTATTCAGGACCTCTCTCTTTCATCAATCCACAGCTGCTCAGCATCTGTATC	1012
Db	994	CTAGCCATCGTCCGCTCGGCGTCATGTCGTTGTTGTTGTTCTCATCCAGAGCTTCGTC	1053
Qy	1013	AGGTTTATCTCCACCCCATGCCCCCTCTCTGTTGGGCTTCCTGGTGGCTGGCTGATG	1072
Db	1054	GATTTACCTCCCGCAAGAGATCTCCCGCTGGCAAGGTTATTACCTGCTCTCATCTC	1113
Qy	1073	TTCTGTGCTCCATGATGTCAGTCTGATCTTACACACTATTACCACTACATCTTTGTG	1132
Db	1114	CTTGTGCCAANTTCGTGAGGCTTTGACGAGCATCATAGTTCAATTTCCGATTCCGAGAAG	1173

QY 1133 ACTGGGTGAAGTTTCGTACTGGGATCATGGGTGTCACTACAGGAAGGCTCTGGTTATC 1192
DB 1174 CTTGGGATGCTTATAGGTCAACTTAATCACTGCACTCTACAAGAAAGGTTTAAAGCTC 1233
QY 1193 ACCAACTCAGTCAAAAGTGGCTCCACTGTGGGGAAATGTTCAACCTCATGTTCAGTGGAT 1252
DB 1234 ACAGGCTCTGGCGTCAGAACACCGCGTAGGACAAATCGTGAATACATGGCCGTAGAT 1293
QY 1253 GCCCAGCGCTTCATGGACCTTGCCGCCCTTCCTCAATCTGCTGTGTGTCAGCACCCCTGCGAG 1312
DB 1294 GCACAACAGCTCTCTGACATGATGCTTCAGCTCCACGCAATCTGCTCATGCTTTGCAA 1353
QY 1313 ATCATCTTGGCGATCTACTTCTCTGCGCAGAACCTAGTTCCTGCTGCTGCTGCTGAGTTC 1372
DB 1354 GTCACCTGTGCACTAGTCTCTCTACCGGAGCCCTAGCGGCTCTGTTATACCGCGT 1413
QY 1373 GCTTTCATGGTCTTCTGATTCCACTCAACGGAGCTGTGGCGTGAAGATGCGGCCCTTC 1432
DB 1414 ATTGGGCTGACTGGAGTGTCTGCTTTCATCTCTCTGGGACTCAGAGAAACACGGATAC 1473
QY 1433 CAGGTAAAGCAAAATGAATTTGAAGACTCGCGCATCAAGCTGATGAGTGAGATCTCTGAAC 1492
DB 1474 CAATTCAGCTTGATGGGAAACCGAGATCTCGATGAGGCCACCAACGAGATGCTCAAT 1533
QY 1493 GGCATCAAGGTGCTGAAGCTGTACGCCCTGGGAGCCCACTTCTTCCGAAAGAGTGGAGGCG 1552
DB 1534 TACATCGAGTGCATCAAGCTTTCAGGCTTGGGAGAAATCATTTTAAACAAGAGGATCTCAA 1593
QY 1553 ATCAGGAGGCTGAGCTCCAGCTGCTGCGCAGCGGCGCTACCTCCACCAACACACCC 1612
DB 1594 TTCAGGAGACATGGAGTTTGGTGGCTTCCAAAGTTTCTTACTCCATTCCTGGGCAATAT 1653
QY 1613 TTCACCTGGATGTGAGCCCTTCTGCTGACCTGATCACCTCTGGGTGATGCTGTAC 1672
DB 1654 ATGTCTCTGGAGCACCGAGTGTATCTCTGCTCTCACCTTCGCCAACCCCTTGC 1713
QY 1673 GTGGACCAACAATGCTGAGCCCGCAGAGGCTTTGTGTGCTGTGCTGTGTTTAAAT 1732
DB 1714 TTGGGAGTCAA-----GCTTGAGCTGGGACTGTGTTCACCAACCAACCAATTTTCAAG 1767
QY 1733 ATCTTAAGACTTCCTCAACATGCTGCCAGTTAATCAGCAACCTGACTCAGGCCAGT 1792
DB 1768 ATCTGCAAGAACCTATCAGGAGCTTCTCAGTCTATGATTTCTCTCGGCAACATG 1827
QY 1793 GTGTCTGAAACGGATCCAGCAATTCCTGAGCCAAAGAGAACTTGACCCCGCAGAGTGTG 1852
DB 1828 ATCTCTCTGGGAGACTGGACTATACATGATGAGCAAGAGCTGTGGAAGATGCTGTG 1887
QY 1853 GAAAGAAAGACCATCTCCCGAGGCTATGCCATCACCATACAGAG---TGGCACCTTCACC 1909
DB 1888 GAGAGAGCCCTGGGTGTGTGATGATTAATCTCCGCTGGAGGTCAGAGATGGAAGCTTTAGT 1947
QY 1910 TGGGCC---AGGACCTGCCGCCCTCTGCACAGCTTAGACATCCAGCTCCCGAAAGGG 1966
DB 1948 TGGGATGATGAGGACAAAGAACCTGCTCTAGTATATCAACTCAAGGTTAAGAAAGGT 2007
QY 1967 GCACTGTGGCGGTGGGCGCTGTGGGCTGTGGGAGTCTCCCTGGTGTCTGCCCTG 2026
DB 2008 GAGCTCACTGGATGTGGAACCGTTGGTTTCAGGGAATCTTCTCTGTAGCTTCGGTT 2067
QY 2027 CTGGGAGATGGAGAGCTAGAGGCAAGTGCACATGAAGGCTCCGTGGCTATGTG 2086
DB 2068 CTTGGTGAATGACAGAAATCTCAGGCGAGGTGAGAGTTTGTGGGAGCAAGTTATGTA 2127
QY 2087 CCCGAGGAGCATGATCCAGAACTGACCTTCTCAGGAAACGTGCTTTTCGGCAAGCC 2146
DB 2128 GCTCAGAGCTGCTGGATGAAACGGGAGGTTTCAAGACAACTCTTGTGGTCTTCCA 2187
QY 2147 CTGAACCCAAAGCGCTACACAGACTCTGGAGGCTGTGCTGTGCTAGCTGACCTGGAG 2206
DB 2188 ATGTTAGAGAGAGTACAAAGTCTCAATCTCTGTTCTTGTGAAAGAACCTACAA 2247
QY 2207 ATGTGCTGTGGTGGGATCAGACAGAGATTGGAGAGAGGSCATTAACCTCTCTGGGCGC 2266

DB 2248 ATGATGGAGTTTGGAGATAAGACTGAGATTGGAGAACGGGAATCAACCTCAGCGGAGG 2307
QY 2267 CAGCGCAGCGGTGAGTCTGCTGCTGAGCTGTTTACAGTGTATCCCATATTTTCTTGTGCTG 2326
DB 2308 CAGAACAACGTATACAGCTCGCACGTGCTCTATCAGGAATGCGATGTATCTTGTCTC 2367
QY 2327 GATGACCCACTGTCCCGGTGGACTCTCATGTGGCCCAAGCACATCTTTGACCAACGTCATC 2386
DB 2368 GAGGATGTTTTAGCGCACTGGATGCTCATCCGGTTTCAGATATTT-----CAAGAAA 2421
QY 2387 GGGCCAGAAGCGTGTGTCAGCAGCAAGACGCGAGTCTGCTGTCAGCAGCAGCATTAGCTTC 2446
DB 2422 TGTGTAAGAGAGCTGTGAAGAGCAAGACGCTATTAACCTGTTACCCATCAAGTGGATTTC 2481
QY 2447 CTGCCCCAGACAGACTTTCATCATTTGCTAGCTGATGGAGAGCTGCTGAGATGGGCCCG 2506
DB 2482 TTGCACAACGTGATGTCATCTTGGTGTATGCGGGATGGAAGATTTGTTGAATCAGGAAA 2541
QY 2507 TACCCAGCCCTGCTGCGCGCAACCGCTCTTTCGCAACTTCTCTGCAACTATGCCCC 2566
DB 2542 TATGAGCAATTAGT-----CAGCTCCGGATTGGATTTTGGGGAACCTTGTGGCTGCA 2592
QY 2567 GATGAGGACCAAGGCACTGAGGAGACGTGGACCGCTTGGAAAGTGCAGAGGATAAG 2626
DB 2593 CATGAGACGTCAATGAGAGCTGTTGAAGCGGTGTCAGACTCTGCAGCAGTCGCCACATCC 2652
QY 2627 GAGGCACTGCTGATTTGAAGACACACTCAGCAACCAACCGGATCTGACAGACAATGATCCA 2686
DB 2653 CCAAGAACAACCACTCTCCCATGCAAGCTCTCCGAGAACGTCATGGAAGTCTCCTCAC 2712
QY 2687 GTCACCTATGTGGTCAGAAAGCACTTATGAGACAGCTCAGTGCCTCTCTCAGATGGG 2746
DB 2713 TTAAGTATCTAAGCAATGAGCATATCAATCATTTCTCGTTCTCAGATCGTAGA---- 2768
QY 2747 GAGGACAGGCTGGCCCTGTACCCCGGAGGACCTGGGTCCATCAGAGAAGTGCAGGTG 2806
DB 2769 -----AGATGGCTCGAAGCTCATCAAGAAGAAGAAGAGG 2803
QY 2807 ACAGAGCGAAGGCAAGTGGGCACTGACCCAGGAGGAGAAAGACGCAATTTGCCACTGTG 2866
DB 2804 AAACGGACAGGTTAGCTTAGGATTTACAAA----- 2835
QY 2867 GAGCTCAGTGTCTTGGGATTATCCAAAGCGCTGGGCTCTGTACCACTGCGCATC 2926
DB 2836 -----CAGTACTGCACTGAGGCTTATGGCTGGTGGGAATTTGCTTGT 2880
QY 2927 TGTCTCTGTATGTGGTCAAAAGTGGCGTGCATTTGGAGCAATGTGTGGCTCAGTGCC 2986
DB 2881 CTGTTCTCTCTGACGCTGGCAGGGATCTCTAATGGCCAGCGATTACTTGGCTTGCAATC 2940
QY 2987 TGGCAAAATGATCCATGSCACAGACTAGACAGACAACACATTCCTGAGGCTGGCGCTC 3046
DB 2941 GAAACATCAGCCAAAATGCA-----ATATCATTTGATGCTTCGGTTTTCATCTCGGA 2994
QY 3047 TATGCTGCTTAGGAATTTCTCAAGGTTCTTGTGTGATGCTGGCAGCCATGGCCATGGCA 3106
DB 2995 TATGTAATTTATGCACTTGTTCATCGTTTGGTGAGCATCGGTCATATTTACGTCACC 3054
QY 3107 GCGGTGGCATCCAGGCTGCCCGTGTGTGGACCAAGGCACTGCTGCACAACAGATACGC 3166
DB 3055 CACTTGGGACTCAAGACGCTCAGATCTTTTCCGACAGATCTTTAATAGTATCTTTACAC 3114
QY 3167 TCGCCACAGTCTCTTTTGACACACACCATCAGCCGCGATCTGAACTGCTTCTCCAG 3226
DB 3115 GCTCCCATGTCTTTTGACACACGCACTCGGGAAGAAATTTCTCAGTGGCGCATCGACT 3174
QY 3227 GACATCTATGTGTGATGAGGTTCTTGGCCCTGTCTCTCATCTGCTCAATCTCTTC 3286
DB 3175 GATCAGACCAATGTCATATCTTAATCGTTTATGCTCGGACTGTGTGCTCAATGTAC 3234
QY 3287 TTCAAGCCCATCTCCACTCTTGTGCTCATCATGGCCAGCACGCGCTCTTCACTGTGCTC 3346

Db 3235 ACCACTCTGCTGACGATTTTTCATAGTTACCTGCCAGTACGCTTGGCCAACTGCATTTCTTT 3294
QY 3347 ATCTGCCCCCTGGCTGTCTCTACACCTTAGTGCAGCGCTTCTATGAGCCACATACAGG 3406
Db 3295 GTGATTCCTCCCTTGGCTGTCTCTAACTATGCTGATGCTGAGCAATATTACCTGCTTCTTCCCGT 3354
QY 3407 CAACCTGAAGCGCTGGAACTAGCTGAGCGCTCACCCTATCTACTCCCACTTTTTCGGAGACA 3466
Db 3355 GAATTAACACCGCATGGACTCAATCACTAAGGCTCCCATATCCACCACTTTCTCTGAAAGT 3414
QY 3467 GTGACTGGTGCAGTGTCTATCCGGGCTTACAACCGCAGCGGGGATTTTGTAGATCATCAGT 3526
Db 3415 ATAGCTGGAGTGAACATCCGATCATTCAGGAAGCAGGAGTTGTTTAGACAGAGAAAT 3474
QY 3527 GATTAAGTGGATGCAACACGAGAGAGCTGTCTACCCCTACATCATCTCCAAACCGGTGG 3586
Db 3475 GTAAAGAGTGTAAATGATATCTCAGGATGGACTTCCACAAACATGCTCCAAAGCAATGG 3534
QY 3587 CTGAGCATCGGAGTGGAGTTCTGCGGGAACCTCGGTGCTCTTTGCTGGCACTATTTGCC 3646
Db 3535 CTCGGTTTCCGCTGGAGCTGGTTGGGAGCTGGGTGCTCTGCACTCTCGGCTTTTCTTATG 3594
QY 3647 GTCATCGGAGGAGCAGCCCTGAAC---CCGGGGCTGTGGGCTTTCTGTGTCTCTACTCC 3703
Db 3595 GTATTGTTACCCAGCAACGTTATCAGACACAGAGAATCTAGGGTTGTCCCTGCTGTACGGA 3654
QY 3704 TTGAGGTGACATTTGCTGTGAAGTGTATGATGAGGAATGATGTCAGATTTGGAAATCTAAC 3763
Db 3655 CTGTCCTGAACTCGGTCTGTCTTTTGGCCATATACATGAGCTGCTTTGTCGAGAACAAG 3714
QY 3764 ATCTGTGCTTGGAGAGGGTCAAGGATCTCTCCAAAGACAGACAGAGCGCCCTGGGTG 3823
Db 3715 ATGTTTTCAGTTGAAGAGTCAACAGCTTCACTGATATTCCTCCAGAAATCCGAGTGGGAG 3774
QY 3824 GTGAAGGAGCGCCCTCCCGAAGTGTGGCCACGTGGGAGGTGGAGTTCCCGGAAT 3883
Db 3775 AGAAAGAAACCCCTTCCACCTTCGAATTTGGCCCTTCCATGGCAATGTACATCTCGAAGAC 3834
QY 3884 TATCTGTGCTTACCGGCTGAGCTGAGCTGTGTGAGAGACCTGTAGTCTGCAATGTG 3943
Db 3835 CTCGAAGTGGCTTACAGACCGCACTTCCACTTTGTCTCAAGGGGATCACTCTTGATC 3894
QY 3944 CACGGTGGCAGAGGTGGGATCTGTGGCGGCACCTGGGGCTTGCAAGTCTTCCATGACC 4003
Db 3895 AAAGGAGAGAGAGTGTGTGTGGAGCAGCAGGGAAGCGGGAATCGACATGATC 3954
QY 4004 CTTTGCTGTTCGCACTCTCGGAGCGGCAAGGGTGAATTCGCAATGTATGGCTCAAT 4063
Db 3955 CAAGTCTTTGTCAGGCTTGTAGAACCATCAGGAGGAAGATATCATAGACGGGATGTAT 4014
QY 4064 GTGCAGACATCGGCTTCCATGACCTGCGCTCTCAGCTGACCATGACCTATCCCGCAGGACCC 4123
Db 4015 ATAAGCACTTAGGGTTACATGATCTCAGTCAAGATTCGGAATCATTCGCGCAAGAACCT 4074
QY 4124 ATCTGTCTCGGGACCTCGCATGAACCTTGACCCCTTCGCGCACTACTCAGAGGAG 4183
Db 4075 GTCTCTTTGAAGAACCTGTGAAGCAACATCGACCGACAGCAATACTCTGAGCAA 4134
QY 4184 GACATTTGGTGGCTTTGGAGCTGTCCCACTGCACACAGCTTTGTGAGCTCCCGCAGCGCA 4243
Db 4135 GAAATCTGGAAGAGCCTGGAACGGTGTCAACTCAAGGATGTCTGAGTACCAAGCCTGAG 4194
QY 4244 GGCTGCACTTCAGTGTCTCAGAGGGGGGGAAGATCTCAGCTGGGCCAGAGCGAGCTC 4303
Db 4195 AAGCTCGATTTCTTTTGGTGTGTGATATGCGGGAAGTGGAGCGTAGGCGCAGAGCGAGCTT 4254
QY 4304 GTGTGCTGCGCGGCTGCTCCGCAAGAGCGCGATCTCTGCTTTTAGACGAGGCCACA 4363
Db 4255 CTATGCTTAGCAGGGTTATGTTTGAACCGCAGCAGACTTCTCTCTAGCAGGAAGCACT 4314
QY 4364 GCTGCCATCGACTGAGACTGACAACTCATCCAGCTACCATCGCAGCCCACTGTTGAT 4423
Db 4315 GCATCGGTGATTTCCCAACCGACGCGGTGATTCAGAAGATCATCAGAGAGACTTTGG 4374

QY 4424 ACCTGCACCTGCTCTGACCATCGCACACCGGCTTAACACTATCATGCTACTACACGAGGTC 4483
Db 4375 TCGTGCACCATCATCAGCATCGCCACCGGATTCCTACAGTGTACGAGCGGCGATCGAGTC 4434
QY 4484 CTGCTCCTGGCAAGAGGAGTAGTAGTGAATTTGATTCTCCAGC 4527
Db 4435 CTTGTCTATTGATGCTGGGAAAGCGAAGAGTTCGATAGCCCGGC 4478

RESULT 13

US-10-042-125A-32

; Sequence 32, Application US/10042125A

; Patent No. US20020164345A1

; GENERAL INFORMATION:

; APPLICANT: Jiang, Yuliu

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.557

; CURRENT APPLICATION NUMBER: US/10/042.125A

; CURRENT FILING DATE: 2001-10-18

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 32

; LENGTH: 418

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 1, 4..352

; OTHER INFORMATION: n = A,T,C or G

US-10-042-125A-32

Query Match 6.6%; Score 335.2; DB 9; Length 418;
Best Local Similarity 98.8%; Pred. No. 9.5e-75;
Matches 337; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4475 ACCAGGTCCTGGTCTGGGCAAAAGGAGTAGTAGTGAATTTGATTTCCAGCCCAACCTC 4534

Db 78 ACTAGGTCCTGGTCTGGGCAAAAGGAGTAGTAGTGAATTTGATTTCCAGCCCAACCTC 137

QY 4535 ATTCACTAGAGGCATCTTCTAGGGATGCCAGAGATGCTGGACTTGCCTAAATATA 4594

Db 138 ATTCACTAGAGGCATCTTCTAGGGATGCCAGAGATGCTGGACTTGCCTAAATATA 197

QY 4595 TTCCTGAGATTTCTCTCTGGCTTTCTCTGGTTTCATCAGGAAGAAATGACACCAATA 4654

Db 198 TTCCTGAGATTTCTCTCTGGCTTTCTCTGGTTTCATCAGGAAGAAATGACACCAATA 257

QY 4655 TGTCGCGAGAATGGACTGTGATAGCAAAACACTGGGGGCACTTAAAGATTTTGCACCTGAA 4714

Db 258 TGTCGCGAGAATGGACTGTGATAGCAAAACACTGGGGGCACTTAAAGATTTTGCACCTGAA 317

QY 4715 AGTCCCTTACAGGTAATCTGTGCTGAATGCTTTAGATGAGGAATGATCCCAAGTGTG 4774

Db 318 AGTCCCTTACAGGTAATCTGTGCTGAATGCTTTANATGAGGAATGATCCCAAGTGTG 377

QY 4775 AATGACACGCTTAAGTTCACAGCTAGTTTGGCCAGTTAGA 4815

Db 378 AATGACACGCTTAAGTTCACAGCTAGTTTGGCCAGTTAGA 418

RESULT 14

US-09-938-842A-436

; Sequence 436, Application US/09938842A

; Patent No. US20020160378A1

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; TITLE OF INVENTION: SAME, AND METHODS OF USE

Db 2740 GCACTTGGAGGGGCGATGGGTAGTGATGATGCTCTCTTTTATGTTACGCTCTTAACAGAACTA 2799
QY 2948 AGTGCCTGCTGATGGAGCAATGTGTGCTCAGTCCCTGGGCAAAATGATGCCATGGCA 3007
Db 2800 TTTGGGTTACTA-----GCAGACGTGGTTGAGTGGAGTGGATGATGAGGAAGTCCA 2853
QY 3008 GACAGTAGACAGAACACATCTCCCTGAGCTGGCGCTCTATGCTGTCTTAGGAATCTG 3067
Db 2854 AAGAGT-----CATGGACCCCTTTCTACAATCTCAATATGACATCTCTCTGTTTGG 2907
QY 3068 CAAGGGTCTTGTGTGATGGGAGCCATGGCCATGGCAGCGGTGGCATCCAGGCTGCC 3127
Db 2908 CAGGTTTGTGATGACATGACCAATTCATATGTTGATGATGATGATGATGATGATGATG 2967
QY 3128 CGTGTGTGACAGGACGTGTCGACAAACAGATGCTGCGGCACAGTCTCTTTTGGAC 3187
Db 2968 AAGAAGTTACACGACAAATATGCTTCAATTCATATGAGGGCCCGATGCTCTTCCAT 3027
QY 3188 ACCACACATCAGGCGCATCTGCTGCTCTCTCAAGACATCTATGCTGTGATGAG 3247
Db 3028 ACCAATCCGTAGGCGGATTAATCAATGATTCGCAAAAGATCTGGGTGATATGATCGA 3087
QY 3248 GTTCTGGCCCTGCTATCTCTGCTGCTCAATCTCTTCAACGCCATCTCCACTCTT 3307
Db 3088 ACTGTGGCGCTCTTTGTAACATGTTTATGGGTCAAGTCTCACAGCTCTTTCAACTGA 3147
QY 3308 GTGGTCAATGAGCCAGCGGCTCTTCACTGTGTGATGATGCTGCTGCTGCTGCTGCTG 3367
Db 3148 GTGTGATTTGGCAATTTGAAGCACTTTGTCTCTGTTGGGCCCATCATGCCCTCTCTGCT 3207
QY 3368 TACACCTTAGTGAGCGCTCTATGAGCCACATCAGGCAACTGAGCGGCTGGATCA 3427
Db 3208 TTTTATGGAGCTTATCTTATATGACAGATTTGAGAGGCAATGATGCTTCAACTATC 3267
QY 3428 GTGAGCGCTCACTATCT 3487
Db 3268 ATTTCAAGATCGCTGTTTATGACAGATTTGAGAGGCAATGATGCTTCAACTATC 3327
QY 3488 CGGCGCTACAGCGAGCGGGATTTTGAATCATCATGATGATGATGATGATGATGATGAT 3547
Db 3328 CGTGTCTTACAAAGCATATGATGATGATGATGATGATGATGATGATGATGATGATG 3387
QY 3548 CAGAGAGTGTACCCCTACATCATCTCAACCGGTGCTGAGCATCGAGTGGAGTTC. 3607
Db 3388 ATCAGATTCACCTTGTCAACATGGGTGCAATCGGTGGCTTGAATCCCTTTAGAACT 3447
QY 3608 GTGGGAACTGCTGTGCTCTTTGCTGCTATTTGCTGCTATCGGGAGGAGCAGCGTG 3667
Db 3448 CTGGGTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3507
QY 3668 AACCGGGGTG-----TGGGCTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3712
Db 3508 GAGAACAACAGGCAATTTGCATCATCAATGGGTGCTTCTCTGATGATGCTTAAATAT 3567
QY 3713 ACATTTGCTGTAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3772
Db 3568 ACTAGCTTGTAAACAGTGTCTGAGACTTGCAGTTTGGCTGAGATATGCTAAACGG 3627
QY 3773 GTGGAGAGGTCAAGAGTACTTCAAGACAGACAGAGAGCGGCTGGTGGTGGAGGC 3832
Db 3628 GTGAGCGGTGTTGGCAATATATAGAGATTCGCCAGAGGCTCCGCTGCTGATGAGAAC 3687
QY 3833 AGCGGCTTCCGAAGTGTGGCCCGACGTGGGGAGGTGAGTTCGGGAATATTTCTGTG 3892
Db 3688 AACCGTCCACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3747
QY 3893 CGTACCGCGCGGCTAGACTGCTGCTGCTGAGAGCTGAGTGTGATGCTGACGCTGGC 3952
Db 3748 CGTATCGGCGCTAGTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3807
QY 3953 GAGAAGTGGGATCTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4012
Db 3808 GATAGGTGGGATTTTGAAGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3867

QY 4013 TTCCGCATCTCTGGAGCGGCAAAAGGTGAATCCGCATTTGATGGCTCAATGTGCAGAC 4072
Db 3868 TTTAAGATTTGGAGGTGGAAGAGGAGGATCTTAATCGATGATGTGACGTTTGAAG 3927
QY 4073 ATCGGCTTCCATACCTCGCTCTCAGCTGACCATCATCCCGCAGGACCCCATCTGTC 4132
Db 3928 TTTGACTGATGGACCTTACGTTAAAGTGTCTCGAATCATTCACAGCTCACCGGTTCTTTC 3987
QY 4133 TCGGGGACCTTCCGCATGAACCTTGACCCCTTGGCAGCTACTCAGAGGAGGACATTTGG 4192
Db 3988 TCAGAACTGTGAGTTCATCTTGAATCTTGAATCTTGTGAACACAATGATGCTGTTGG 4047
QY 4193 TGGCTTTGGAGCTGTCCCACTTGCACAGTGTGTGAGCTCCCGCAGGAGCCCTGAC 4252
Db 4048 GAATCTCTAGAGGGGACACTTGAAGGATACCATCCCGCAGAAATCTCTTGGTCTGAT 4107
QY 4253 TTCCAGTCTCAGAGGGGGGAGAACTCAGCGTGGGCCAGAGGAGCTGCTGTGCTG 4312
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QY 4313 GCCGAGCCCTGCTCCGCAAGAGCGCATCTCTGTTTGTAGAGGCGCACAGCTGCCATC 4372
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QY 4433 GTCTGACCATCGACACCGGCTTAAACATATCATGAGTACAGGAGTCTGCTGCTGCTG 4492
Db 4288 ATGCTCATTTATCGCTACCGCTCTCAATACCATCATTTGACTGTGACAAATTTCTCGTCT 4347
QY 4493 GACAAAGAGTAGTGTGATTTGATTTCTCCAGCAACCTCATTTGACGCTAGAGGATC 4552
Db 4348 GATTTCTGAGAGTTCAGAAATTCAGTTCACCGGAGAACCTTTTCAATGAGGAAGC 4407
QY 4553 TTCTAC 4558
Db 4408 TCTTTC 4413

RESULT 15

US-09-864-761-16892
; Sequence 16892, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn. Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16892
; LENGTH: 329
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005921.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 19
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.76
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 4.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 9.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
; OTHER INFORMATION: EST_HUMAN HIT: BF336682.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: O15438, EVALUE 7.00e-44
; OTHER INFORMATION: NT HIT: g19955971, EVALUE 0.00e+00
US-09-864-761-16892

Query Match 6.1%; Score 311; DB 10; Length 329;
Best Local Similarity 100.0%; Pred. No. 1e-68;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GGTCTTGGTGATGCTGGCAGCATGCCATGGCAGGGGTGGCATCCAGGCTGCCCGTG 60
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Db 61 TGTTCACCCAGGCACCTGCTGCACAAAGATACGCTCGCCACAGTCTCTTTTGACACCA 120
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Db 121 CACCATCAGCCCGCATCCTGAATGCTTCTCCAAAGACATCTATGCTGTTGATGAGGTTT 180
QY 3252 TGGCCCTCTCATCTCATGCTGCTCAATCTCTTTCACGCCCATCTCCACTCTTGTGG 3311
Db 181 TGGCCCTCTCATCTCATGCTGCTCAATCTCTTTCACGCCCATCTCCACTCTTGTGG 240
QY 3312 TCATATGCCCGCAGCCGGCTCTTTCACCTGTGCTCATCTCTGCCCCCTGGCTGCTCTACA 3371
Db 241 TCATATGCCCGCAGCCGGCTCTTTCACCTGTGCTCATCTCTGCCCCCTGGCTGCTCTACA 300
QY 3372 CCTTAGTGCAG 3382
Db 301 CCTTAGTGCAG 311

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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:05:00 ; Search time 101.285 Seconds
(without alignments)
15378.431 Million cell updates/sec

Title: US-09-647-140A-5

Perfect score: 5079

Sequence: 1 cccatgagccctgtcg.....ctgatgaataaaactacag 5079

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1737.8	34.2	5011	1	US-08-463-092B-1
3	1737.8	34.2	5011	2	US-08-462-109A-1
4	1737.8	34.2	5011	2	US-08-460-907B-1
5	1737.8	34.2	5011	3	US-08-463-179A-1
6	1737.8	34.2	5011	3	US-08-461-384B-1
7	1737.8	34.2	5011	3	US-08-407-207A-1
8	1736.2	34.2	5011	1	US-08-463-092B-3
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19	406.2	8.0	4931	4	US-09-208-716-2
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21	374.8	7.4	2454	3	US-08-476-900A-32
22	374.8	7.4	2454	3	US-08-488-546A-32
23	356	7.0	4781	2	US-09-001-273-1
24	356	7.0	4781	4	US-08-843-459A-1
25	356	7.0	4847	3	US-09-061-400-1
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28 351.4 6.9 4877 3 US-08-476-900A-7 Sequence 7, Appli
29 351.4 6.9 4877 3 US-08-476-900A-8 Sequence 8, Appli
30 351.4 6.9 4877 3 US-08-488-546A-7 Sequence 7, Appli
31 351.4 6.9 4877 3 US-08-488-546A-8 Sequence 8, Appli
32 351 6.9 2294 2 US-08-404-531B-30 Sequence 30, Appl
33 351 6.9 2294 3 US-08-476-900A-30 Sequence 30, Appl
34 351 6.9 2294 3 US-08-488-546A-30 Sequence 30, Appl
35 333.4 6.6 5110 2 US-08-404-531B-5 Sequence 4, Appli
36 333.4 6.6 5110 2 US-08-404-531B-5 Sequence 5, Appli
37 333.4 6.6 5110 3 US-08-476-900A-4 Sequence 4, Appli
38 333.4 6.6 5110 3 US-08-476-900A-5 Sequence 5, Appli
39 333.4 6.6 5110 3 US-08-488-546A-4 Sequence 4, Appli
40 333.4 6.6 5110 3 US-08-488-546A-5 Sequence 5, Appli
41 322.8 6.4 5232 4 US-08-972-927-1 Sequence 1, Appli
42 318.6 6.3 1308 2 US-08-404-531B-1 Sequence 1, Appli
43 318.6 6.3 1308 2 US-08-404-531B-2 Sequence 2, Appli
44 318.6 6.3 1308 3 US-08-476-900A-1 Sequence 1, Appli
45 318.6 6.3 1308 3 US-08-476-900A-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-141-893-1
; Sequence 1, Application US/08141893
; Patent No. 5489519
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/141,893
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923; 08/029,340
; FILING DATE: 27-OCT-1992; 8-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Deconti, Giulio A. Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PQI-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5149
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..4788
; US-08-141-893-1
Query Match 34.2%; Score 1737.8; DB 1; Length 5011;
Best Local Similarity 62.2%; Pred. No. 0;
Matches 2882; Conservative 0; Mismatches 1662; Indels 87; Gaps 6;

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QY 2437 CATTAGCTTCTGCCCCAGACAGACTTTCATATTGTGCTAGCTGATGAGCAGGTGTCTGA 2496
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Db 4140 CACGATCAATGGGGAGAAAAGTCTGGGCTGGGCGGAGCTGGGAAGTCTGTC 4199
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Db 4200 CTTGACCTTGGCTTATTTTCGATCAACAGTCTCCGAGGAGAGATCATCATGATGG 4259
QY 4057 CCTCAATGTGGCAGACATCGGCTCCATGACCTGCGCTCTCAGCTGACCATCATCCGCA 4116
Db 4260 CATCAACATGCCAAGATCGGCTTCACGACCTCCGCTTCAAGATCACCATCATCCCCA 4319
QY 4117 GGACCCCATCTGTTCTCGGGGACCTCGCATGAACCTGGAACCCCTTCGGGAGCTACTC 4176
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QY 4177 AGAGGAGACATTTGGTGGGCTTTGGAGCTGTCCCACTGCACACGTTGTGTGAGTCCCA 4236
Db 4380 GGATGAAGAGCTTGGAGCTCCCTGGAGCTGGCCCACTCCAGGAGTCTGCTGAGCCCT 4439
QY 4237 GCCGCGGCTGAGCTTCCAGTGTCTCAGAGGGGGGAGAGATCTCAGCGTGGCGCAGAG 4296
Db 4440 TCCTGACAAGCTAGACCATGAATGTGACAGAGGCGGGAGAACCTCAGTGTGCGGACGG 4499
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QY 4357 GGCACAGCTGCCATCGACCTGGAGACTGACACACCTCATCCAGCTACCATCGCACCA 4416
Db 4560 GGCACAGCTGCCATCGACCTGGAGACTGACACACCTCATCCAGCTACCATCGCACCA 4619
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QY 4477 CAGGCTCTGCTGCTGACACAAAGAGTGTAGCTGTAATTTGATTCTCCAGCCCAACCTCAT 4536
Db 4680 AAGGCTGATGCTGCTGACACAAAGAGTGTAGCTGTAATTTGATTCTCCAGCCCAACCTCAT 4739
QY 4537 TGCAGCTAGGAGCTGCTTCTACGGGTGCGCAGAGATGCTGGACTTGCCTTAAATATATT 4596
Db 4740 GCAGCAGAGAGAGCTGCTTCTACAGCATGCGCAAGAGCGCGGCTTGTGTGAGCCCCAGA 4799
QY 4597 CTTGAGATTTC 4607
Db 4800 GCTGGCATATC 4810

RESULT 2

US-08-463-092B-1

; Sequence 1, Application US/08463092B

; Patent No. 5766880

; GENERAL INFORMATION:

; APPLICANT: Cole, Susan P.C.

; APPLICANT: Deeley, Roger G.

; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING

; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS

; CITY: Kingston

; STATE: Ontario

; COUNTRY: CANADA

; ZIP: K7L 3N6

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/463,092B

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/966,923

; FILING DATE: 27-OCT-1992

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/029,340

; FILING DATE: 8-MAR-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/141,893

; FILING DATE: 26-OCT-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/407,207

; FILING DATE: 20-MAR-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Steeg, Carol Miernicki

; REGISTRATION NUMBER: 39,539

; REFERENCE/DOCKET NUMBER: Q1546

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (613) 545-2342

; TELEFAX: (613) 545-6853

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..4788
; US-08-463-092B-1

Query Match 34.2%; Score 1737.8; DB 1; Length 5011;
Best Local Similarity 62.2%; Pred. No. 0;
Matches 288; Conservative 0; Mismatches 1662; Indels 87; Gaps 6;

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Db 219 CGCGATGGCTCCGACCCGCTCTGGGACTGGAATGTACGTGGGATACACGACACCCGGA 278
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RESULT 3
US-08-462-109A-1
; Sequence 1, Application US/08462109A
; Patent No. 5882875
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Dealey, Roger G.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,109A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. Jr.
; REGISTRATION NUMBER: 31,503

; REFERENCE/DOCKET NUMBER: P01-002CP4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5011 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 196..4788

; US-08-462-109A-1

Query Match 34.2%; Score 1737.8; DB 2; Length 5011;

Best Local Similarity 62.2%; Pred. No. 0;

Matches 2882; Conservative 0; Mismatches 1662; Indels 87; Gaps 6;

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QY 2557 CTATGCCCCGATGAGGACCAAGGCACTTGGAGGACAGCTGGACCGCTTGAAGGTGC 2616
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Db 4200 CTTGACCTTGGGCTTATTTCCGATCAACGAGTCTGCCGAAGGAGATCATCATCGATGG 4259


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: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII text
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: 05/08/463,179A
: FILING DATE:
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/966,923
: FILING DATE: 27-OCT-1992
: APPLICATION NUMBER: 08/029,340
: FILING DATE: 8-MAR-1993
: APPLICATION NUMBER: 08/141,893
: FILING DATE: 26-OCT-1993
: APPLICATION NUMBER: 08/407,207
: FILING DATE: 20-MAR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: DeConti, Giulio A. Jr.
: REGISTRATION NUMBER: 31,503
: REFERENCE/DOCKET NUMBER: PQI-002CP8
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 227-7400
: TELEFAX: (617) 227-5941
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5011 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 196...4788
: US-08-463-179A-1

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Query Match          34.2%; Score 1737.6; DB 3; Length 5011;
Best Local Similarity 62.2%; Pred. No. 0;
Matches 2882; Conservative 0; Mismatches 1662; Indels 87; Gaps 6;

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DB 219 -CGCCGATGGCTCGGACCCGCTGGGACCTGGGATGCACTGGGATACCAAGCAACCCGA 278

QY 85 CCTCACTCCCTGCTCCAGAACTCCCTGCTGGCTGGGTGCTGCTGCTGCTGCTGCTGCTG 144
DB 279 CTTCAACAGTCTTTCAGAACAGCTCTCTGCTGGGTGCTGCTGCTGCTGCTGCTGCTG 338

QY 145 CGCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 204
DB 339 CTGTTTCCCTTCTACTTCTCTATCTCTCCGACATGACCGAGGCTACATTCAGATGAC 398

QY 205 CCACCTGTCCAGCTCAAGATGGTCTGCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTG 264
DB 399 ACCTCTCAACAAACAAACAACTGGGATTTTGGTGTGGATCTGCTGCTGCTGCTGCTG 458

QY 265 CTTTCTTACTCTCTCCATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 324
DB 459 CTTCTCTACTCTTCTGGGAAGAGTGGGGCATATTCCTGGCCCGGCTGCTGCTGCTG 518

QY 325 CACCCCTTGGTGGGGGTCAACATGCTGCTGGCCACCTGCTGATACAGATGAGCG 384
DB 519 CAGCCCAACTCTCTGGGCATCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 578

QY 385 GTGAGGCGGTACAGTCTGCGGGGTCTCTATATCTGCTGCTGCTGCTGCTGCTGCTG 444
DB 579 GAGGAAGGAGTTCAGTCTTCAAGGATCATGCTCACTTCTGCTGCTGCTGCTGCTG 638

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QY 625 CCCTGAGACAGCGCTGGCTTCTCTCCCGCTGTTTCTTCTGGTGGTTTCACAAAGATGGC 684
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QY 1006 CCTGATCAGGTTTATCTCCAAACCCATGGCCCTCTCTGGTGGGCTTCTCTGGTGGCTG 1065
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RESULT 6

US-08-461-384B-1
; Sequence 1, Application US/08461384B
; Patent No. 6025473
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario

COUNTRY: CANADA
ZIP: K7L 3N6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,384B
FILING DATE: 05-JUN-95
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-OCT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-OCT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: Q1547
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 196..4788
US-08-461-384B-1

Query Match 34.2%; Score 1737.8; DB 3; Length 5011;
Best Local Similarity 62.2%; Pred. No. 0;
Matches 2882; Conservative 0; Mismatches 1662; Indels 87; Gaps 6;
QY 25 CGGGGAGCTCGGCTCCAAAGTCTGGGACTCCAACTCTGTGTGCACACAGAAACCCGGA 84
Db 219 CGCGGATGGCTCGGACCGCTCTGGGACTGGAATGTACGTGGGAATACACAGCAACCCGGA 278
QY 85 CCTCACTCCCTGCTTCCAGAACTCCCTGCTGGCTGGGTCCTGCACTACCTGTGGGT 144
Db 279 CTTCAACCAAGTCTTTTCAGAAACACGGTCTCTGCTGGTGGCTTGTGTTTACCTCTGGGC 338
QY 145 CGCCCTGCTGCTGCTACTTGTCTACCTGCGGACCAATGTGCTGGCTACATCATCTCTC 204
Db 339 CTGTTTCCCTCTCTACTTCTCTATCTCTCCGACATGACCGAGGCTACATTCAGATGAC 398
QY 205 CCACCTGTCCAACTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 264
Db 399 ACCTCTCAACAAACCAAACTGCTTGGGATTTTCTGCTGGATCTCTGCTGGGCGAGA 458
QY 265 CTTTCTTACTCTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 324
Db 459 CTTCTTCTACTCTTCTTGGGAAAGAAAGTCTGGGCGCATATCTCTGGCCCGCAGTGTCTGGT 518
QY 325 CACCCCTTGTGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 384
Db 519 CAGCCCAACTCTCTGGGATCATCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 578
QY 385 GCTGAGGGGCTACAGTCTTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 444
Db 579 GAGGAAGGGAGTTCAGTCTTTCAGGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 638
QY 445 CGCCATCGTCCCAATTCGCTTCCAGATCTCTTTAGCCAAAGGAGGCTGAGATCTCAGA 504
Db 639 TGCCCTAGCCATCTCTGAGATCCAAAATTTATGACAGCTTAAAGAGGATGCCCGAGTGA 698

QY 505 CCCCTTCGGCTTACCACCTTCTACATCCACTTTGGCCCTGGTACTCTCTGCCCTCATCTT 564
DB 699 CCTGTTTCGTGACATCACTTTCTACGTCTACTTTCTTCTTCTTACTCAATCACTGCTCT 758
QY 565 GGCCTGCTTACAGGAGAAACCTCCATTCTTCGCGAAAGATGTCGACCTCAACCCCTA 624
DB 759 GTCTCTTTCAGATCGCTCACCCCTGTTCTCGGAACCAATCCACGACCCCTAATCCCTG 818
QY 625 CCTGAGACCAAGCCTGGCTTCTCTCCGCTGTCTTCTGGTGGTTTCACAAAGATGGC 684
DB 819 CCCAGAGTCCAGCGCTTCTTCTCTGTCAGGATCACCTTCTGGTGGATCACAGGGTTGAT 878
QY 685 CATCTATGGCTACCGGATCCCTTGGAGGAGAAAGACCTCTGGTCCCTAAAGGAAGAGA 744
DB 879 TGTCCGGGGCTACCGCGAGCCCTGGAGGGCAGTGACCTCTGGTCTTAAACAAGAGGA 938
QY 745 CAGATCCAGATGTGTGTCAGCAGCTGCTGGAGGCATGGAGGA----- 788
DB 939 CACGTCGGACAAAGTCGTGCTGTTTGGTAAAGAACTGGGAAGAGGAATCGGCCAAGAC 998
QY 789 -----AGCAGAAAGAGCAGCGCACACAAAGGCTTCAGCAGCACCTGGGAAAAA 840
DB 999 TAGGAACAGCCGTGAAGGTTGTGTACTCTCTCAAGGATCTGCCAGCCGAAGAGAG 1058
QY 841 TGCCTCCGGGAGGACGAGGTGCTGCTGGG-----CCCGGCCCAGGCC 885
DB 1059 TTCCAAGTGGATCGGAATGAGGAGTGGAGGCTTTGATCGTCAAGTCCCCACAGAAGGA 1118
QY 886 CCGGAAGCCCTCTCTCTGAAGCCCTGCTGGCCACCTTCCGCTCCAGCTTCCTCATCAG 945
DB 1119 GTGGAACCCCTCTCTGTTTAAGGTGTATACAAGACCTTTGGGCCCTACTTCTCATGAG 1178
QY 946 TGCTGCTTCAAGCTTATCAGGACCTGCTCTCTCATCAATCCACAGCTGCTCAGCAT 1005
DB 1179 CTCTCTTCAAGCCATCACGACCTGATGATGTTTCCGGGCCGAGATCTTAAAGTT 1238
QY 1006 CTTGATCAGGTTTATCTCAACCCCATGGCCCTCTGCTGGGCTTCTGGTGGCTGG 1065
DB 1239 GCTCATCAAGTTCGTGAATGACACGAAGGCCACAGACTGGCAGGGCTACTTCTACCCGT 1298
QY 1066 GCTGATGTTCTGTGCTCCATGATGACGCTCGCTGATCTTACAACACTATPACCACTACAT 1125
DB 1299 GCTGCTGTTTGTCACTGCCCTGCTGAGACCCCTGCTGCTGCACCACTACTTCCACATCTG 1358
QY 1126 CTTTGTGACTGGGTAAGTTTCGTATGGGATCATGGGTGCTATCTACAGGAAGGCTCT 1185
DB 1359 CTTGCTAGTGGCATGAGGATCAAGACCGCTGTCATTGGGGCTGCTATCGGAAGGCCCT 1418
QY 1186 GGTATACCAACTCAGTCAAACTGCTGCTCACTGTGGGGAATGTCAACCTCATGTC 1245
DB 1419 GGTGATCACCATAATCAGCCAGAAAACTCTCCACGCTCGGGGAGATGTCAACCTCATGTC 1478
QY 1246 AGTGGATGCCAGGCTTCATGACCTTGGCCCTTCTCAATCTGCTGTTGGTTCAGCAC 1305
DB 1479 TGTGGAGCTCAGAGGTTTCATGACTTGGCCACCTGATTAACATGATGCTGGTCAGCCCC 1538
QY 1306 CTTGACGATCATCTGTCGATCTACTTCTCTGCGAAGAACCTAGGCTCCCTGTCTCTGGC 1365
DB 1539 CTTGCAAGTCACTCTTCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1598
QY 1366 TGGAGTCCCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1425
DB 1599 TGGAGTGGCGGTGATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1658
QY 1426 CGCTTCCAGGTAAGCAATGAATGAAGGACTCGCGCATCAAGCTGATGATGATGAT 1485
DB 1659 GACGTATCAGGTGGCCCATGAAGAGCAAGCAAACTGCGATCAAGCTGATGAACGAAT 1718
QY 1486 CTTGAAGCGCATCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1545
DB 1719 TCTCAATGGGATCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1778

QY 1546 GGAGGSCATCAGCGAGGTGAGCTCCAGTGTGTCGCACGGCGCTTACTCTCACACCAC 1605
DB 1779 GCTGGCCATCAGCGAGGAGGTGAAGTGTGAAGAAGTCTGCTTACTCTGTCAGCCGT 1838
QY 1606 AACCACTTTCACCTGGATGTGAGCCCTTCTGCTGAGCCCTGATCACCTCTGGGTGTA 1665
DB 1839 GGGCACCTTTCACCTGGGTGTGACGCCCTTCTGCTGGCTTGTGACACATTTGCCCTCTA 1898
QY 1666 CGGTACGTGGACCCAAACAATGTGCTGACGCCGAGAGGCTTTGTCTGTGCTCTT 1725
DB 1899 CGTGACCATTTGAGGAGCAACAATCTGTGATGCCAGACAGCTTCTGCTTGGCCCTT 1958
QY 1726 GTTTAATATTTAAGACTTCCCTCTCAACATGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1785
DB 1959 GTTCAACATCTCCGCTTCCCTTGAACATTTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCT 2018
QY 1786 GGCAGTGTGCTCTGAAACGATCCAGCAATTTCTGAGCCAAAGAGGAATTTGACCCCA 1845
DB 2019 GCGAGTGTCTCCCTCAACAGCTGAGGATCTTCTCTCCATGAGGAGCTGGAACCTGA 2078
QY 1846 GAGTGTGGAAGAAAGACCATCTCCCGAGC-----TATGCCATCACCATACACAG 1896
DB 2079 CAGCATGAGCGACGCTGTCAAGACGCGCGGGGCGACGAACAGCATCACGCTGAGGAA 2138
QY 1897 TGGCACCTTACCTTGGGCGCAGGACCTGCCCCCTCTGTCACAGCTTACAGATCCAGGT 1956
DB 2139 TGGCACATTCACCTGGCGCAGGAGCGACCTCCACACTGAATGGCATCACCTTCTCCAT 2198
QY 1957 CCGGAAAGGGGACCTGCTGGCGCTGCTGGGCTGCTGGGCTGCTGGGCTGCTGGGCTGCTGG 2016
DB 2199 CCGGAAAGGGTCTGCTGGGCTGCTGGGCTGCTGGGCTGCTGGGCTGCTGGGCTGCTGG 2258
QY 2017 GTCGCCCTGCTGGGAGAGATGGAAGCTAGAAGCAAGTGCACATCAAGGGCTCCGT 2076
DB 2259 CTCAGCCCTCTTGGCTGAGATGGACAAAGTGGAGGGGCGACGTATCAAGGGCTCCGT 2318
QY 2077 GGCCTATGTGCCCGCAGCGGATGATCCAGAACTGCACTTTCAGAAAGAAAGCTGCTTT 2136
DB 2319 GGCCTATGTGCCACAGCGGCTGGATTCAGAACTGATTTCTCTCCGAGAAACATCTTTT 2378
QY 2137 CCGGAAAGCCCTGAACCCCAAGCGCTACAGCAGACTCTGGAGGCTGCTGGCTGCTGCTGCT 2196
DB 2379 TGGATGTGAGTGGAGGAAACCATATTTACAGGTCCTGTATACAGGCTGCTGCTGCTGCT 2438
QY 2197 TGACCTGGAGATGCTGCTGCTGGGATCAGACAGAGATTGGAGAGGAGGATTAACCT 2256
DB 2439 AGACCTGGAATCTTCCCGAGTGGGATCGGACAGAGATTGGGAGAGGAGGCTGAGCT 2498
QY 2257 GTCGGGGGCCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2316
DB 2499 GTCGGGGGACAGAGCGGCTGAGCCTGCGCGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 2558
QY 2317 TTTCTGCTGATGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2376
DB 2559 TTACCTTCTGATGATCCCTCTCAGCAGTGGATGCCCATGTGGGAAACACATCTTTGA 2618
QY 2377 CCAGCTCATCGGGCCAGAGGCTGCTGCGAGCGAAGCGCAGTGTGCTGCTGCTGCTGCTGCT 2436
DB 2619 AATGTGATTGGCCCAAGGGATGCTGAAGAAAGAGCGCGGATCTTGGTCAGGACAG 2678
QY 2437 CATTAGCTTCTGCCCCAGACAGACTTATCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2496
DB 2679 CATGAGCTTCTGCGCAGGTGAGCTCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2738
QY 2497 GATGGCCCTTACCAGCCCTGCTGCGGCGAAGGCTCTTGGCAACTTCTCTGCA 2556
DB 2739 GATGGCTCTTACCAGGAGCTTGGCTGCGAGACGCGCTTCTGCTGCTGCTGCTGCTGCT 2798
QY 2557 CTATGCCCTGATGAGGACCAAGGACCTGCGAGGACAGCTGCGCGCTGCTGCTGCTGCTGCT 2616
DB 2799 CTATGCCAGCACAGAGGAGGACGAGTGCAGAGGAGAACGGGCTGCTGCTGCTGCTGCT 2858
QY 2617 AGAGGTAAGGAGGCACTGCTGATTTGAAGACACACTCAAGCAACACAGGATCTGACAGA 2676

Db 1719 TCTCAATGGGATCAAGTCTAAAGCTTTATGCTGGAGCTGGCATTCAGAGACAGGT 1778
QY 1546 GGAGGGCATCAGCAGGGTGAAGTCCAGCTGCTGCCACGGCGCCCTACCTCCACACCCAC 1605
Db 1779 GCTGGCCATCAGCAGGAGGAGTGAAGTGTCTGAAGAAGTCTGCCCTACCTGTGAGCCGT 1838
QY 1606 AACCACTTCACCTGATGTGACAGCCCTTCTGCTGAGCCCTGATCACCCTCTGGGGTGA 1665
Db 1839 GGGCAGCTTCACCTGGGTGTGACAGCCCTTCTGCTGGGCTTGTGCACATTTCCCGCTGA 1898
QY 1666 CGTGTACGTGGACCCCAAAATGCTGGACGCCGAGAGGCGCTTGTGCTGTGCTGCTT 1725
Db 1899 CGTGACCATTCAGGAGAACACATCTGATGCCAGACAGCCCTGCTGTCTTTGGCCTT 1958
QY 1726 GTTAAATATCTTAAGACTTCCCTCTCAACATGCTGCCCGCTTAAATCAGCAACCTGACTCA 1785
Db 1959 GTTCAACATCTCCGCTTCCCTGAAACATCTTCTCCCATGGTCTCAGCAGCATCTGTGA 2018
QY 1786 GGCCAGTGTCTCTGAAGGATCCAGCAATTCCTGAGCCAAAGAGAACTTGACCCCA 1845
Db 2019 GGGAGTGTCTCCCTCAACAGCTGAGGATCTTCTCTCCCATGAGGAGCTGGAACCTGA 2078
QY 1846 GAGTGTGGAAGAAAGACCATCTCCCGAGCG-----TATGCCATCACCATACACAG 1896
Db 2079 CAGCATCAGAGCAGCGCTGTCAAGACGGCGGGGCCAGACAGCATCACCCTGAGGAA 2138
QY 1897 TGCCACCTTCACCTGGGCCAGGACCTGCCCGCCACTCTGCACAGCTTACAGATCCAGGT 1956
Db 2139 TGCCACATTCACCTGGCGCAGGAGCGACCTCCACACTGAATGGCATCACCTTCCCAT 2198
QY 1957 CCGGAAGGGGACTGGTGGCGGTGTGGGCGTGTGGGCTGTGGGAGTCTCCCTGGT 2016
Db 2199 CCGGAAGGTGTGGTGGCGGTGTGGGCGGAGGTGGGCTGGGAAAGTGTGCCCTGCT 2258
QY 2017 GTCTGCCCTGTGGGAGAGATGGAGAAGCTAGAAGCAAGTGCACATGAAGGGCTCCGT 2076
Db 2259 CTCAGCCCTTGGGTGAGATGGACAAAGTGGAGGGCAGCTGGGTATCAAGGGCTCCGT 2318
QY 2077 GGCCTATGTGCCCGCAGCGCATGGATGGATCGACAACTGCATCTCTCAGGAAACAGTCTTT 2136
Db 2319 GGCCTATGTGCCACAGCAGCGCTGGATTCAGAAATGATCTCTCCGAGAAACATCCTTT 2378
QY 2137 CGGCAAGCCCTGAACCCCAAGCGCTACAGCAGACTCTGGAGGCTGTGCCCTGCTAGC 2196
Db 2379 TGATGTCACTGGAGGAACCATATTACAGGTCCGTGATACAGGCTGTGCCCTCTCC 2438
QY 2197 TGACCTGGAGATGCTGCTGTGGGATCAGACAGAGATTGGAGAGAGGCAATTAACCT 2256
Db 2439 AGACCTGGAATCCTGCCAGTGGGATCGGACAGAGATTGGGAGAGGGCGTGAACCT 2498
QY 2257 GTCTGGGGCCAGCGGCTGAGTGTGGCTGAGTGTGGTGTGATGATGATGATGATGAT 2316
Db 2499 GTCTGGGGACAGAAAGCAGCGGTGAGCTGTGCCCGCGGTGTACTCCAAACGCTGACAT 2558
QY 2317 TTTCTGTGTGATGACCCACTGTCCGCTGGACTCTCATGTGGCAAGCAATCTTTGA 2376
Db 2559 TTACCTCTTCGATGATCCCTCTCAGCAGTGGATGCCATGAGGAAACACATCTTTGA 2618
QY 2377 CCACCTCATCGGGCCAGAGGGCTGTGGCAGCGAAGACCGAGTGTGTCACGACCG 2436
Db 2619 AAATGTGATGGCCCAAGGGATGCTGAAGAACAGACCGGATCTTGTTCAGCACAG 2678
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Db 2679 CATGAGCTACTTCCGCGAGGTGAGCTCATCATCTGATGATGATGATGATGATGATGAT 2738
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Db 2739 GATGGGCTCCTACAGAGAGCTGCTGGCTCGAGACGGCGCTTGGCTGAGTTCTCGGTAC 2798
QY 2557 CTATGCCCCCGATGAGGACCAAGGGCACTGGAGGAGACCTGGACCGCGCTTGGAGGTC 2616

Db 2799 CTATGCCAGCAGCAGCAGGAGCAGGATGCAGAGGAGAAACGGGCTACGGGCGTCAAGGG 2858
QY 2617 AGAGGATAAGGAGGCACTGCTGATTTGAAGACACACACTCAGCAACACACAGGATCTGACAGA 2676
Db 2859 TCCAGGGAAGGAGCAAGCAAAATGGAGATGGCAT----- 2894
QY 2677 CAATGATCCAGTCACTATGTGTGTCAGAGCAGTATTTATGAGACAGTGTGATGCTGCTGTC 2736
Db 2895 -----GCTGGTACGGACAGTGCAGGGAAGCACTCAGAGCAGCTCAGCAGCTCCTC 2948
QY 2737 CTCAGATGGGAGGACAGGCTGGCGCTGTACCCCGAGGACACTGGGTCCATCAGAGAA 2796
Db 2949 CTCCTATAGTGGGACA-----TCAGCAGGCACCACAACAGCAGCAGAACTGCAGAAA- 3003
QY 2797 GGTGCAGGTGACAGAGCGAAGCAGATGGGCACATGACCCAGGAGGAGAGAGCAGCCAT 2856
Db 3004 ---GCTGAGGCCAAGAGGAGGAGACCTGGAAGCTGATGAGGCTCACAAGGGCGCAGAC 3059
QY 2857 TGGCACTGTGGAGCTCAGTGTGCTGGGATTTATGCCAAGCGCTGGGCTCTGTATCAC 2916
Db 3060 AGGCAAGGTCAAGCTTTCCGTGTACTGGGACTATCATGAAGGCCATCGGACTCTTCACTC 3119
QY 2917 GCTGGCCATCTCTCCTGTATGTGGGTCAAAGTGGGCTGCCATTTGAGCCCAATGTGTG 2976
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QY 2977 GCTCAGTGCCTGGCAAAATGATGCCATGGCAGACAGTAGACAGAAACAACTTCCCTGAG 3036
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QY 3037 GCTGGGCTGTATGCTGCTTTAGGAATCTGCAAGGGTCTTGGTGTATGTGGCAGCCAT 3096
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QY 3097 GGCATGGCAGCGGTGGCATCCAGGCTGCCGTGTGTTGACCAAGCAGCATGCTGCACAA 3156
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QY 3157 CAAGATACGCTGCCACAGTCTTCTTTGACACACACACATCAGCGCGCATCTCTGAACTG 3216
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QY 3217 CTTCTCAAGGACATCTATGCTGTTGATGAGTGTGCGGCCCTGTCTATCTCATCTGCTGT 3276
Db 3420 CTTCTCAAGGAGCTGGACAGTGGACTCCATGATCCCGGAGGTCTCAAGATGTTTCAT 3479
QY 3277 CAATCTCTTCTCAAGCCCATCTCCACTCTTGTGGTCAATCATGCGCAGCAGCGCTCTT 3336
Db 3480 GCGCTCCCTGTTCAACGTCATTTGGTGGCTGCATCTGTTATCTGCTGCCACAGCCCATCGC 3539
QY 3337 CACTGTGGTCACTGCCCTGGCTGTGCTGTACACTTATAGTACAGCGCTTCTATGACGC 3396
Db 3540 CGCCATCATCATCCCGCCCTTGGCTCTACTTCTTCTGTCAGAGGTTCTACGTTGCG 3599
QY 3397 CACATCAGGCACTGAAGCGGTGGAATCAGTCAAGCGCTCAGCTATCTACTCCCACTT 3456
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QY 3457 TTTCCGAGACAGTCACTGTGCGCACTGTCTCCCGGCTTACAACCGCAGCGGATTTTGA 3516
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QY 3517 GATCATCAGTGAATTAAGGTGGATGCCAACAGAGAGTGTACCCCTACATCATCTC 3576
Db 3720 CCACCAAGTGAACCTGAAGGTGGACGAGAACAGAGGCGCTATTACCCAGCATCTGGGC 3779
QY 3577 CAACCGGTGGCTGAGCATCGGAGTGGAGTCTGTGGGAAGTGGTGGTGGTGGTGGTGGTGG 3636
Db 3780 CAACAGGTGGCTGGCGCTGGCGTGGAGTGTGTGGCAACTGATCTCTGTTGTTGTC 3696
QY 3637 ACTATTGGCGTCACTGGGAGGAGCAGCCCTGAACCCGGGGCTGTGGGCGCTTCTGTGTC 3696
Db 3840 CTTGTTGGGTGATCTCCAGGCACAGCCCTCAGTGTGGCTTGTGGGCGCTCTCAGTGTGTC 3899

QY 265 CTTTCTTTTACTCTCCATGGCCTGTGTCCATGGCGGGCCCTGCGCCCTGTTTCTTTGT 324
Db 459 CTTCTTTCTACTCTTTTGGGAAAGAGTGGGGGCAATATCTCGTCCGCCAGGTGTTCTGGT 518
QY 325 CACCCCTTGGTGGGTGACACCATGTGTGTGGCCACCCCTGCTGATACAGTATGAGCG 384
Db 519 CAGCCCAACTCTCTGGGATACACAGCTGTGTGTACCTTTTAAATTCAGTGGAGAG 578
QY 385 GTGTCAGGGGTTACAGTCTTCGGGGTTCCTCAATATCTTGTGTCTGTGTGTGTGTGT 444
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QY 445 CGCATCTGTCCTTCCGCTCCAGATTCCTTTTAGCCAGGCGAGAGGTGAGATCTCAGA 504
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QY 1186 GGTATCACCAACTCAGTCAAAAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1245
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QY 1246 AGTGGATCCCCAGCTTCATGAGACCTTGGCCCTTCTTCAATCTGTGTGTGTGTGTGTGT 1305
Db 1479 TGTGGACGCTCAGAGGTTTCAATGGACTTGGCCACGATACATTAACATGATCTGTGTGACGCC 1538

QY 1306 CTTGCAGATCATCTCTGGGATCTACTTCTCTTCCCTGTGCGCAAACTAGTCTCTGTCTGTGGC 1365
Db 1539 CTTGCAAGTATCATCTTCTCTACCTCTGTGGCTGAATCTGGGCCCTTCCGCTCTGTGGC 1598
QY 1366 TGGAGTCCGCTTTTATGCTGTGTGATTCACATCAACGAGAGCTGTGGCCGTGAAGATGCG 1425
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QY 1606 AACACCTTCCACTGGATGTGACGCCCTTCTCTGTGTGACCCCTGATCACCCCTCTGGGTGA 1665
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QY 1726 GTTATAATATCTTAAGACTTCCCTCAACATGCTGCCCCAGTTTAAATAGCACCTGACTCA 1785
Db 1959 GTTCAACATCTCCGGTTCCTCTGAACATTTCCCTCATCAGCAGCATCCCTGTGCGA 2018
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Db 2079 CAGCATCGAGCGAGCGCTCTCAAGACGCGGGGCGCAACAGCATCACCGTGAGGA 2138
QY 1897 TGCACCTTCCACTGGGCCAGGACCTGCCCCACACTCTCACAGCCTAGACATFCCAGGT 1956
Db 2139 TGCCACATCTACCTGGCCAGGAGCGACCTCCACACTGAATGGCATCACCCTTCTCCAT 2198
QY 1957 CCGGAAAGGGCACTGCTGCTGCTGTGGGGCTGTGGGGCTGTGGGAAGTCTCCCTCGT 2016
Db 2199 CCCCAGAGTGTCTTGTGTGGCTGTGGGCCAGGTGGGTGCGGAAAGTCTGCTCCCTGCT 2258
QY 2017 GTCTGCCCTGCTGGGAGAGATGAGAGAGCTAGAAGGCAAGTGCACATGAAGGGCTCCGT 2076
Db 2259 CTCAGGCCCTTGTGGCTGAGATGGACAAGTGGAGGGGACGTGGCTATCAAGGGCTCCGT 2318
QY 2077 GGCTATGTGCCCCAGCAGGCGATGGATFCCAGAACTGCACACTTTCAGGAAACAGTGTCTTT 2136
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QY 2137 CGGCAAGCCCTGAACCCCAAGCGCTACACAGAGACTCTGTGGGGCTGTGCTTGTGTAGC 2196
Db 2379 TGGATGTCAGCTGGAGGAACCATATTACAGGTCCGTGATACAGGCTGTGCCCTCTCC 2438
QY 2197 TGACCTGGAGATGCTGCTGTGGGATCAGACAGAGATTGGAGAGAGGGCATTAACCT 2256
Db 2439 AGACCTTGGAAATCTCTCCAGTGGGATCGGACAGAGATTGGGAGAGGGCGGTGAACCT 2498
QY 2257 GTCTGGGGCCAGCGCAGCGGTGAGTCTGAGCTGCGAGCTGTTTACAGTATGATGCCGATAT 2316
Db 2499 GTCTGGGGNACAGCAGCGCGTGTGAGCTTGGCCCGGCGCTGTACTTCCAACTGTACAT 2558
QY 2317 TTTCTTGTGATGACCCCACTGTCCCGGTGTGAGCTCTCATGTGGCCCAAGCACATCTTTGA 2376
Db 2559 TTACCTCTTCGATGATCCCTCTCTCAGCAGTGGATGCCCATGTGGGAAACACATCTTTGA 2618
QY 2377 CCACGTATCGGCCAGAGAGCGCTGTGTGCGAGGCAAGACCGGAGTGTGTGTGAGCACGG 2436

Db 2619 AATGATGGCCCAAGGGGATGCTGAAGAAACAGCGGGATCTGGTCAACGCACAG 2678
 QY 2437 CATTAGCTTCTGCCCCAGACAGACTTCATCATTTGCTAGCTGATGACAGAGTGTCTGA 2496
 Db 2679 CATGAGCTACTTGGCGAGGTGAGCTCATCATCTGATGAGTGGCGCAGATCTCTGA 2738
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 Db 2799 CTATGCCAGCAGAGCAGGAGGAGGATGACAGGAGAAACGGGTTCACGGGCGFCACGG 2858
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 Db 2859 TCCAGGGAAGGAACCAATGGAGATGGCAT----- 2894
 QY 2677 CAATGATCCAGTACCTATGTTGCCAGAACAGTATTATGAGACAGCTGAGTGCCTGTC 2736
 Db 2895 -----GCTGGTCAGCGACAGTGCAGGGAAGCAACTGCAGAGACAGCTCAGCAGCTCCTC 2948
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 Db 3240 GCTGAGCGCTATGAGAGCCCTGGGCATTTCAAGAGGATCGCGTGTGGCTACTCCAT 3299
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RESULT 9
US-08-462-109A-3
; Sequence 3, Application US/08462109A
; Patent No. 5882875
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deelev, Roger G.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,109A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PQI-002CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..4788
US-08-462-109A-3

Query Match 34.2%; Score 1736.2; DB 2; Length 5011;
Best Local Similarity 62.2%; Pred. No. 0;
Matches 2881; Conservative 0; Mismatches 1663; Indels 87; Gaps 6;

QY 25 CGGGAGCTCGGCTCCAAAGTTCTGGAGCTCCAACTGTGTGTCACACAGAAAACCCGGA 84
Db 219 CGCCGATGGCTCCGACCCGCTCTGGAGTGAATGTCAGTGGTAATACCAAGCAACCCCGA 278

QY 85 CTTCACTCCCTCTCCAGAACTCCCTGTGGCGTGGGTGCGCTGCATCTACCTGTGGGT 144
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QY 145 CGCCCTGCGCTCTACTTGCCTACCTCGGGCACCATTGTCGTGGCTACATCATCTCTC 204

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QY 205 CCACCTGTCCAAGCTCAAGATGGTCTCTGGGTCTCTCTGTGGTGGCTCTCTCTGGCGGA 264
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QY 265 CTTTCTTCT 324
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Db 1059 TTCCAAGTGGATGCGAATGAGGAGGTGGAGGCTTTGATGCTCAAGTCCCAAGAGGA 1118
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QY 1066 GCTGATGTTCTCTGTCTCCATGATGAGTCTGCTGATCTTTACAAACACTATTACCACTACAT 1125
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DB 4320 GGACCTGTTGTTGCTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTG 4379
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QY 4597 CTTGAGATTTT 4607
DB 4800 GCTGGCATACT 4810

RESULT 10
US-08-460-907B-3
; Sequence 3, Application US/08460907B
; Patent No. 5891724
; GENERAL INFORMATION:
; APPLICANT: Deeley, Roger G.
; APPLICANT: Cole, Susan P.C.
; TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
; TITLE OF INVENTION: RESISTANCE ON A CELL
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,907B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; LENGTH: 5011 base pairs
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; NAME/KEY: CDS
; LOCATION: 196...4788
US-08-460-907B-3

Query Match	34.2%	Score 1736.2	DB 2	Length 5011
Best Local Similarity	62.2%	Pred. No. 0		
Matches 2881	Conservative	0	Mismatches 1663	Indels 87
Gaps				

QY	25	CGGGAGCTGGCTCCAAGTTCTGGGACTCCAACCTGTCTGTGCACAGAAACCCGGA	84
DB	219	CGCCGATGGCTCCGACCCGCTCTGGGACTTGGAAATCTCAGTGGAAATACCAAGAACCCGGA	278
QY	85	CCTCACTCCCTGCTTCCAGAACTCCCTGCTGGCTTGGGTGGCCCTGCATCTACCTGTGGGT	144
DB	279	CTTCACCAAGTCTTTCAGAACACAGCTCTCGTGTGGGTGCTTGTTTTACCTCTGGGC	338
QY	145	CGCCCTGCCCTGCTACTTGTCTACTCTAGCTGGGACCAATTTGCTGGTGCATCATCTCTC	204
DB	339	CTGTTCCCTCTACTTCTCTCTAFTCTCTCCGACATACCCGAGGTACATTCAGATGAC	398
QY	205	CCACCTGCCAAGCTCAAGATGGTCTCGGTGCTCTGCTGTGGTGCCTCTCTGGCGGA	264
DB	399	ACCTCTCAACAAAACCAAACTGCCCTGGGATTTTGTGTGGATFCGTCTGTGGGCGAGA	458
QY	265	CCTTTTCTACTCTCTTCTGGGAAAGTTCGGGATATCTCTGGCCCAAGTTCCTGGT	324
DB	459	CCTCTCTACTCTTCTGGGAAAGTTCGGGATATCTCTGGCCCAAGTTCCTGGT	518
QY	325	CACCCCTTGGTGTGGGGTCAACATCTGCTGGCCACCCTGCTGTGATACAGATGACGG	384
DB	519	CAGCCCAACTCTCTTGGGCATACACACCTGCTTCTACCTTTTAAATTCAGCTGGAG	578
QY	385	GCTGAGGGCTACAGTCTCGGGGCTCTCATATCTTCTTGGTTCCTGTGTGGTCTG	444
DB	579	GAGGAAGGATTCAGTCTTCAGGATCATGCTCACTTCTTGGCTTGGTGGCCCTAGTGTG	638
QY	445	CGCCATCTCCATTCCTCCCTCCAAGATCCTTTTAGCCAAAGCAGAGGCTGAGATCTCAGA	504
DB	639	TGCCCTAGCCATCTGAGATCAAAATTTAGACAGCTTTAAAGAGGATGCCAGGTGA	698
QY	505	CCCTTCGGCTTACCACCTTCTACATCCACTTGGCCCTGCTACTCTCTGCCCTCATCTT	564
DB	699	CTGTGCTGACATCACTTTCTACGTCTACTTTTCTTCCCTTACTCAATTCAGCTCGCTT	758
QY	565	GGCTGCTTCAGGAGAACTCCATTTTCTCGCAAGAAATGTCGACCTCAACCCCTA	624
DB	759	GTCTGTTTTCAGATCGCTCACCCCTGTTCTCGGAACCACTCCACGACCTTAATCCCTG	818
QY	625	CCCTGAGACCAAGCTGCTTCTCTCCGCTGTCTTCTGCTGGTTCACAAAGATGGC	684
DB	819	CCCAGAGTCCAGCGCTCTCTCTGTGCGAGGATCACCTTCTGCTGGATCACAGGTTGAT	878
QY	685	CATCTAGGCTACCGGATCCCTCTGGAGGAGAGACCTCTGGTCCCTTAAAGGAAGAGA	744
DB	879	TGTCGGGGCTTACCGCCAGCCCTTGGAGGGCAGTGACCTCTGGTCTTAAACAAGGAGA	938
QY	745	CAGATCCAGATGTGTGTCAGCAGCTGTCTGGAGCATGGAGGA-----	788
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QY	789	-----AGCAGGAAAGCAGACGGCACGACACAAGCTTTCAGCAGCACCTGGGAAAA	840
DB	999	TAGGAAGCAGCGGTGAAGGTTGTACTCTCTCAAGGATCTCTGCCAGCCGAAAGAG	1058
QY	841	TGCTTCGGGAGCAGAGGTGCTGTGGTG-----	885
DB	1059	TTCAAGGTGGATGAGGAGGTGGAGGCTTTGATCGTCAAGTCCCTCCACAGAAGA	1118
QY	886	CCGGAAGCCCTCTCTCTGAGGCCCTGCTGGCCACCTTCGGCTCCAGCTTCTTCATCAG	945
DB	1119	GTGGAACCCCTCTGTTTAAAGGTGTATACAGACCTTTGGGCCCTTACTTCTCATGAG	1178
QY	946	TGCTGCTTCAAGCTTATCCAGGACCTGCTCTCTCTTCAATCCACAGCTGCTCAGCAT	1005
DB	1179	CTTCTTCTTAAGGCCATCCAGACCTGATGATGTTTTCGGGGCCGAGATCTTAAAGTT	1238
QY	1006	CCTGATCAGGTTTATCTCCAAACCCCATGGCCCCCTCTGTGGGGCTTCTTGGTGGCTG	1065

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QY	1066	GCTGATGTTCTGTCTCCATGATGAGTGCCTGATCTTACAACTATTTACCACTACAT	1125
DB	1299	GCTGTGTTTGTCTACTGCTCTGACACCCCTCGTCTGCACCACTTCTTCCATCTG	1358
QY	1126	CTTTGTGACTGGGGTGAAGTTTCTGACTGGGATCATGGGTGTCTATCACAGGAAGCTCT	1185
DB	1359	CTTCTGCTGAGTGCATGAGGATCAAGACCCGCTGCTATTTGGGGTGTCTATCGGAAGCCCT	1418
QY	1186	GTTTATCACCAACTCAGTCAAAACGTCGCTCCACTGTGGGGGAAATTTGCAACCTCATGTC	1245
DB	1419	GCTGATACCAATTCAGCCAGAAAAATCTCCACGGTCGGGAGATTGTCAACCTCATGTC	1478
QY	1246	AGTGGATGCCAGCGCTTCATGAGACCTTGCCTCCCTTCTCAATCTGCTGTGTGTCAGCACC	1305
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QY	1366	TGGAGTCTCTTCTATGGTCTTCTGATTTCCACTCAACGAGGCTGTGGCGCTGAAGATGCG	1425
DB	1599	TGGAGTGGCGGTAGTGTCTCATGTGTGCTCAATGTGTGATGGGATGAAGACCAA	1658
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QY	1546	GAGGGCATCAGGCAAGGTGAGTCCAGCTGCTGCGCAGCGGCGCTACCTCCACACCAC	1605
DB	1779	GCTGGCCATCAGGCAAGGAGGCTGAAGTGTCTGAAGAAGTCTGCTACCTTCTGACGCGT	1838
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QY	1666	CGTGTACGTGACCCCAAACTGTCTGGAGCCGAGAGGCTTGTGTCTGTCTCTT	1725
DB	1899	CGTGACCATTCAGAGAACACATCTCTGATGCCAGACAGCTTCTGTCTTGGCCTT	1958
QY	1726	GTTTAATATCTTAAGACTTCCCTCAACATGCTGCCAGTTAATTCAGCAACCTTGACTCA	1785
DB	1959	GTTCAACATCTCGGTTTCCCTGAACATTTCCCTTCCCTTCCCTGATCAGCAGCATCGTGCA	2018
QY	1786	GGCAGTCTGTCTGTGAAGCATCCACATTTCTGAGCCCAAGGAGAACTTGACCCCA	1845
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QY 2137 CGGCAAGCCCTGAOCCCAAGCGCTACACAGAGACTCTGGAGCCCTGTGCCCTTGGCTAGC 2196
Db 2379 TGGATGTGAGCTGGAGGAACCATATTACAGGTCCGTGATACAGGCCCTGTGCCCTCCCTCCC 2438
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Db 4440 TCTGACAGCTAGACCAATGATGTCGAGAGGCGGGGAGAACTTCTAGTGTGCGGCGAGCG 4499

[illegible]

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RESULT 11
US-08-463-179A-3
: Sequence 3, Application US/08463179A
: Patent No. 6001563
: GENERAL INFORMATION:
: APPLICANT: Cole, Susan P.C.
: APPLICANT: Deeley, Roger G.
: TITLE OF INVENTION: METHODS FOR IDENTIFYING CHEMOSENSITIZERS
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD
: STREET: 60 State Street, suite 510
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII text
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/463,179A
: FILING DATE:

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QY	625	CCCTGAGACGCGCTGGCTTTCTCTCCCGCCTGTTTTTCTGGTGGTTTACAAAGATGCC	684
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Db	1059	TTCCAAGTGGATGCGAATGAGAGGTGAGGCTTTGATCGTCAAGTCCCCACAGAAAGA	1118
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QY 2677 CAATGATCCAGTCACTATGCTGCTCCAGAGCAGTTTATGAGACAGCTGAGTGCCTGTC 2736
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Db 4080 CCGAATCTACTGCTGCGCTTACCGAGAGGACTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4139
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RESULT 12
US-08-461-384B-3
; Sequence 3, Application US/08461384B
; Patent No. 6025473
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,384B
; FILING DATE: 05-JUN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1547
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 196..4788
US-08-461-384B-3

Query Match 34.2%; Score 1736.2; DB 3; Length 5011;
Best Local Similarity 62.2%; Pred. No. 0;
Matches 2881; Conservative 0; Mismatches 1663; Indels 87; Gaps 6;

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Db 4800 GTTGGCATATC 4810

RESULT 13

US-08-463-092B-5

Sequence 5, Application US/08463092B

Patent No. 5766880

GENERAL INFORMATION:

APPLICANT: Cole, Susan P.C.

APPLICANT: Deele, Roger G.

TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING

NUMBER OF INVENTION: MULTIDRUG RESISTANCE PROTEINS

TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS

NUMBER OF INVENTION: 9

CORRESPONDENCE ADDRESS:

ADDRESS: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS

CITY: Kingston

STATE: Ontario

COUNTRY: CANADA

ZIP: K7L 3N6

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,092B

FILING DATE: 05-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/966,923

FILING DATE: 27-OCT-1992

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/029,340

FILING DATE: 8-MAR-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/141,893

FILING DATE: 26-OCT-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/141,893

FILING DATE: 26-OCT-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: Q1546
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5889 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 6 4589
US-08-463-092B-5

Query Match 31.8%; Score 1612.6; DB 1; Length 5889;

Best Local Similarity 60.8%; Pred. No. 0;

Matches 2794; Conservative 0; Mismatches 1699; Indels 102; Gaps 6;

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RESULT 14
 US-08-462-109A-5
 ; Sequence 5, Application US/08462109A
 ; Patent No. 5882875
 ; GENERAL INFORMATION:
 ; APPLICANT: Cole, Susan P.C.
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING
 ; TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: LAHIVE & COCKFIELD
 ; STREET: 60 State Street, suite 510
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/462,109A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/966,923
 ; FILING DATE: 27-OCT-1992
 ; APPLICATION NUMBER: 08/029,340

FILED DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-OCT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: POI-002CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5889 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 6 4589
us-08-462-109A-5

Query Match 31.8%; Score 1612.6; DB 2; Length 5889;
Best Local Similarity 60.8%; Pred. No. 0;
Matches 2794; Conservative 0; Mismatches 1699; Indels 102; Gaps 6;

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DB 109 ACACGGTCTCACATGGGTGCTGTTTCTACCTGCTGCTGTTTCCCTCTACTTCT 168
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QY 465 CCAAGATCTTTTACCAAGGAGGAGGTGAGATCTCAGACCCCTTCGCTTCCACCACT 524
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QY	3954	AGAAAGTGGGATCGTGGGCCCGCACTGGGGCTGGCAAGTCTTCCATGACCCTTTGCTGTG	4013
Db	3958	AAAAGTGGGATTTGTAGTCTGTACGGAGCTGGGAAATCATCTCTCACCCCTGGGTTGT	4017
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QY	4074	TGGGCTCCATGATCGGCTCTAGCTGACCATCATCCGAGGAGCCCATCTCTTCT	4133
Db	4078	TCGGCTGCACAAACCTCGCTTCAAGATCACCATCATTCACAGGATCTGTTTGTCT	4137
QY	4134	CGGGACCCCTGGCATGATGAACCTGGACCCCTTCGGCAGCTACTCAGAGGAGGACATTTGGT	4193
Db	4138	CGGTTTCCCTCCGATGAACCTTGGACCCCTTTCAGTCAGTATTCTGATGAAGAAGTCTGGA	4197
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Db	4198	TGGCCCTGGAGCTTGCTCACCTAAAGGGCTTTGTGTACGCTTGCCTGACAGCTGAACC	4257
QY	4254	TCCAGTGTCTCAGAGGGCGGGGAGAAATCTACGGCTGGCGGAGAGGACGCTGTGTGCTGG	4313
Db	4258	ATGATGTGTCAGAAGGTGCGAGAGAACCTGAGTGTGGGCGAGCGACAGCTTGTGTGCTGG	4317
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RESULT 15

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US-08-460-907B-5
: Sequence 5, Application US/08460907B
: Patent No. 5891724
:
: GENERAL INFORMATION:
: APPLICANT: Deeley, Roger G.
: APPLICANT: Cole, Susan P.C.
: TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
: TITLE OF INVENTION: RESISTANCE ON A CELL
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESS: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
: STREET: Queen's University at Kingston
: CITY: Kingston
: STATE: Ontario
: COUNTRY: CANADA
: ZIP: K7L 3N6
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII text
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/460,907B
: FILING DATE: 05-JUN-1995
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/966,923

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Search completed: December 18, 2002, 21:35:15
 Job time : 169.285 secs

(FOX-) FOX CHASE CANCER CENT.

Kruh G, Lee K, Belinsky M, Bain L;

WPI; 1999-610812/52.

P-FSDB; RAY43543.

New transporter gene useful for screening for anti-cancer drugs

Claim 23; Page 138-140; 153pp; English.

The present sequence encodes a human MPR-related ABC transporter (MOAT) protein, designated MOAT-D. The protein comprises a multi-domain structure including a tandem repeat of nucleotide binding folds appended C-terminal to a hydrophobic domain, having Walker A and B ATP binding sites and several potential membrane spanning domains. The MOAT nucleic acids are useful for screening a test compound for inhibition of MOAT mediated transport, indicated by restoration of anticancer drug sensitivity, which in turn causes a reduction of transporter mediated cellular efflux of anticancer agents. MOAT DNA or RNA may be used as probes to detect the presence or expression of genes encoding MOAT proteins. Anti-MOAT antibodies are useful for detecting and quantitating MOAT proteins.

Sequence 5079 BP; 1040 A; 1476 C; 1388 G; 1175 T; 0 other;

Query Match 100.0%; Score 5079; DB 20; Length 5079;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5079; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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121 GGTGCTGTGATACCTGTGGGTGCGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
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Qy 4741 ATGCTTTAGATGAGGAATGATCCCAAGTGTGAATGACACGCTTAAGTCAAGTAG 4800
Db 4741 ATGCTTTAGATGAGGAATGATCCCAAGTGTGAATGACACGCTTAAGTCAAGTAG 4800
Qy 4801 TTTGAGCCAGTGTAGACTAGTCCCGGCTCCCGATTCCTCAACTGAGTGTATTTGGCACAC 4860
Db 4801 TTTGAGCCAGTGTAGACTAGTCCCGGCTCCCGATTCCTCAACTGAGTGTATTTGGCACAC 4860
Qy 4861 TGCACCTGTTTCAATTAACGATTTATGAATGACCTCTCTCTCCCTCTGATTTTTCAT 4920
Db 4861 TGCACCTGTTTCAATTAACGATTTATGAATGACCTCTCTCTCCCTCTGATTTTTCAT 4920
Qy 4921 ATTTTCAAGTTTCTGTTCTGTTTTTAAATAAAGCTTTTCTCTCTGGAACAGAAGA 4980
Db 4921 ATTTTCAAGTTTCTGTTCTGTTTTTAAATAAAGCTTTTCTCTCTGGAACAGAAGA 4980
Qy 4981 CAGCTGCTGGGTGAGCCACCCCTAGGAACCTCAGTCTGTACTGTGGGTGCTGCTGAA 5040
Db 4981 CAGCTGCTGGGTGAGCCACCCCTAGGAACCTCAGTCTGTACTGTGGGTGCTGCTGAA 5040

Qy 5041 TCCATTAATAATGGGAGTACTGATGAATAATAAACTACAG 5079
Db 5041 TCCATTAATAATGGGAGTACTGATGAATAATAAACTACAG 5079

RESULT 2

ABK61466
ID ABK61466 standard; cDNA; 5193 BP.

XX ABK61466;

XX 18-JUN-2002 (first entry)

XX Human cDNA encoding protein NOV14.

XX Human; gene; ss; NOVX; gene therapy; cardiomyopathy; atherosclerosis;
cell signal processing disorder; metabolic pathway modulation disorder;
diabetes; cancer; adenocarcinoma; lymphoma; prostate cancer;
uterus cancer; immune response; graft-versus-host disease;
acquired immunodeficiency syndrome; AIDS; asthma; Crohn's disease;
hypertension; congenital heart defects; multiple sclerosis; inflammation;
Albright hereditary osteodystrophy.

XX Homo sapiens.

XX WO200216599-A2.

XX 28-FEB-2002.

XX 27-AUG-2001; 2001WO-US26510.

XX 25-AUG-2000; 2000US-228191P.

XX 08-FEB-2001; 2001US-267300P.

XX 20-FEB-2001; 2001US-269961P.

XX 20-MAR-2001; 2001US-277337P.

XX (CURA-) CURAGEN CORP.

XX (CORT-) COR THERAPEUTICS INC.

XX Burgess CE, Conley PB, Grosse WM, Hart M, Kekuda R, Shimkets RA;

XX Spytek KA, Szekeres ES, Tomlinson JE, Topper JN, Yang R;

XX WPI; 2002-280937/32.

XX P-PSDB; AAU91309.

XX New polypeptides for treating or preventing a disorder associated with
them, in humans, e.g. cardiomyopathy, atherosclerosis or cancers -

XX Claim 1; Page 104-105; 263pp; English.

XX The invention relates to an isolated polypeptide (NOVX) a mature
form of NOVX, a NOVX variant (differing by no more than 15%), the
nucleotide encoding NOVX (or its complement, fragment or variant).
NOVX is NOV1-14, 15a, 15b, 16a, and 16b. The NOVX polypeptide, nucleic
acid encoding it and antibody against it, are useful for treating or
preventing (e.g. by gene therapy) a NOVX-associated disorder in humans,
e.g. cardiomyopathy, atherosclerosis, a disorder related to cell signal
processing and metabolic pathway modulation, diabetes or cancers. The
NOVX polypeptide and nucleic acids are also useful for determining the
presence of predisposition to the diseases. The NOVX nucleic acid and
polypeptide are especially useful in therapeutic or prophylactic
applications for disorders associated with aberrant NOVX expression or
activity, e.g. cancers (e.g. adenocarcinoma, lymphoma, prostate cancer or
uterus cancer), immune response, graft-versus-host disease, acquired
immunodeficiency syndrome (AIDS), asthma, Crohn's disease, hypertension,
congenital heart defects, multiple sclerosis, inflammation or Albright
hereditary osteodystrophy and many other diseases listed in the
specification. The DNA encoding the protein is useful in gene therapy
for treating the conditions. This is also useful in detection assays,
chromosome mapping, tissue typing, diagnostic or prognostic assays, or
for developing a powerful assay system for functional analysis of
various human disorders, as well as in diagnostic applications. The

CC present sequence encodes a NOVX protein.

XX Sequence 5193 BP; 1083 A; 1511 C; 1410 G; 1189 T; 0 other;

SQ Query Match 99.9%; Score 5071.6; DB 24; Length 5193;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5074; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	1	CCCCATGACGCCCTGTGCGGTTCGCGGAGCTCGGCTCCAAAGTCTTGGAGCTCCAACCT	60
Db	67	CCCCATGACGCCCTGTGCGGTTCGCGGAGCTCGGCTCCAAAGTCTTGGAGCTCCAACCT	126
Qy	61	GTCGTGCACACAGAAACCGGAGCTCAGTCCCTGCTTCAGAACTCCCTGCTGCGCTG	120
Db	127	GTCGTGCACACAGAAACCGGAGCTCAGTCCCTGCTTCAGAACTCCCTGCTGCGCTG	186
Qy	121	GGTGCCTGTCATACCTGTGGGTGCGCCCTGCGCTGCTTACTTGCTTACCTCGGACCA	180
Db	187	GGTGCCTGTCATACCTGTGGGTGCGCCCTGCGCTGCTTACTTGCTTACCTCGGACCA	246
Qy	181	TTGTGCTGGCTACATCATCTCTCCACCTGTCCAAAGCTCAAGATGTCCTGGGTGCTCT	240
Db	247	TTGTGCTGGCTACATCATCTCTCCACCTGTCCAAAGCTCAAGATGTCCTGGGTGCTCT	306
Qy	241	GCTGTGGTGCCTCTCTGGGCGGACCTTTTACTTCTTCCATGCGCTGGTCCATGGCGG	300
Db	307	GCTGTGGTGCCTCTCTGGGCGGACCTTTTACTTCTTCCATGCGCTGGTCCATGGCGG	366
Qy	301	GGCCCTGCCCTCTTTTCTTGTACCCCTTGTGTGGGTGGGGTCAACATGCTGCTGGC	360
Db	367	GGCCCTGCCCTCTTTTCTTGTACCCCTTGTGTGGGTGGGGTCAACATGCTGCTGGC	426
Qy	361	CACCTGCTGATACAGTATGAGCGGCTGCAGGCGGTACAGTCTTCGCGGGTCTCATAT	420
Db	427	CACCTGCTGATACAGTATGAGCGGCTGCAGGCGGTACAGTCTTCGCGGGTCTCATAT	486
Qy	421	CTTCTGTTCTGTGTGGTCTGGGCGCATGCTGCCATTCGCTCCAGATCTCTTTTACG	480
Db	487	CTTCTGTTCTGTGTGGTCTGGGCGCATGCTGCCATTCGCTCCAGATCTCTTTTACG	546
Qy	481	CAAGCAGAGGTTGAGATCTCAGACCCCTTCCGCTTACACACCTTCTACATCCACTTGC	540
Db	547	CAAGCAGAGGTTGAGATCTCAGACCCCTTCCGCTTACACACCTTCTACATCCACTTGC	606
Qy	541	CCTGGTACTCTCTGCCCTCATCTTGGCTGCTTCAGGAGAAACCTCCATTTTCTCCGC	600
Db	607	CCTGGTACTCTCTGCCCTCATCTTGGCTGCTTCAGGAGAAACCTCCATTTTCTCCGC	666
Qy	601	AAAGAAATGTCGACCTTAACCCCTACCTTGACACAGCGCTGCTTCTCCGCTGTT	660
Db	667	AAAGAAATGTCGACCTTAACCCCTACCTTGACACAGCGCTGCTTCTCCGCTGTT	726
Qy	661	TTTCTGTTGTTTCAAGATGGCATCTATGGCTACCGGCTCCCTTGGAGGAGAAGA	720
Db	727	TTTCTGTTGTTTCAAGATGGCATCTATGGCTACCGGCTCCCTTGGAGGAGAAGA	786
Qy	721	CCTCTGTTCCCTAAAGGAAGGAGCAGATCCAGATGGTGTGACGAGCTGCTGGAGGC	780
Db	787	CCTCTGTTCCCTAAAGGAAGGAGCAGATCCAGATGGTGTGACGAGCTGCTGGAGGC	846
Qy	781	ATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	840
Db	847	ATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	906
Qy	841	TGCTCCGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	900
Db	907	TGCTCCGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	966
Qy	901	CCTGAAGGCCCTGTGCGCCACCTTTCGGCTCCAGCTTCTCATAGTGCCTGCTTCAAGCT	960
Db	967	CCTGAAGGCCCTGTGCGCCACCTTTCGGCTCCAGCTTCTCATAGTGCCTGCTTCAAGCT	1026
Qy	961	TATCCAGACCTGCTCTCTTTCATCAATCCACAGCTGCTCAGCATCTGATCAGGTTTAT	1020

Db	1027	TATCCAGACCTGCTCTCTTTCATCAATCCACAGCTCTCAGCATCTGATCAGGTTTAT	1086
Qy	1021	CTCAACCCCATCGCCCTCTCTGGTGGGCTTCCCTGGTGGGCTGATGTTCCCTGTG	1080
Db	1087	CTCAACCCCATCGCCCTCTCTGGTGGGCTTCCCTGGTGGGCTGATGTTCCCTGTG	1146
Qy	1081	CTCCATGATGACGTGCTGATCTTACAACACTATTACCACTATCTTCTGACTGGGT	1140
Db	1147	CTCCATGATGACGTGCTGATCTTACAACACTATTACCACTATCTTCTGACTGGGT	1206
Qy	1141	GAAGTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1200
Db	1207	GAAGTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1266
Qy	1201	AGTCAACAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1260
Db	1267	AGTCAACAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1326
Qy	1261	CTTTCATGGACCTTTCCT	1320
Db	1327	CTTTCATGGACCTTTCCT	1386
Qy	1321	GGGATCTACTTCTCTGCGAGAACCTTAGTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1380
Db	1387	GGGATCTACTTCTCTGCGAGAACCTTAGTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1446
Qy	1381	GGTCTTCTGATTCCTCACTCAACGAGCTGTGGCGGTGAAGATGGCGGCTTCCAGGTAAA	1440
Db	1447	GGTCTTCTGATTCCTCACTCAACGAGCTGTGGCGGTGAAGATGGCGGCTTCCAGGTAAA	1506
Qy	1441	GCAAAATGAAATTCAGAGCTCGCGCATCAAGCTGATGATGATGATGATGATGATGATGAT	1500
Db	1507	GCAAAATGAAATTCAGAGCTCGCGCATCAAGCTGATGATGATGATGATGATGATGATGAT	1566
Qy	1501	GGTGTGAAAGCTGTACGCTTGGAGGCCAGCTTCTTGAAGCAGGTGGAGGCTATCAGGCA	1560
Db	1567	GGTGTGAAAGCTGTACGCTTGGAGGCCAGCTTCTTGAAGCAGGTGGAGGCTATCAGGCA	1626
Qy	1561	GGTGTGCTCCAGCTGCTGCGCAGCGGCGCTTACCTCCACACCAACACCTTACCTG	1620
Db	1627	GGTGTGCTCCAGCTGCTGCGCAGCGGCGCTTACCTCCACACCAACACCTTACCTG	1686
Qy	1621	GATGTGACGCCCTTCTGCTGACCTGATCACCCTCTGGGTGATGATGATGATGATGATGAT	1680
Db	1687	GATGTGACGCCCTTCTGCTGACCTGATCACCCTCTGGGTGATGATGATGATGATGATGAT	1746
Qy	1681	AAACAATGTGTGGAGCGCGAGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1740
Db	1747	AAACAATGTGTGGAGCGCGAGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1806
Qy	1741	ACTTCCCTTCAACATGCTGCCCTTCAATCAGCAACCTGACTCAGGCCAGTGTGTCT	1800
Db	1807	ACTTCCCTTCAACATGCTGCCCTTCAATCAGCAACCTGACTCAGGCCAGTGTGTCT	1866
Qy	1801	GAACGAGATCCAGCAATTCCTGAGCCCAAGAGAACTTACCCCGAGAGTGTGAAAGAAA	1860
Db	1867	GAACGAGATCCAGCAATTCCTGAGCCCAAGAGAACTTACCCCGAGAGTGTGAAAGAAA	1926
Qy	1861	GACCATCTCCCGAGGCTATGCCATCACCATACAGAGTGGACCTTACCTGGGCCAGGA	1920
Db	1927	GACCATCTCCCGAGGCTATGCCATCACCATACAGAGTGGACCTTACCTGGGCCAGGA	1986
Qy	1921	CCTGCCCTTCTCTGACAGCTTAGACATCCAGGTCCCGAAGAGGCGACTGTGGCGCT	1980
Db	1987	CCTGCCCTTCTCTGACAGCTTAGACATCCAGGTCCCGAAGAGGCGACTGTGGCGCT	2046
Qy	1981	GGTGGGCGCTGTGGGCTGTGGGAAGTCCCTTGGGTGTGTGTGTGTGTGTGTGTGTGTGT	2040
Db	2047	GGTGGGCGCTGTGGGCTGTGGGAAGTCCCTTGGGTGTGTGTGTGTGTGTGTGTGTGTGT	2106
Qy	2041	GAAGCTAGAGGCAAGTGCATGAAGGCTCCGTGGCTATGTGCCCCAGCAGGATG	2100

Db 2107 GAAGCTAGAGGCAAGTGCACATGAAGGGCTCCGTGGCCTATGTGCCACGAGGCATG 2166
Qy 2101 GATCCAGACTGCACCTTTCAGGAAAACGTGCTTTTCGGGCAAAAGCCCTGAAACCCCAAGCG 2160
Db 2167 GATCCAGAACTGCACCTTTCAGGAAAACGTGCTTTTCGGGCAAAAGCCCTGAAACCCCAAGCG 2226
Qy 2161 CTACACGACACTCTGAGGCGCTGCTGCTAGCTAGCTGACCTGAGATGCTGCTGCTGGTGG 2220
Db 2227 CTACACGACACTCTGAGGCGCTGCTGCTAGCTAGCTGACCTGAGATGCTGCTGCTGGTGG 2286
Qy 2221 GGATCAGACAGAGATTGGAGAGAGGCAATTAACCTGCTCTGGGGGCCAGCGCGACGGGT 2280
Db 2287 GGATCAGACAGAGATTGGAGAGAGGCAATTAACCTGCTCTGGGGGCCAGCGCGACGGGT 2346
Qy 2281 CAGTCTGGCTGAGCTGTTTACAGTAGTGGCGATATTTCTGCTGAGTACCCACTGTC 2340
Db 2347 CAGTCTGGCTGAGCTGTTTACAGTAGTGGCGATATTTCTGCTGAGTACCCACTGTC 2406
Qy 2341 CGCGGTGACTCTCATCTGCGCAAGCACATCTTTTGACACGCTCATCGGCCAGAGGCGT 2400
Db 2407 CGCGGTGACTCTCATCTGCGCAAGCACATCTTTTGACACGCTCATCGGCCAGAGGCGT 2466
Qy 2401 GCTGGCAGGCAAGACGGAGTGTGTGAGCGACGCGCATTAAGCTTCTGCCCCAGACAGA 2460
Db 2467 GCTGGCAGGCAAGACGGAGTGTGTGAGCGACGCGCATTAAGCTTCTGCCCCAGACAGA 2526
Qy 2461 CTTGATCATTTGCTAGCTGATGAGACAGGTGTCTGAGATGGGCCCGTACCCAGCCCTGCT 2520
Db 2527 CTTGATCATTTGCTAGCTGATGAGACAGGTGTCTGAGATGGGCCCGTACCCAGCCCTGCT 2586
Qy 2521 GCAGCGCAACGGCTCCTTTGCCAACTTCTCTGCACTATGCCCCCGATGAGGACCAAGG 2580
Db 2587 GCAGCGCAACGGCTCCTTTGCCAACTTCTCTGCACTATGCCCCCGATGAGGACCAAGG 2646
Qy 2581 GCACCTGGAGGACAGCTGGACCGCGTTGGAGGTGACAGAGATTAAGAGGACACTGCTGAT 2640
Db 2647 GCACCTGGAGGACAGCTGGACCGCGTTGGAGGTGACAGAGATTAAGAGGACACTGCTGAT 2706
Qy 2641 TGAAGACACTCAGCAACACACAGGATCTGACAGACAATGATCCAGTCACTATGTGGT 2700
Db 2707 TGAAGACACTCAGCAACACACAGGATCTGACAGACAATGATCCAGTCACTATGTGGT 2766
Qy 2701 CCAGAGCAGTTTATGACAGCTGAGTGCCTCTCTCAGATGGGAGGACAGGCTCG 2760
Db 2767 CCAGAGCAGTTTATGACAGCTGAGTGCCTCTCTCAGATGGGAGGACAGGCTCG 2826
Qy 2761 GCCTGTACCCCGGAGGCACCTGGGTCCATCAGAGAAGGTGACAGAGCGCAAGGC 2820
Db 2827 GCCTGTACCCCGGAGGCACCTGGGTCCATCAGAGAAGGTGACAGAGCGCAAGGC 2886
Qy 2821 AGATGGGCACTGACCCAGGAGAGAAAGAGCCATTGGCACTGTGAGCTCAGTGTGT 2880
Db 2887 AGATGGGCACTGACCCAGGAGAGAAAGAGCCATTGGCACTGTGAGCTCAGTGTGT 2946
Qy 2881 CTGGGATTATGCAAGGCGCTGGGGTCTCTACACGCTGGCCATCTCTCCTGTATGT 2940
Db 2947 CTGGGATTATGCAAGGCGCTGGGGTCTCTACACGCTGGCCATCTCTCCTGTATGT 3006
Qy 2941 GGGTCAAGTGGCGCTGCCATTGGAGCCAAATGTGTGGCTCAGTGCCTGGCAAAATGATG 3000
Db 3007 GGGTCAAGTGGCGCTGCCATTGGAGCCAAATGTGTGGCTCAGTGCCTGGCAAAATGATG 3066
Qy 3001 CATGGCAGACAGTAGACAGAAACAACTTCCCTGAGGCTGGGCGCTATGCTGCTTTAGG 3060
Db 3067 CATGGCAGACAGTAGACAGAAACAACTTCCCTGAGGCTGGGCGCTATGCTGCTTTAGG 3126
Qy 3061 AATTCTGAGGGTCTTGTGTATGCTGGCAGCCATGGCCATGGCAGCGGTGGCATCCA 3120
Db 3127 AATTCTGAGGGTCTTGTGTATGCTGGCAGCCATGGCCATGGCAGCGGTGGCATCCA 3186
Qy 3121 GGTGCGCGGTGCTTGACACGAGCACTGCTGACACAAAGATACGCTTCGCCACAGTCTTT 3180
Db 3187 GGTGCGCGGTGCTTGACACGAGCACTGCTGACACAAAGATACGCTTCGCCACAGTCTTT 3246

Qy 3181 CTTTGACACCACACCATCAGGCCGCTCCTGAATGCTTCTCAAGGACATCTATGTCTG 3240
Db 3247 CTTTGACACCACACCATCAGGCCGCTCCTGAATGCTTCTCAAGGACATCTATGTCTG 3306
Qy 3241 TGATGAGGTTCTGGGCCCTGTCACTCCTCATGCTGCTCAATCTCTTCAACGCCATCTC 3300
Db 3307 TGATGAGGTTCTGGGCCCTGTCACTCCTCATGCTGCTCAATCTCTTCAACGCCATCTC 3366
Qy 3301 CACTCTTGTGTGCTATCATGCGCAGCACCGCTCTTCACTGTGCTCATCTCCTCCCTGGC 3360
Db 3367 CACTCTTGTGTGCTATCATGCGCAGCACCGCTCTTCACTGTGCTCATCTCCTCCCTGGC 3426
Qy 3361 TGTGCTCTACACCTTAGTGCAGCGCTTCTATGACGCCACATCACGCCAACTGAAGCGGT 3420
Db 3427 TGTGCTCTACACCTTAGTGCAGCGCTTCTATGACGCCACATCACGCCAACTGAAGCGGT 3486
Qy 3421 GGAATCAGTCAAGCGCTCACCTATCTACTCCGACTTTTCGGAGACAGTACTGGTGCAG 3480
Db 3487 GGAATCAGTCAAGCGCTCACCTATCTACTCCGACTTTTCGGAGACAGTACTGGTGCAG 3546
Qy 3481 TGTCTATCCGGCGCTACAAACCGCAGCGGATTTTCAGATCATCACTGATTAAGGTGA 3540
Db 3547 TGTCTATCCGGCGCTACAAACCGCAGCGGATTTTCAGATCATCACTGATTAAGGTGA 3606
Qy 3541 TGCCAAACAGAGAGTCTTACCCCTACATCATCTCCAAACCGGTGGCTGAGCATCGGAGT 3600
Db 3607 TGCCAAATCAGAGAGTCTTACCCCTACATCATCTCCAAACCGGTGGCTGAGCATCGGAGT 3666
Qy 3601 GGAGTCTGTGGGAACTCGCTGGTGTCTTTTGTGCTCACTATTTGCCGTCTATCGGAGGAG 3660
Db 3667 GGAGTCTGTGGGAACTCGCTGGTGTCTTTTGTGCTCACTATTTGCCGTCTATCGGAGGAG 3726
Qy 3661 CAGCTTGAACCCCGGGCTGGTGGGCTTCTGTGTCTCTCTTGTGAGGTGACATTTGC 3720
Db 3727 CAGCTTGAACCCCGGGCTGGTGGGCTTCTGTGTCTCTCTTGTGAGGTGACATTTGC 3786
Qy 3721 TCTGAACCTGGATGATAGAAATGATGTGAGATTTGAAATCTAACATCTGAGGAG 3780
Db 3787 TCTGAACCTGGATGATAGAAATGATGTGAGATTTGAAATCTAACATCTGAGGAG 3846
Qy 3781 GGTCAAGAGTACTTCCAAAGACAGACAGAGCGCCCTGGGTGGTGGAAAGCAGCGGCC 3840
Db 3847 GGTCAAGAGTACTTCCAAAGACAGACAGAGCGCCCTGGGTGGTGGAAAGCAGCGGCC 3906
Qy 3841 TCCCGAAGGTTGGCCCGCCACCTGGGAGGTGAGTTCCGGAATTTATCTGTGCGTACCG 3900
Db 3907 TCCCGAAGGTTGGCCCGCCACCTGGGAGGTGAGTTCCGGAATTTATCTGTGCGTACCG 3966
Qy 3901 GCGGGCTAGACCTGTGTGAGAGACCTGAGTGTGATGTGACACGCTGGCGAGAGGT 3960
Db 3967 GCGGGCTAGACCTGTGTGAGAGACCTGAGTGTGATGTGAGTGGCTCAATGTGCGAGAC 4026
Qy 3961 GGGGATCTGGCGCGCACTGGGCTGGCAAGTCTTCCATGACCCCTTTGCCCTTCCGCA 4020
Db 4027 GGGGATCTGGCGCGCACTGGGCTGGCAAGTCTTCCATGACCCCTTTGCCCTTCCGCA 4086
Qy 4021 CCTGGAGCGCGCAAGGTTGAAATCCGATTTGATGGCTCAATGTGCGAGACATCGGCT 4080
Db 4087 CCTGGAGCGCGCAAGGTTGAAATCCGATTTGATGGCTCAATGTGCGAGACATCGGCT 4146
Qy 4081 CCATGACCTGGCTCTCAGCTGACCATCATCCCGAGGACCCCATCTCTGTTCTCGGGAC 4140
Db 4147 CCATGACCTGGCTCTCAGCTGACCATCATCCCGAGGACCCCATCTCTGTTCTCGGGAC 4206
Qy 4141 CCTGCGCATGAACCTGACCCCTTCGGCAGCTACTCAGAGGAGGACATTTGGTGGCTTT 4200
Db 4207 CCTGCGCATGAACCTGACCCCTTCGGCAGCTACTCAGAGGAGGACATTTGGTGGCTTT 4266
Qy 4201 GGAGTCTGCCACCTGACAGTGTGTGAGTCTCCAGCGCAGCGCTGAGTTCACATG 4260
Db 4267 GGAGTCTGCCACCTGACAGTGTGTGAGTCTCCAGCGCAGCGCTGAGTTCACATG 4326

QY 4261 CTCAGAGGGCGGGAGAACTCTCAGCGTGGGCCAGAGGAGCTCGTGTGCTGCGCCGAGC 4320
 Db 4327 CTCAGAGGGCGGGAGAACTCTCAGCGTGGGCCAGAGGAGCTCGTGTGCTGCGCCGAGC 4386
 QY 4321 CCTGCTCGCAAGAGCGGATCTCTGGTCTTTAGACGAGGCCACAGCTGCCATCGACTGGA 4380
 Db 4387 CCTGCTCGCAAGAGCGGATCTCTGGTCTTTAGACGAGGCCACAGCTGCCATCGACTGGA 4446
 QY 4381 GACTGACAACTCATCCAGGCTACCATCGGACCCAGTTTGATACCTGCAGTGTCTGAC 4440
 Db 4447 GACTGACAACTCATCCAGGCTACCATCGGACCCAGTTTGATACCTGCAGTGTCTGAC 4506
 QY 4441 CATCGCACACCGGCTTAACACTATCATGACTACACAGGCTCCCTGGGCAAGG 4500
 Db 4507 CATCGCACACCGGCTTAACACTATCATGACTACACAGGCTCCCTGGGCAAGG 4566
 QY 4501 AGTAGTACCTGAATTTGATTTCTCCAGCCAACTCATTTGAGCTAGAGGATCTTCTACGG 4560
 Db 4567 AGTAGTACCTGAATTTGATTTCTCCAGCCAACTCATTTGAGCTAGAGGATCTTCTACGG 4626
 QY 4561 GATGCCAGAGATGCTGAGCTTGCCTAAATATATTTCTGAGATTTCTCTGGCCTTTC 4620
 Db 4627 GATGCCAGAGATGCTGAGCTTGCCTAAATATATTTCTGAGATTTCTCTGGCCTTTC 4686
 QY 4621 CTGTTTTCATCAGAGGAATGACACCAATATGTCGGCAGATGAGCTGATAGCAA 4680
 Db 4687 CTGTTTTCATCAGAGGAATGACACCAATATGTCGGCAGATGAGCTGATAGCAA 4746
 QY 4681 ACATGGGGGACCTTTAGATTTTGCACCTGTAAGTGCCTTACAGGCTAACTGTGCTGA 4740
 Db 4747 ACATGGGGGACCTTTAGATTTTGCACCTGTAAGTGCCTTACAGGCTAACTGTGCTGA 4806
 QY 4741 ATGCTTTAGATGAGGAATGATCCCAAGTGGTGAATGACACGCTTAAGGTCACAGCTAG 4800
 Db 4807 ATGCTTTAGATGAGGAATGATCCCAAGTGGTGAATGACACGCTTAAGGTCACAGCTAG 4866
 QY 4801 TTTGAGCAGTTAGACTAGTCCCGGCTCCCGATTTCCCACTGAGTGTATTTTGCACAC 4860
 Db 4867 TTTGAGCAGTTAGACTAGTCCCGGCTCCCGATTTCCCACTGAGTGTATTTTGCACAC 4926
 QY 4861 TGCACCTTTTCAATCAACGATTTTATGAATGACCTCTGTCCTCTCTGATTTTTCAT 4920
 Db 4927 TGCACCTTTTCAATCAACGATTTTATGAATGACCTCTGTCCTCTCTGATTTTTCAT 4986
 QY 4921 ATTTCTAAAGTTTCGTTCTGTTTCTTTTAAATAAAGCTTTTCTCTGTCGAAACAGAGA 4980
 Db 4987 ATTTCTAAAGTTTCGTTCTGTTTCTTTTAAATAAAGCTTTTCTCTGTCGAAACAGAGA 5046
 QY 4981 CAGCTGTGGGTGACGAGCCACCCCTAGGAACCTCAGTCTGCTGCTGCTGCTGCTGAA 5040
 Db 5047 CAGCTGTGGGTGACGAGCCACCCCTAGGAACCTCAGTCTGCTGCTGCTGCTGCTGAA 5106
 QY 5041 TCCATTAATAATGGGAGTACTGATGAATAAATACTACA 5078
 Db 5107 TCCATTAATAATGGGAGTACTGATGAATAAATACTACA 5144

RESULT 3
 AAT94052
 ID AAT94052 standard; cDNA; 4762 BP.
 XX
 AC AAT94052;
 XX
 DT 01-APR-1998 (first entry)
 XX

Human multidrug resistance-associated protein 3 (hMRP3) cDNA sequence.
 DE
 KW Canalicular multispecific organic anion transporter protein;
 KW cMOAT protein; ATP-binding cassette transporter family; ABC transporter;
 KW hepatobiliary excretion; multidrug resistance-associated protein; MRP3;
 KW cMOAT protein activity; multidrug resistance-related protein; MDR-1;
 KW Dubin-Johnson disease; Rotor disease; ss.
 XX

OS Homo sapiens.
 XX Key Location/Qualifiers
 FH CDS 71..4657
 FT /*tag= a
 XX
 PN WO97311111-A2.
 XX
 PD 28-AUG-1997.
 XX
 PF 21-FEB-1997; 97WO-NL00079.
 XX
 PR 22-FEB-1996; 96EP-0200460.
 XX
 PA (MEDI-) ACAD MEDISCH CENT AMSTERDAM.
 PA (HETN-) HET NEDERLANDS KANKER INST.
 PA (INTR-) INTROGENE BV.
 XX
 PI Borst P, Bosma PJ, Evers R, Oude Elferink RPJ;
 PI Paulusma CC;
 XX
 DR WPI: 1997-435163/40.
 DR P-PSDB; AAW33363.
 XX
 XX DNA encoding human and rat canalicular multispecific organic anion
 PT transporter proteins - useful for diagnosis and treatment of
 PT Dubin-Johnson disease and Rotor disease
 XX
 PS Disclosure: Fig 17A; 106pp; English.
 XX
 CC The present cDNA sequence encodes a human multidrug resistance-associated
 CC protein 3 (MRP3). The MRP3 gene has been localised to chromosome 17. The
 CC MRP3 protein is a member of the ATP-binding cassette (ABC) transporter
 CC family of anorganic anion transporters. MRP3 is a 4 domain protein, with
 CC 2 ATP-binding domains, and 2 domains with transmembrane regions. The
 CC protein is a homologue of MRP1, which is involved in ATP-dependent
 CC transport of glutathione conjugates such as dinitrophenyl glutathione.
 CC These substrates are also transported by a novel canalicular
 CC multispecific organic anion transporter (cMOAT) protein. The ATP
 CC dependent cMOAT transporter system mediates hepatobiliary excretion in
 CC the liver. cMOAT may be a liver-specific homologue of multidrug
 CC resistance-associated protein. The nucleic acids are used to provide
 CC cells with cMOAT protein activity. cMOAT protein activity in cells can
 CC be enhanced by increasing the level of glutathione, glucuronide and/or
 CC sulphate. Antisense constructs, especially derived from another multidrug
 CC resistance (MDR)-related protein, e.g. MDR-1, to the nucleic acids and
 CC vectors can be used to decrease the level of cMOAT in a cell. The nucleic
 CC acids and proteins can be used especially in diagnosis of Dubin-Johnson
 CC disease, Rotor disease or another disease involving cMOAT. The cMOAT gene
 CC may also be used as a selectable marker gene.
 XX
 SQ Sequence 4762 BP; 935 A; 1423 C; 1325 G; 1073 T; 6 other;

Query Match 90.3%; Score 4586.8; DB 18; Length 4762;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 4645; Conservative 2; Mismatches 24; Indels 7; Gaps 4;
 QY 1 CCCCATGACGCGCTGTGCGGTTCCGGGAGCTCGGCTCCAGTCTCGGACTCCAACT 60
 Db 67 CCCCATGACGCGCTGTGCGGTTCCGGGAGCTCGGCTCCAGTCTCGGACTCCAACT 126
 QY 61 GTCGTGTGCACACAGAAAAACCCGGACCTCAGTCCCTGCTTCCAGAACTCCCTGCGCTG 120
 Db 127 GTCGTGTGCACACAGAAAAACCCGGACCTCAGTCCCTGCTTCCAGAACTCCCTGCGCTG 186
 QY 121 GGTGCTGTGCATCTACCTGTGGTGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 Db 187 GGTGCTGTGCATCTACCTGTGGTGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 246
 QY 181 TTGTCGTGGCTACATCATCTCTCCACCTGTCCAGCTCAGAGTGGTCTGCTGCTGCTGCT 240
 Db 247 TTGTCGTGGCTACATCATCTCTCCACCTGTCCAGCTCAGAGTGGTCTGCTGCTGCTGCT 306

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RESULT 4
ABN96910
ID ABN96910 standard; DNA; 1977 BP.
XX AC ABN96910;
XX 13-AUG-2002 (first entry)
XX DE Gene #3408 used to diagnose liver cancer.
XX KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KW metastatic liver tumour; cytostatic; expression profile; disease state;
KW disease progression; drug toxicity; drug efficacy; drug metabolism.
XX OS Homo sapiens.
XX XX WO200229103-A2.
XX PD 11-APR-2002.
XX PF 02-OCT-2001; 2001WO-US30589.
XX PR 02-OCT-2000; 2000US-237054P.
XX PA (GENE-) GENE LOGIC INC.
XX PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
XX DR WPI; 2002-426119/45.
XX PT Diagnosing and detecting the progression of liver cancer,
PT hepatocellular carcinoma or metastatic liver tumor in a patient,
PT involves detecting the level of expression of two or more genes in a
PT liver tissue sample
XX PS Claim 1; SEQ ID NO 3408; 298pp; English.
XX CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC tumour in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytostatic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 1977 BP; 450 A; 537 C; 513 G; 469 T; 8 other;

Query Match 34.4%; Score 1749.4; DB 24; Length 1977;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 1889; Conservative 0; Mismatches 49; Indels 15; Gaps 10;

QY 3134 TTGCACAGGCACTGTGTCACAAAGATAGCTGCGCACAGTCTCTTGTGACACCACA 3193
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QY 3252 TGGCCCTGTCTATCCCTCAT--GCTGCTCAATTCCTTCTCAACGCCATCTCCACTTGTG 3310
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QY 3547 CCAGAGAAGTCTACCCCTACATCATCTCCAAACCGGTGGCTGAGCATCGGAGTGGAGTT 3606
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QY 3727 CTGGATGATACGAATGATGTCTAGATTTGGAATCTAACATCTGCTGTGGAGAGGTGCA 3786
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Db 659 GGAGTACTTCCAAAGCAGAGACAGAGCGCCCTGGTGGTGGAG--CAGCCGCCCTCCCGA 716
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QY 3847 AGGTTGGCCCCACGTGGGAGGTGGAGTTCCGGGAATTAATCTGTGCGCTACCGCGCGGG 3906
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QY 4327 CCGCAAGAGCGGCATCTCTGTTTGTAGACAGGCGCACAGCTGCCATCGAGCTGGAGACTGA 4386
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XX DT 15-MAY-2002 (first entry)
XX DE Ovary cancer related gene sequence SEQ ID NO: 6335.
XX KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX KW gene; ds.
XX OS Homo sapiens.
XX PN WO200194629-A2.
XX XX 13-DEC-2001.
XX PF 30-MAY-2001; 2001WO-US10838.
XX PR 05-JUN-2000; 2000US-209473P.
XX PR 05-JUN-2000; 2000US-209531P.
XX PR 18-SEP-2000; 2000US-233133P.
XX PR 18-SEP-2000; 2000US-233617P.
XX PR 20-SEP-2000; 2000US-234009P.
XX PR 20-SEP-2000; 2000US-234034P.
XX PR 20-SEP-2000; 2000US-234052P.
XX PR 22-SEP-2000; 2000US-234509P.
XX PR 22-SEP-2000; 2000US-234567P.
XX PR 25-SEP-2000; 2000US-234923P.
XX PR 25-SEP-2000; 2000US-234924P.
XX PR 25-SEP-2000; 2000US-235077P.
XX PR 25-SEP-2000; 2000US-235082P.
XX PR 25-SEP-2000; 2000US-235134P.
XX PR 25-SEP-2000; 2000US-235280P.
XX PR 26-SEP-2000; 2000US-235637P.
XX PR 26-SEP-2000; 2000US-235638P.
XX PR 27-SEP-2000; 2000US-235711P.
XX PR 27-SEP-2000; 2000US-235720P.
XX PR 27-SEP-2000; 2000US-235840P.
XX PR 27-SEP-2000; 2000US-235863P.
XX PR 28-SEP-2000; 2000US-236028P.
XX PR 28-SEP-2000; 2000US-236032P.
XX PR 28-SEP-2000; 2000US-236033P.
XX PR 28-SEP-2000; 2000US-236034P.
XX PR 28-SEP-2000; 2000US-236109P.
XX PR 28-SEP-2000; 2000US-236111P.
XX PR 29-SEP-2000; 2000US-236842P.
XX PR 29-SEP-2000; 2000US-236891P.
XX PR 02-OCT-2000; 2000US-237172P.
XX PR 02-OCT-2000; 2000US-237173P.
XX PR 02-OCT-2000; 2000US-237278P.
XX PR 02-OCT-2000; 2000US-237294P.
XX PR 02-OCT-2000; 2000US-237295P.
XX PR 02-OCT-2000; 2000US-237316P.
XX PR 03-OCT-2000; 2000US-237425P.
XX PR 03-OCT-2000; 2000US-237598P.
XX PR 03-OCT-2000; 2000US-237604P.
XX PR 03-OCT-2000; 2000US-237606P.
XX PR 03-OCT-2000; 2000US-237608P.
XX PR 01-NOV-2000; 2000US-244867P.
XX PR 01-NOV-2000; 2000US-245084P.
XX PA (AVAL-) AVALON PHARM.
XX PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
XX PI Soppet DR, Weaver Z;
XX XX WPI: 2002-188264/24.
XX XX Screening for anti-neoplastic agent involves exposing cells to a
XX PT chemical agent to be tested for anti-neoplastic activity, and
XX PT determining a change in expression of a gene of a signature gene set
XX XX
XX PS Claim 1; SEQ ID 6335; 44pp; English.

XX The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABU61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.
XX XX
XX Sequence 1977 BP; 450 A; 537 C; 513 G; 469 T; 8 other;
Query Match 34.4%; Score 1749.4; DB 24; Length 1977;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 1889; Conservative 0; Mismatches 49; Indels 15; Gaps 10;
QY 3134 TTGCACGAGGCGTGTGCACAAAGATACGCTCGCCACAGTCTCTTTGACACCACA 3193
DB 1 TTGCACGAGGCGTGTGCACAAAGATACGCTCGCCACAGTCTCTTTGACACCACA 60
QY 3194 CCATCAGGCGGCGATCCTGAACTCTTCCAAAGGACATCTATGTGCG--TTGATGAGGTTG 3251
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QY 3427 AGTCAGCGCTACCTATCTACTCTCCACTTTTCGGAGACAGTCTGCTGGCCAGTGTCTAT 3486
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DB 360 CCGGGCTTACACCGCAGCGCGGATTTTGAGATCATCATGATCACTAAGTGGATGCCAA 419
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QY 3607 CGTGGGAACTGGGTGCTCTTTGCTGCATCTTTGCGGTCTATTTGGGAGGAGGAGCCCT 3666
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QY 3787 GGAGTACTTCAAGACAGACAGAGCGCGCTTGGGTGGTGGAGGAGGAGGAGCCCTCCCGA 3846
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Db 717 AGGTGG-CCCAAGTGGGGAGGTGGAGTTCGGGAATATTCTGTGCGCTACCGGCCGGG 775
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Db 1494 TTCATAGGAAGGAATGACACCAATATATGTCGAGAAATGGACTTGATAGCAACACTG 1553
QY 4687 GGGGCACTTTAAGA-TTTTGACCTGTAAGTGTGCTTACAGGGTAACTGTGCTGAATGCT 4745
Db 1554 GGGGCACTTTAAGATTTTGGCACCTTTAAAGTGGCTTACAGGGTAACTGTGCTGAATGCT 1613
QY 4746 TTAGATGAGAAATGATCCCAAGTGTGAATGACAGCGCTAAGGTACAGCTAGTTGA 4805
Db 1614 TTAGATGAGAAATGATCCCAAGTGTGAATGACAGCGCTAAGGTACAGCTAGTTGA 1673
QY 4806 GCCAGTTAGACTAGTCCCGGCTTCCCGATTCCCAACTGAGTGTATTGTGACACTGCAC 4865
Db 1674 GCCAGTTAGACTAGTCCCGGCTTCCCGAATCCCAACTGAGTGTATTGTGACACTGCAC 1733
QY 4866 TGTTTTCAATAACGATTTTATGAATGACCTGTGCTCCCTGATTTTTCATATTTT 4925
Db 1734 TGTTTTCAATAACGATTTTATGAATGACCTGTGCTCCCTGATTTTTCATATTTT 1793
QY 4926 CTAAGATTTCTGTTCTTTTAAATAAAGCTTTTTCCTCTCTGGACAGACAGCT 4985
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Db 1794 CTAAGATTTCTGTTCTTTTAAATAAAGCTTTTTCCTCTCTGGACAGACAGCT 1853
QY 4986 GCTGGCTCAGGCAACCCCTAGGAACCTCAGTCTGTACTCTGGGTGCTGCCTGAATCCAT 5045
Db 1854 GCTGGCTCAGGCAACCCCTAGGAACCTCAGTCTGTACTCTGGGTGCTGCCTGAATCCAT 1913
QY 5046 TAAAAATGGAGTACTGATGAATAAAACTACA 5078
Db 1914 TAAAAATGGAGTACTGATGAATAAAACTACA 1946

RESULT 7
AAQ65377
ID AAQ65377 standard; cDNA; 5011 BP.
XX
AC AAQ65377;
XX
DT 14-OCT-1994 (first entry)
XX
DE Multidrug resistance protein.
XX
KW Multidrug resistance protein; MRP; H69AR; cancer cell line;
stem cell; cardiac muscle; transgenic animal; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 196..4791
FT /*tag= a
XX
PN W09410303-A.
XX
PD 11-MAY-1994.
XX
PF 27-OCT-1993; 93WO-CA00439.
XX
PR 27-OCT-1992; 92US-0966923.
PR 08-MAR-1993; 93US-0029340.
XX
PA (TOOH ) UNIV QUEBENS KINGSTON.
XX
XX Cole SPC, Deeley RG;
XX
XX WPI; 1994-167460/20.
XX
XX P-PSDB; AAR54928.
XX
XX Multi-drug resistance gene - encodes protein capable of
conferring multi-drug resistance on cells, useful in diagnostic
and treatment methods
XX
XX Disclosure; Page 62-68; 101pp; English.
XX
XX The multidrug resistant cancer cell line H69AR (ATCC CRL 11350) was
used to identify cDNA encoding a novel protein associated with
multidrug resistance, MRP. MRP may be expressed in e.g.
hematopoietic stem cells or cardiac muscle, or in
transgenic animals, or can be used to raise antibodies.
XX
XX Sequence 5011 BP; 1064 A; 1497 C; 1394 G; 1056 T; 0 other;

Query Match 34.2%; Score 1737.8; DB 15; Length 5011;
Best Local Similarity 62.2%; Pred. No. 0;
Matches 2882; Conservative 0; Mismatches 1662; Indels 87; Gaps 6;
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QY 25 CGGGGAGCTCGGCTCCAGTTCGGGACTCCAACTGTGTGACACAGAAAACCCCGA 84
Db 219 CGCGGATGGCTCCGACCGCTCTGGGACTGGAATGTCACGTGGAATACCAACCCCGA 278
QY 85 CCTCAGTCCCTGCTTCCAGAACTCCCTGCTGCGCTGGGTGCGCTCATCTGCTGGT 144
Db 279 CTTCCACCAAGTCTTTTCAAGAACAGCTCCTGCTGTTGGGTGCTTTTACCTCTGGC 338
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QY	145	GC	CCCTGCGCCCTGCTACCTGCTCTACCTGCGGCACCAATGCTCGTGGCTACATCATCATCTCTC	204
DB	339	CT	GTGTTCCCTTCTACCTTCTCTATCTCTCCCGACATGACCGAGGCTACATTCAGATGAC	398
QY	205	CC	ACCTGTCCAAAGCTCAAGATGGTCTGGGTGTCCTGCTGTGGTGCCTCTCTGCTGGCGGA	264
DB	399	AC	CTCTCAACAAACCAAACTGCCCTTGGGATTTTGTGTGGATCGTCTGCTGGCGCAGA	458
QY	265	CC	TTTTTACTCTCTCCATGGCTGTGCATGCGCGGGCCCTGCCCTGTTTCTTTCTTGT	324
DB	459	CT	CTTCTACTCTTCTGCGGAAGAAGTCGGGCATATTCCTGGCCCCAGTGTTCCTGGT	518
QY	325	CAC	CCCCCTTGGTGGGGGTACCAATGCTGTGGCCACCTGCTGATACAGATGAGCG	384
DB	519	CAG	CCCAACTCTCTTGGGCATCACACGCTGCTTGTCTACCTTTTAAATTCAGCTGGAG	578
QY	385	GCT	CAGGGCGTACAGTCITCGGGGTCCCTCAATATCTTCTGTGGTTCCTGTGTGGTCTG	444
DB	579	GAG	AAGGGAGTTCAGTCTTTCAGGGATCATGCTCACTTCTGTGGTGTGAGCCCTAGTGTG	638
QY	445	CG	CATCGTCCCATTCCTGCTCCAAAGATCCTTTTTCGCAAGGCAGAGGCTGAGATCTCAGA	504
DB	639	TG	CCCTAGCCATCTCTGAGATCCAAAATATAGACGCTTAAAGAGGATGCCAGGTGGGA	698
QY	505	CCC	TTCGGCTTACCACACCTTCTACATCCACTTTTGCCCTGGTACTCTCTGCCCTCATCTT	564
DB	699	CT	GTGTCGTGACATCACTTCTTACGTCTACTTTTCCCTTCTACTCATTCAGCTCGTCTT	758
QY	565	GG	CTGCTCAGGAGAAACCTCCATTTTCTCCGCAAGAATGTFCGACCCTAACCCCTA	624
DB	759	GT	CTGTCTTCAGATCGCTCACCCCTGTTCGCGAAACCATCCACGACCCCTAATCCCTG	818
QY	625	CC	TGAGACACGCGTGGCTTCTCTCCCGCTGTTTCTCTGGTGGTTCACAAAGATGGC	684
DB	819	CC	AGATCCAGCGCTCTCTCTGTCGAGGATCACTTCTGGTGGATCAGAGGTTGAT	878
QY	685	CAT	CTATGGCTACCGCATCCCTCGAGGAGAGGACCTCTGGTCCCTTAAAGGAGAGGA	744
DB	879	TG	TCCGGGGCTACCGCCAGCCCTCGAGGCGAGTCACTCTGGTCTTAAACAGAGGGA	938
QY	745	CAG	ATCCAGATGGTGGTGCAGCAGCTGCTGAGGCATGGAGG-----	788
DB	939	CAG	CTGGGAACAAGTCTGCTGCTTGTGGTAAAGAACTGGAAGAGGAATGCGCCAAAGC	998
QY	789	-----	AGCAGAAACAGACGCGACGACACAAAGCTTTCAGCAGCACCTGGGAAAAA	840
DB	999	TAG	AGCAGCGCGTGAAGTGTGTACTCTCCCAAGATCTGCCAGCGCGAAGAGAG	1058
QY	841	TG	CTCGGGGAGGAGGTGCTGTGGTG-----CCGGCCCGAGGCC	885
DB	1059	TT	CAAGTGGATGCGAATGAGAGGTGGAGGCTTGTATGCTCAAGTCCCCACAGAAGGA	1118
QY	886	CG	GAGCCCTCTCTTCTCAAGGCCCTGCTGGCACTTCGCTCCAGTCCAGCTCTCATCAT	945
DB	1119	GT	GGAACCCCTCTCTTTAAGGTGTATACAAAGACCTTTGGGCGCTACTTCTCATFAG	1178
QY	946	TG	CTGCTTCAAGCTTATCCAGGACTGTCTCTCTTCATCAATCCACAGCTGCTCAGCAT	1005
DB	1179	CT	TCTTTCAGGGCATCCAGACCTGATGATGTTTCCGGGCGGCGATCTTAAAGTT	1238
QY	1006	CT	GATCAGGTTATCTCAACCCCATGGCCCCCTCTGTGTGGGGCTTCTGTGGTCTG	1065
DB	1239	GCT	CACTAAAGTTCGTGAATGACAAAGGCCACAGCTTGGCAGGGCTACTTCTACACCGT	1298
QY	1066	GCT	GATGCTTCTGCTCCTCATCATGACGATCGCTGATCTTACAAACATTTTACACATCAT	1125
DB	1299	GCT	GCTGTTGTGCTACTGCTGCTCGACACCCCTCGTGTGTCACCACTACTTCCACATCTG	1358
QY	1126	CT	TGTGTACTGGGTGAAGTTCGTACTTGGGATCATGGGTCTCATCTACAGGAAGGCTCT	1185
DB	1359	CT	TGCTAGTGCATGAGGATCAAGACCGTGTCTATGGGGCTCTCTATCGGAAGGCCCT	1418
QY	1186	GG	TATACCAACTCAGTCAAAACGTCGCTGCCACTGTGGGGGAAATTTGTCACCTCATGTC	1245

Db	1419	GGTGATACCAATTCACGCCAAGAAATCCTCCACGGTGGGGAGATTGTCACACCTCATGTC	1478
Qy	1246	AGTGGATGCCAGCGCTCATGACCTTGGCCCTTCTCCTCAATCTGCTGTGGTTCAGCACC	1305
Db	1479	TGTGGACGCTCAGAGTTTATGACATTTGGCCACGTACATTTAAATGATCTGGTTCAGCCCC	1538
Qy	1306	CTGCAAGATCATCCTGGCGATCTACTTCCCTGGCAGAACCTAGTCCCTCTGTCTCTGGC	1365
Db	1539	CCTGCAAGTCACTCTTGTCTCTACCTCTGTGGCTGAATCTGGGCCCTTCCGTCCTGGC	1598
Qy	1366	TGGAGTCTGCTTTCATGGTCTTGTCTGATTCACATCAACGAGAGCTGTGCGCGTGAAGATGCG	1425
Db	1599	TGGAGTGGGGGTGATGGTCTCATGGTGGCCGCTCAATGCTGTGATGGCATGAAGACCAA	1658
Qy	1426	CGCTTTCAGGTAAACCAATGAATGAAGGACTCGCGCATCAAGCTGATGATGATGATGAT	1485
Db	1659	GACGATACAGTGGGCCCATGAAGAGACAAGACAATTCGATCAAGCTGATGAACGAAT	1718
Qy	1486	CCTGAACGCATCAAGGTGCTGAAGCTGTACGCTGGGAGCCAGCTTCTCTGAAGCAGGT	1545
Db	1719	TCTCAATGGATCAAAAGTCTAAAGCTTTATGCTGGAGCTGGCATTCAGGACACAGGT	1778
Qy	1546	GGAGGCATCAGCAGGGTGATCTCAGCTGTCTGCGCAGCGCGCCCTACTCTCCACACCAC	1605
Db	1779	GCTGGCCATCAGCAGGAGGAGCTGAAGGTGCTGAAGAGTCTGCCTACCTGTCAAGCCGT	1838
Qy	1606	AACCACTTCACCTGGATGTCAGCGCCCTTCTCTGGTGAACCTCATCACCTCTGGGGTGA	1665
Db	1839	GGGACCTTCACCTGGGTCTGCACGCCCTTCTCTGGTGGCTTCTGTGCACATTTGCCCTCA	1898
Qy	1666	CGTGTACGTGGACCCAAACAATGCTGTGACGCCGAGAGAGCCCTTGTGTCTGTGTCTT	1725
Db	1899	CGTGACCATTGACGAGAACACATCTGGATGCCACAGACGCTTCTGTCTTTGGCCTT	1958
Qy	1726	GTTTAAATATCTTAAGACTTCCCTCAACATGCTGTGCCCCAGTTAATCAGCAACCTGACTCA	1785
Db	1959	GTTCAACATCTCCCGTTTCCCTCGAACATTTCTCCCATGCTCATCAGCAGCATCTGTCA	2018
Qy	1786	GGCCAGTGTCTCTGAACGGATCCAGCAATTCCTGAGCCAGAGAGAACTTGACCCCCA	1845
Db	2019	GGCAGTGTCTCCCTCAAAAGCCTGAGGATCTTCTCTCCCATGAGGAGCTGGAACCTGA	2078
Qy	1846	GAGTGTGAAGAAAGACCATCTCCCCAGGC-----TATGCCATCACCATACACAG	1896
Db	2079	CAGCATCGAGCAGCGCCCTGTCAAAGACGCGGGGSCACGAACAGCATCACCTGAGGA	2138
Qy	1897	TGGCACTTCACCTGGGCCAGGACCTGCCCCCACTCTGCACAGCCTAGACATPCAGGT	1956
Db	2139	TGCCACATTCACCTGGGCCAGGAGGACCCCTCCACACTGAATGGCATCACCTTCTCCAT	2198
Qy	1957	CCGGAAGGGGCACGTGTGGCCGTGTGTGGGCTGTGGGCTGTGGGAAGTCTCTCCCTGGT	2016
Db	2199	CCCCAGAGGTGCTTTGGTGGCCGTGGTGGCCAGGTGGGCTCGGGAAGATTGTTCCTGCT	2258
Qy	2017	GTCTGCCCTGTCTGGAGAGATGGAGAAGCTAGAAGGCAAGTGCATGAAGGGCTCCCGT	2076
Db	2259	CTCAGCCCTCTTGGCTGAGATGGACAAAGTGGAGGGGCACGTGGCTATCAAGGGCTCCGT	2318
Qy	2077	GGCCTATGTGCCCAGCAGGATGATTCAGAACTGCATCTTCAGGAAAAAGTGGCTTTT	2136
Db	2319	GGCCTATGTGCCACAGCAGGCCCTGGATTTCAGAAATGATTTCTCTCCGAAAAAATCTCTTT	2378
Qy	2137	CGGCAAGCCCTGAACCCCAACCGCTACCAAGCAGACTCTGGAGGCTGTGCCTTGTCTAGC	2196
Db	2379	TGGATGTCAAGTGGAGGAACCATATTCATAGGTCCGTGTACAGGCTGTGGCCTCTCC	2438
Qy	2197	TGACCTGGAGATGCTGCCTTGTGGGATCAGACAGAGATTGGAGAGAAGGCATTAACT	2256
Db	2439	AGACCTGGAATCTTGCCCACTGGGGATCGGACAGAGATTGGGAGAGGGCGTGAACCT	2498
Qy	2257	GTCTGGGGGCCAGCGGCACGCGGTCTGCTCTGCTCTGAGCTGTTTACAGTGTGCCGATAT	2316

Db 2499 GTCTGGGGCAGAGCAGCGCTGACGCTGGCCCGGCGCTGTACTCCAAGCGTGACAT 2558
QY 2317 TTTCTTGCTGGATGACCCACTGTCCGGGTGGACTCTCATGTGGCCAAACACATCTTTGA 2376
Db 2559 TTACTCTTTCATGATCCCTCTCAGCAGTGGATGCCATGTGGAAAAACACATCTTTGA 2618
QY 2377 CCAGCTCATCGGGCCAGAGCGCTGTGGCAGGCAAGACGCGAGTGTGGTGAGCCAGG 2436
Db 2619 AATGTGATTTGGCCCAAGGGATGCTGAAGAACAAAGACGGGATCTTGGTCAACGACAG 2678
QY 2437 CATTAGCTTCTGCTCCCCAGACAGACTTCATCTATGTGTAGCTGATGGACAGGTGTCTGA 2496
Db 2679 CATGAGTACTTGGCCGAGGTGGACGTCTCATCTGTCATGATGGCGGCAAGATCTCTGA 2738
QY 2497 GATGGGCCGTACCCAGCCCTGTGTGACGCCAACGGCTTCTTTCGCAACTTTTCTCTGCAA 2556
Db 2739 GATGGGCTCTTACCAGGAGTGTGTGGCTCGAGACGGCGCTTCTGCTGAGTTCTCTCGGTAC 2798
QY 2557 CTATGCCCCGATGAGCAACCAAGGCACTTGGAGGACAGCTGGACCGGTTGGAAGTGC 2616
Db 2799 CTATGCCAGCACAGAGGAGGAGGATGAGAGGAAGCGGTCAACGGCGTCAGCGG 2858
QY 2617 AGAGGATAAGGAGGCACTGTGATTGAAGACACACTCAGCAACACACAGGATCTGAACAGA 2676
Db 2859 TCCAGGAGGAAGCAAGCAATGAGATGGCAT----- 2894
QY 2677 CAATGATPCCAGTCACTTATGTGTCCAGAACAGTATTATGAGACAGCTGAGTGCCTGTCTC 2736
Db 2895 -----GCTGTGACGACAGTGCAGGGAAGCAACTCAGAGACAGCTCAGCAGCTCCTC 2948
QY 2737 CTCAGATGGGGAGGACAGGCTGGCTGTATCCCGGAGGACCTGGTCCATCAGAGAA 2796
Db 2949 CTCCTATAGTGGGGACA-----TCAGCAGGCAACCAACAGCAGCCGACAACTGCAGAAA- 3003
QY 2797 GGTGCAAGTACAGAGGCGAAGGAGCAGATGGGCACTGACCCAGGAGGAGAAAGCAGCCAT 2856
Db 3004 ----GCTGAGGCCAAGAGGAGGAGACTGGAAGCTGATGGAGGCTACAGAGGCGCAGAC 3059
QY 2857 TGGCACTGTGGAGTCACTGTGTCTGGGATTAAGCCAGGCCGTGGGCTCTGTACCAAC 2916
Db 3060 AGGCGCAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAGGCCATCGGACTTCTTCATCTC 3119
QY 2917 GCTGGCCATCTGTCTCTGTATGTGGTCAAAGTGGCGCTGCCATTTGGAGCCATGTGTG 2976
Db 3120 CTTCTCAGCATCTTCTTTTCAATGTATAACCATGTGTCCGCGCTGGCTTCCAACTATTG 3179
QY 2977 GCTCAGTGCCTGGACAAATGATGCCATGGCAGACAGTAGACAGAAACACTTCCCTGAG 3036
Db 3180 GCTCAGCCTCTGGACTGATGACCCCATCTGTCAGGGGACTCAGAGGACACAGAAAGTCCG 3239
QY 3037 GCTGGCGCTCTATGTCTTTAGGAATTCGCAAGGGTTCTTGGTGTATGCTGGCAGCCAT 3096
Db 3240 GCTGAGCGTCTATGGAGCCCTGGGCATTTTCAAGGGATCGCCGTGTTTGGCTACTCCAT 3299
QY 3097 GGCCATGGCAGCGGTGGATCCAGGCTGCCGTGTGTCACAGGCACTGTGCAACAA 3156
Db 3300 GGCCGTGTCATCGGGGGGATCTTGGCTTCCCGCTGTCTGACGCTGGACCTGTGTCACAG 3359
QY 3157 CAAGATACGCTGCCACAGTCTTCTTGAACACACACACACACACACACACACACACAC 3216
Db 3360 CATCTTGGGTCAACCATGAGCTTTTGGAGCGGACCCCGAGTGGGAACCTGGTGAACCG 3419
QY 3217 CTTCTCAAAGGACATATGTCTGTGATGAGGTCTTGGCCCTCTGTCACTCTCATGTGCT 3276
Db 3420 CTTCTCAAAGGAGCTGGACACAGTGGACTCCATGATCCCGAGGTCATCAAGATGTTTCA 3479
QY 3277 CAATTCCTTCTTCAAGCCATCTTCACTCTTGTGGTCACTCATGCCAGCAGCGGCTCTT 3336
Db 3480 GGCTCCCTGTTTCAAGGTCTTATGGTGGCTGCTGATCTGCTGCGGCAACGCGGCTTCGC 3539
QY 3337 CACTGTGGTCACTGCCCCCTGTGCTGTACACCTTAGTACAGGCTTCTATGACG 3396
Db 3540 CGCCATCATATCCCGCCCTTGGCTCATCTACTTCTTCTCGTCCAGAGGTTCTACGTGGC 3599

QY 3337 CACATCACGCAACTGAAGCGCTGGAATCAGTCAGCGGCTCACCTATCTACTCTCCACTT 3456
Db 3600 TTCTCTCCGCGCAGCTGAAGCGCTCGAGTCGTCAGCGCTCCCGGCTATTTCCCATTT 3659
QY 3457 TTCGAGACAGTACTGTCGACAGTGTCTATCCGGGCTTACAAACCGCAGCCGGATTTGA 3516
Db 3660 CAACGAGACCTTGTGGGGGTGAGGTCATTCGAGCCTTCGAGGAGCAGGAGCGCTTCAT 3719
QY 3517 GATCATCATGATACTAAGGTGGATCCCAACAGAGAGCTGCTACCCCTACATCATCTC 3576
Db 3720 CCACGAGTACCTGAAGGTGGAGAGACCAAGAGGCTATTACCCAGCATCTGTGGC 3779
QY 3577 CAACGGTGGCTGAGCATCGGAGTGGAGTGTGTTGGGAACTCGTGGTGTCTTTGCTGTC 3636
Db 3780 CAACAGGTGGCTGGCGGTGGAGTGTGTGGCAACTGCATCGTCTCTTTGCTGTC 3839
QY 3637 ACTATTTGCCGTCTATCGGGAGGAGGAGCTGAACCCGGGCTGTGGGCTTTCTGTGTC 3696
Db 3840 CCTGTTTGGGTGATCTCCAGGCAAGCTCAGTCTGGCTTGGTGGGCTCTCAGTGTCTC 3899
QY 3697 CTACTCTTTCAGGTGACATTTGCTCTGAAGTGGATGATGACAAATGATCTCAGATTTGA 3756
Db 3900 TTACTCATTTGAGGTCAACACGTACTTGAAGTGGCTGGTTCGGATGTCTCTGAAATGGA 3959
QY 3757 ATCTAACATCTGGCTGTGGAGAGGTTCAAGAGTACTTCCAAAGACAGACAGAGCGCC 3816
Db 3960 AACCAACATCTGGCGGTGGAGAGGCTCAAGAGTATTTCAGAGACTGAGAGGAGCGCC 4019
QY 3817 CTGGTGTGGAAGGAGCGCCCTCCGAAAGGTTGGCCCCACGCTGGGGAGGTGGAGTT 3876
Db 4020 CTGCAAAATCCAGGAGACACGTCCGCCAGCAGTGGCCCCAGGTGGGCGGAGTGAAT 4079
QY 3877 CCGAAATTTATCTGTGGCTACCGCGCGGCTAGACTGTGTGCTGAGAGACTCAGTCT 3936
Db 4080 CCGAAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4139
QY 3937 GCATGTGCAGGTGGCGAAGGTGGGATCTGGGCGGCTGCTGGGCGCTGCTGCTGCTGCT 3996
Db 4140 CACGATCAATGGGAGAGAAAGTTCGGATCAAGAGTCTGCCAAGGAGAGATCATCGATG 4199
QY 3997 CATCACCTTTGCTGCTCCGATCTCTGGAGCGGCAAGGTTGAAATCCGATTTGATGG 4056
Db 4200 CCGACCTGGGCTTATTTTCGGATCAAGAGTCTGCCAAGGAGAGATCATCGATGG 4259
QY 4057 CCAATGTGGCAGACATCGGCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4116
Db 4260 CATCAACATCGCAAGATCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4319
QY 4117 GGACCCCATCTGTTCTCGGGGACCTCGCATGAACCTGGACCCCTTCGGCAGCTACTC 4176
Db 4320 GGACCTGTTTGTGTTTTCGGGTTCCCTCCGATGAACCTGGACCCCTTCAGCCAGTACTC 4379
QY 4177 AGAGGAGACATTTGGTGGGCTTTGGAGCTGTCCACCTGCACAGTGTGTGAGCTCCCA 4236
Db 4380 GGATGAAGAAGTCTGGAGCTCCCTGGAGCTGGCCACCTGAAGGACTTCTGCTGCTGCTGCT 4439
QY 4237 GCGGCGAGGCTGACATTCAGTCTCAGAGGCGGGGAGATCTCAGCTGGGCGCAG 4296
Db 4440 TCTTGACAAGCTAGACCATGAATGTGCAAGAGGGGAGAAACCTCAGTGTGGGCGACG 4499
QY 4297 GCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4356
Db 4500 CCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4559
QY 4357 GGCCACAGTGCATCGACTGAGAGTGAACCTCATCCAGGCTACCATCCGACCCA 4416
Db 4560 GGCCACGCGAGCTGGACCTGGAAGAGGAGGAGCTCATCCAGTCCACCATCCGACACA 4619
QY 4417 GTTGTATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4476
Db 4620 GTTCGAGGACTGCACCGTCTCTACCATCGGCGGCTCAACCATCATCATGGACTACAC 4679

Db 1179 CTTCTTCTTAAGCCATCCAGCCAGCTGATGTTTTCGGGGCGCAGATCTTAAAGTT 1238
Qy 1006 CCGTATCAGGTTTATCTCCAAACCCATGAGCCCTCTCTGTTGGGGCTTCTGGTGGCTGG 1065
Db 1239 GCTCATCAAGTTCTGATGACAGGAAGGCCCACTGCGAGGGCTACTTCTACACCGT 1298
Qy 1066 GCTGATGTTCTGTGCTCCATGATGACGAGTCCGTGATCTTAAACACATATTACCACATAT 1125
Db 1299 GCTGCTGTTTCTACTGCTCCCTGCGAGACCCCTCGTGTGCACAGTACTTCCACATCTG 1358
Qy 1126 CTTTGTGACTGGGTGAAGTTTCTACTTGGGATCATGGGTGTCTATCAGAGAAAGGCTCT 1185
Db 1359 CTTGCTCAGTGGCATGAGGATCAGACCGGTGTCTATGGGGCTGTCTATCGGAAGGCCCT 1418
Qy 1186 GGTATCACCAACTCAGTCAAACTGGTCCACCTGTCACCTGAGGAAATTTCAACCTCATGTC 1245
Db 1419 GGTGATCACCAATTACGCCAGAAAACTCTCCACGGTGGGGGAGATTGTCAACCTCATGTC 1478
Qy 1246 AGTGGATGCCAGCGCTTCATGGACCTTGGCCCTTCTCTCAATCTGCTGTGGTGAGCAC 1305
Db 1479 TGTGGAGCGCTCAGAGGTTCTATGGTACTTGGCCACGCTACATTAACATGATCTGGTCAGCC 1538
Qy 1306 CCTGCAGATCATCTGCGGATCTACTTCTCTGCGCAGAACCTAGTCCCTCTGCTGGC 1365
Db 1539 CTTCAAGTCTATCTGCTCTCTACTCTCTGCTGGCTGAATCTGGGCCCTTCCGCTTGGC 1598
Qy 1366 TGGAGTCGCTTTCATGTTCTGCTGATTCCACTCAAGGGAGCTGTGGCCGTGAAGATGCG 1425
Db 1599 TGGAGTGGCGTGTGCTCTCATGTTGCGGCTCAATGCTGTGATGGGATGAAGACAA 1658
Qy 1426 GCGCTTCCAGTAAAGCAATGAATTTGAAGGACTCGGCATCAAGCTGATGAGTGAAT 1485
Db 1659 GACGTATCAGTGGTGGCCACATGATGAAGCAAGCAATCGGATCAAGTGAATGAAGCAAT 1718
Qy 1486 CCTGAAGCGGATCAAGTGTGTAAGTGTACGCTGGGAGCCAGCTTCTCTGAAGCAGGT 1545
Db 1719 TCTCAATGGGATCAAGTGTAAAGCTTATGCTTGGGAGCTGGCATTCAGGACAGGT 1778
Qy 1546 GAGGGGATCAGGAGGGTGAAGTCTCAGCTGCTCGCACGGCCCTTACCTCCACACAC 1605
Db 1779 GCTGGCCATCAGGAGGAGGCTGAAGTGTCTGAAGAGTCTGCCCTACCTGTACGCGT 1838
Qy 1606 AACCACTTACCTGGATGTGACGCCCTTCTCTGGTGAACCTGATACCCCTCTGGGTGA 1665
Db 1839 GGGACCTTACCTGGGTGTGACGCCCTTCTGGTGGCCCTTGTGTCATTTGCCGCTA 1898
Qy 1666 CGTGTAGTGGACCCAAACAAATGTGTGGAGCGCGAGAGGCCCTTGTGTGTGTCTT 1725
Db 1899 CGTGACCATTTGACGAGAACAACTCTGGATGCCACAGCCCTTCTGTCTTGGCCCT 1958
Qy 1726 GTTATPATCTTAAAGCTTCCCTCAACATGCTGCCCCAGTTAATCAGCAACCTGACTCA 1785
Db 1959 GTTCAACATCTCGGTTTCCCTTGAACATTTCTCCCATGCTATCAGCAGCATCGTGCA 2018
Qy 1786 GGCAGTGTCTGTAAAGCGATCCAGCAATTTCTGAGCCCAAGAGAACTTGACCCCA 1845
Db 2019 GGGAGGTCTCCCTCAAGCGCTGAGGATCTTCTCTCCCATGAGAGGTGGAACCTGA 2078
Qy 1846 GAGTGTGGAAGAAAGAACCATCTCTCCAGCG-----TATGCCATCACCATAFACAG 1896
Db 2079 CAGCATCGAGCGGCTGTCAAGACGGGGGGGACCAACAGCATACCGTGAGGAA 2138
Qy 1897 TGGACCTTCACTGGGCCAGGACCTTGGCCCACTCTGCACAGCCATAGACATCCAGGT 1956
Db 2139 TGGCACATTCACCTGGGCCAGGAGCGACCTCCACACATGAATGGCATCACCTTCTCCAT 2198
Qy 1957 CCGAAGGGGCACTGTTGGCCGTGTGGGGCTGTGGGTGTGGGAAGTCTCCCTGGT 2016
Db 2199 CCGGAAGGTGCTTGTGGCCGTGTGGGGAGGTGGGGTGGGGAGGTTGTCCTGCT 2258
Qy 2017 GTCTGCCCTCTGGGAGAGATGGAGAGCTAGAGGCAAGATGCACATGAAGGGCTCCGT 2076

Db 2259 CTCAGCCCTCTTTGGCTGAGATGCACAAAGTGGAGGGGCACTGGGCTATCAAGGGCTCCCT 2318
Qy 2077 GGCCTATGTGCCCCAGCAGGCAATGGATCCAGAACTGCACCTCTTTCAGGAAAAAGTGTCTTT 2136
Db 2319 GGCCTATGTGCCCCAGCAGGCGCTGGATTTCAGAAATGATTCTCTCCGAGAAAAATCCTTTT 2378
Qy 2137 CGGAAAGCCCTGAACCCCAAGCGCTACACAGAGACTCTGGAGGCGCTGTGCTTGTGTAGC 2196
Db 2379 TGGATGTGAGCTGGAGGAACCAATATTACAGTCCGTGATACAGGCTGTGCCCTCTCTCC 2438
Qy 2197 TCACCTGGAGATGCTGCTGTTGGGATCAGACAGAGATTGGAGAGAGGGCATTAACCT 2256
Db 2439 AGACCTGGAATCTCTGCCAGTGGGATCGGACAGAGATTGGCGAGAGGGCGTGAACCT 2498
Qy 2257 GTCTGGGGCCAGCGCGGCTCAGTCTGCTCGAGCTGTTTACAGTGATGCCGATAT 2316
Db 2499 GTCTGGGGACAGAGCAGCGCTGAGCCTGCCCGGCCGTGTACTCCAAGCTGACAT 2558
Qy 2317 TTTCTTGTGGATGACCACTGTCCGCGTGGACTCTCATGTGGCCAAAGACACATCTTTGA 2376
Db 2559 TTACCTCTTCGATGATCCCTCTCAGCAGTGTATGCCATGTGGGAAAAACACATCTTTGA 2618
Qy 2377 CCACGTATCGGGCCAGAAAGCGCTCTGGCAGGCAAGAGCGGAGTGGTGGTACGACGG 2436
Db 2619 AATGTGATGGCCCAAGGGGATGCTGAAGAAACAGACGCGGATCTTGGTCACGCACAG 2678
Qy 2437 CATGTAGCTTCTGCCCCAGACAGACTTCATCATTTGTGTAGCTGATGGACAGGCTGTCTGA 2496
Db 2679 CATGAGCTACTTGGCGAGGTGGAGCTCATCATCTCATGTAGTGGCGGCAAGATCTCTGA 2738
Qy 2497 GATGGGCCCTTACCAGCCCTGTCTCAGCGCAACGGCTCTTTTGCCAACTTTCTCTGCAA 2556
Db 2739 GATGGGCTCTTACCAGGAGCTGTGCTCGAGACGGCGCTTCGCTGAGTCTCTGCTGAC 2798
Qy 2557 CTATGCCCCGATGAGGACCAAGGCGCTGTGGAGCAGCTGCGACCGCTTGGAGGTGC 2616
Db 2799 CTATGCCAGCAGACAGGAGGAGGATGAGAGAGAACGGGTACGGGCGTCAGCGGCTCAGCGG 2858
Qy 2617 AGAGGATGAAGGAGGAGCTGCTGATTGAAGACACACTCAGCAACCAACAGCGATCTGCACGA 2676
Db 2859 TCCAGGGAAGGAAGCAAGCAATGAGAAATGGCAATGGCAAT----- 2894
Qy 2677 CAATGATCCAGTCACTACCTATGTGGTCCAGCAAGAGTATTTATGAGACAGCTGAGTGCCTGTC 2736
Db 2895 -----GCTGTGAGCGAGCTGAGTGGAGGAGCACTGAGGAGAGAGCTCAGCAGCTCCTC 2948
Qy 2737 CTCAGATGGGAGGAGCAGGCTGCGGCTGTACCCCGAGGAGCAGCTGGTCCATCAGAGAA 2796
Db 2949 CTCCTATAGTGGGACA-----TCAGCAGCAGCAACCAAGCAGCAGCCAGACTGCGAGAAA- 3003
Qy 2797 GGTGACAGTGAAGAGGCGAAGGAGATGGGCACTGACCCAGGAGAGAGAAAGCAGCCAT 2856
Db 3004 ----GCTGAGGCCAAGAGAGGAGAGACCTGGAAGCTGATGGAGGCTGACAGGCCAGAC 3059
Qy 2857 TGGCACTGTGGAGCTCAGTGTCTTGGGATTTATGCCAAGGCGGTGGGCTGTGTACAC 2916
Db 3060 AGGCAGGTCAAGCTTTTCCGCTGTACTGGGACTACATGAAGGCCATCGGACTCTTCATCTC 3119
Qy 2917 GCTGGCATCTGTCTCTGTATGTGGGTCAAAGTGGCGCTGCCATTTGGAGCCAAATGTGTG 2976
Db 3120 CTTCTCAGCATCTTCTTTTCATGTGTAACTGTGTCCGCGCTGGCTTCCAACTATGT 3179
Qy 2977 GCTCAGTGCCTGGCAATATGATGGCAGACAGTAGACAGAACAACTTCCCTGAG 3036
Db 3180 GCTCAGCCTCTGGACTGATGACCCCATCGTCAACGGGACTCAGGAGCAGACAGAAAGTCG 3239
Qy 3037 GCTGGGCGTCTATGCTGCTTTAGGAATTTCTCAAGGGTCTTGTGTGTGTGTGGCAGCCAT 3096
Db 3240 GCTGAGGCTCTATGAGCCCTTGGGCAATTTCAAGGGGATCGCGGTGTGTGGCTACTCTCAT 3299
Qy 3097 GGCATGCGACGGGTGGCATCCAGGCTGCCGCTGTGTGTCACAGGAGCTGCTGTCACAA 3156
Db 3300 GGCCTGTCCATCGGGGGGATCTTGGCTTCCGCTGTCTGCACGCTGGACCTGCTGCACAG 3359

QY 3157 CAAGATACGCTGCCACAGCTCTTCTTTTGACACACACACATCAGCGCGCATCTCTGAAGT 3216
DB CATCTCGCTGCTACCAAGCTATGCTTTTGGAGGACGCCAGTGGAAACCTGTGTGAACCG 3419
QY 3217 CTTCTCAAGGACATCTATGCTGTGATGAGGTCTTGCCCTCTCATCTCATCTCATGCTGCT 3276
DB CTTCTCAAGGAGCTGGACACAGTGGACTCCATGATCCCGGAGGTCAATGAATGTTTCAT 3479
QY 3277 CAATTCCTTCTTCAAGCCCATCTCCACTCTGTGGTTCATATGCGCCACAGCAGCGCTCTT 3336
DB GGGCTCCCTGTTCAACGCTCATTTGGTGCCTGATCGTTATCTCTGTCGCCAGCCCATCGC 3539
QY 3337 CACTGTGGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3396
DB CGCATCATCATCCCGCCCTTGGCCCTCATCTACTTCTTCTGTCGAGAGGTCTACGTGGC 3599
QY 3397 CACATCAGGCACTGAAGCGGCTGGAATCAGTCAGCGCTCAGCTACCTATCTACTTCCACTT 3456
DB TTCTCCCGGACGCTGAAGCGCTCGAGTCGGTCAGCGCTCCCGGCTCTATTCCCATTT 3659
QY 3457 TTCGAGACAGTACTGCTGCCAGTGTCTATCCGGGCTTACAACCGCAGCGGATTTTGA 3516
DB CAACGAGACCTTCTGGGGTCAAGCTATTCGAGCCTTCGAGGAGCAGGAGCGCTTCAT 3719
QY 3517 GATCATCAGTACTAAGTGTGATGCCAACACAGAGAGCTGTACCCCTACATATCTC 3576
DB CCACGAGAGTACTGAAGGTGGACGAGACACAGAGGCTATTACCCAGCATCTGTCG 3779
QY 3577 CAACCGTGGCTGAGCATCGGAGTGGAGTTCGTGGGGAAGTCTGCTGCTCTTTCTGTC 3636
DB CARACGTTGGTGGCGTGGCGCTGGAGTGTGGGCACTGCTGCTGCTGCTGCTGCTGCTGCTG 3839
QY 3637 ACTATTTCGCTATCCGAGGAGCAGCTGTAACCCCGGCTGGTGGGCTTCTGCTGCTGCTG 3696
DB CCTGTTTGGGTGATCTCCAGGACAGCTCAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 3899
QY 3697 CTACTCTTGCAGTACATTTCTCTGACTGATGATGATGATGATGATGATGATGATGATGAT 3756
DB TTACTCATTTGCAAGTCAACAGCTTACTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 3959
QY 3757 ATCTAATCATCTGGCTGTGGAGAGTCAAGGAGTACTCCAGACAGACAGAGAGCGCC 3816
DB AACCACATCTGGCTGTGGAGGCTCAAGGAGTATTCAGAGACTGAGAAGAGGCGCC 4019
QY 3817 CTGGGTGGTGAAGCAGCGCCCTCCGAAAGTGTGGCCCGCAGCTGGGAGGTGGAGTT 3876
DB CTGGCAATCCAGGAGACACGTCGCCCGCAGCAGCTGGCCCGCAGGTGGCGGAGTGAAT 4079
QY 3877 CCGGAATTATCTGCTGCTACCGCGCGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3936
DB CCGGAATCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4139
QY 3937 GCATGTGACGCTGGCGAAGTGGGATCTGGGCGCAGCTGGGCGTGGCAAGTCTTC 3996
DB CACGATCAATGGGGAGAAAGTGGCATCTGGGCGGAGCGGAGCTGGGAAGTCTGTC 4199
QY 3997 CATGACCTTTCCCTGTTCCGATCTTGGAGCGGCAAGGTTGAAATCCGCAATTGATGG 4056
DB CTTGACCTGGGCTTATTTCCGATCAACGAGTCTCCGAGGAGAGATCATCATGATGG 4259
QY 4057 CTTCAATGTGGAGACATCGGCTCATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4116
DB CATCAATCACTCAAGATCGGCTGACGAGACCTGCGCTTCAAGATCAATCATATCCCA 4319
QY 4117 GGACCCCATCTCTGCTGCGGACCTGGCATGACCTGGACCTTCGGCAGCTACTC 4176
DB GGACCTGTTTGTTCGGTTCCTCGAATGAACTGGACCTTACGACCTGCTGCTGCTGCTGCTGCT 4379
QY 4177 AGAGGAGACATTTGGTGGCTTTGGAGCTGTCCACCTGACAGCTTTGTGAGCTTCCA 4236
DB GGATGAGAGAGTCTGGACCTCCTGGAGCTGCGCCACCTGAGAGGACTCTGCTGCTGCTGCTGCT 4439

QY 4237 GCCGGAGCGCTGAGCTTCCAGTCTCAGAGGGGGGAGAAATCTCAGCTGGGCGCAGAG 4296
DB TCCTTGACAAGCTAGACCATGAATGTGCAAGAGCGGGGAGAACCTCAGTGTGGGCGCG 4499
QY 4297 GCAGCTCTGTGCTTGGCCCGAGCCCTGCTCCGCAAGAGCGCATCTCTGCTGCTTTAGACA 4356
DB CCAGCTTGTGTGCTTGGCTAGCCCGGCGCTGCTGAGGAAGACGAGATCTTGTGTTGATGA 4559
QY 4357 GGCCACAGCTGCCATCGACCTGGAGACTGACAACCTCATCCAGGCTACCATCCGACCCA 4416
DB GGCCACGGCAGCCGTGACCTTGGAAACGGAGACCTCATCCAGTCCACCATCCGACACA 4619
QY 4417 GTTGTATACCTGCACTCTCTGACCATCGCACACCGGCTTAACACTATCATGGACTACAC 4476
DB GTTCGAGGACTGCAACCGCTCTCACCATCGCCCGCTCAACCATCATCATGGACTACAC 4679
QY 4477 CAGGCTCTGCTGCTGCAACAGAGTAGTAGCTGAATTTGATTTCTCCAGCCACCTCAT 4536
DB AAGGCTGATCGTCTTGGACAAAGAGAAATCCAGAGTACGGCGCCCATCGGACCTCT 4739
QY 4537 TGCAGTAGAGGCTCTTCTACGGGATGGCCAGAGATGCTGAGCTTGCCTAAATATATT 4596
DB GCAGCAGAGAGGCTTCTTACAGCATGGCCAAAGACGCCGCTTGGTGTGAGCCCGAGA 4799
QY 4597 CCTGAGATTTC 4607
DB GCTGGCATATC 4810

RESULT 9
AAV31497
ID AAV31497 standard; cDNA; 5011 BP.
XX
AC AAV31497;
XX
DT 14-AUG-1998 (first entry)
DE
DE Human multidrug resistance-associated protein (MRP) encoding cDNA.
XX
KW Multidrug resistance-associated protein; MRP; tumour; human;
KW multidrug resistance; MDR; ds.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..195
FT CDS /*tag= a
196..4791
FT /*tag= b
/*product= *human multidrug resistance-associated protein*
FT 3'UTR 4792..5011
FT /*tag= c
XX
XX US5766880-A.
XX
XX
PD 16-JUN-1998.
XX
PF 05-JUN-1995; 95US-0463092.
XX
XX 05-JUN-1995; 95US-0463092.
PR 27-OCT-1992; 92US-0966923.
PR 08-MAR-1993; 93US-0029340.
PR 26-OCT-1993; 93US-0141893.
PR 20-MAR-1995; 95US-0407207.
XX
XX (TOOH) UNIV QUEENS KINGSTON.
XX
XX Cole SP, Deeley RG;
XX WPI: 1998-361687/31.
DR P-PSDB; AAW57485.
XX
PT DNA encoding protein associated with multi-drug resistance - useful

QY 685 CATCTATGGCTACCGCATCCCTCGAGAGAGAGGACCTCTGGTCCCTAAAGAGAGGA 744
DB 879 TGTCGGGGCTACCGCGAGCCCTCGAGGGCAGTAGACCTCTGGTCTTAAACAAAGAGGA 938
QY 745 CAGATCCAGATGTGGTGGCAGCAGCTGCTGGAGGCATGGAGGA-----788
DB 939 CACGTGCGAACAAGTCGTGCCTGTTTGGTAAGAACTGGAAGAAGGAATGCGCCCAAGAC 998
QY 789 -----AGCAGAAAGACAGACGGCAGACACAAGGCTTCAGCAGCACCTGGGAAAAA 840
DB 999 TAGGAAGCAGCGGTGAAGGTTGTACTCTCCCAAGGATCTGCCAGCCGCAAGAGAG 1058
QY 841 TGCTCCCGCAGAGCAGAGGTCTCTCTGGTG-----CCGCCCCAGGCC 885
DB 1059 TTCCAAGGTGATGCGAATGAGAGGTGGAGGCTTTGTATCGTCAAGTCCCCACAGAAGA 1118
QY 886 CCGAAGCCCTCTCTCTGAAGGCCCTGCTGGCCACCTTCGGCTCCAGCTTCCCTCATCAG 945
DB 1119 GTGGAACCCCTCTCTGTTAAGGTGTTATACAGACCTTTGGGCCCTACTTCCCTCATGAG 1178
QY 946 TGCTGCTTCAAGCTTATCCAGGACCTCTCTCTCTCATCAATCCACAGCTGCTCAGCAT 1005
DB 1179 CTCTCTTCAAGGCCATCCAGCAGCTGATGATGTTTCCGGGCCGAGATCTTAAAGTT 1238
QY 1006 CTTGATCAGGTTTATCTCCAACCCCATGGCCCCCTCTCTGGTGGGCTTCTCTGGTGG 1065
DB 1239 GCTCATCAAGTTCGTGAATGACAGCAAGGCCCCAGACTGGCAGGGCTACTTCTACACCGT 1298
QY 1066 GCTGATGTTCTGCTCCATGATGACGCTGCTGATCTTACAACACTATTACCAGTACAT 1125
DB 1299 CTGCTGTTTCTACTGCTGCTGACAGCCCTGCTGCTGACCAAGTACTTCCACATCTG 1358
QY 1126 TTTTGTGACTGGGGTGAAGTTTCGTACTGGGATCATGGGTGTCTATCAGGAAGGCTCT 1185
DB 1359 CTTGCTAGTGGCATGAGGATCAAGACCGCTGTCTATTTGGGCTGCTATCGGAAGGCCCT 1418
QY 1186 GGTATACCAAACTCAGTCAAACTGGCTGCACATGCTGGGGGAAATGTCAACCTCATGTC 1245
DB 1419 GGTATACCAAACTCAGCAGAAAATCCTCCAGGTCGGGGAGATTTCAACCTCATGTC 1478
QY 1246 AGTGGATGCCAGCGCTCATGGAACCTTGGCCCTCTCTCAATCTGCTGTGGTCAAGACC 1305
DB 1479 TGTGGAGCTCAGAGGTTCTAGGACTTGGCCACGTAACATTAACATGATCTGGTCAAGCCC 1538
QY 1306 CTTGAGATCATCTGGGATCTACTTCTCTGGCAGAACCTAGTCTCCTCTGCTGGC 1365
DB 1539 CTTGCAAGTCACTCTGCTCTACTCTCTGCTGCTGTAATCTGGGCCCTTCCGCTCTGGC 1598
QY 1366 TGGAGTCGCTTTCATGGTCTTCTGATTCCTCACTCAACGGAGCTGTGGCCGTGAAGATCG 1425
DB 1599 TGGAGTGGCGGTGATGGTCTCATGGTGGCCGCTCAATGCTGTGATGGCGATGNAAGCCAA 1658
QY 1426 CGCCTTCCAGGTAAGCAAAATGAAGACTCGCGCATCAAGCTGATGAGTGAGAT 1485
DB 1659 GACGTATCAGGTGCCACATGAGAGCAAGAAATCGGATCAAGCTGATGAAGAAAT 1718
QY 1486 CTTGAACGGCATCAAGGTGCTGAAGCTGTACGCTGGAGCCAGCTTCTCTGAAGCAGGT 1545
DB 1719 TCTCAATGGGATCAAGTGTCTAAAGCTTTATGCTGGGAGCTGCAATTCAGAGCAAGGT 1778
QY 1546 GGAGGGATCAGGAGGTGAGTCCAGCTGCTGCGCAGCGCGGCTTACCTTCCACACAC 1605
DB 1779 GCTGGCCATCAGGAGGAGGCTGAAGGTGCTGAAGAAGTCTGCCACTTGTCTCAGCGGT 1838
QY 1606 AACCACCTTACCTTGGATGTACGCCCTTCTCTGCTGACCTGATCACCTCTGGGTGA 1665
DB 1839 GGGACCTTACCTTGGGTCTGACGCCCTTCTGGTGGCTTGTGACATTTGGCGTCTA 1898
QY 1666 CGTGTAGTGACCCCAACAAATGTCTGGAGCGCGAGAAGGCCCTTGTGTCTGTCTCT 1725
DB 1899 CGTGACCATTGACAGAACACATCTCTGGATGCTGCCACACAGCCCTTCTGTCTTGGCCCT 1958
QY 1726 GTTTAATATCTTAAGACTTCCCTCTCAACATGCTGCCCCAGTTAATACAGCAACCTGACTCA 1785

DB 1959 GTTCAACATCTCCGGTTTCCCTGAACATTTCCCCATGTCATCAGCAGCATCGTGCA 2018
QY 1786 GGCAGGTGCTCTCTGAACGGATCCAGCAATTTCTTGGAGCAAGAGAACTTGACCCCCA 1845
DB 2019 GCGAGGTCTCTCCCTCAAGCGCTGAGGATCTTTCTCTCCCATGAGAGCTGGAACCTGA 2078
QY 1846 GAGTGTGGAAGAAAGAACCATCTCCCCAGGC-----TATGCCATCACCATAACAG 1896
DB 2079 CAGCATCGAGCAGCGCTCTCAAGACGCGGGGGCAACAGCATCACCCTGAGGAA 2138
QY 1897 TGGCATTCTACCTTGGGCCAGGACCTTGGCCCCACTTCTCACAGCCTAGACATCCAGT 1956
DB 2139 TGGCATTCTACCTTGGGCCAGGACCTTGGCCCCACTTCCACATGAATGGCATCCTTCTCAT 2198
QY 1957 CCGGAAGGGCAGCTGCTGGCCGTGGTGGGCCCTGTGGGCTGTGGGAAGTCTTCCCTGGT 2016
DB 2199 CCGGAAGGTGCTTGTGGCCGTGGTGGGCCAGGTGGGCTGCGGAAGTGTGCTCCCTGCT 2258
QY 2017 GTCTGCCCTGCTGGGAGAGATGGAAGAGCTFAGAAGCAAGTGCACATGAAGGCTCCGT 2076
DB 2259 CTCAGCCCTCTGGCTGAGATGGAACAAAGTGGAGGGGCGAGTGGCTATCAAGGGCTCCGT 2318
QY 2077 GGCCTATGTGCCCGCAGCAGGATGGATCCAGAACTGCACCTTCTCAGGAAAAACGTGCTTTT 2136
DB 2319 GGCCTATGTGCCACAGCAGGCTGGATTCAGATGATTCTCTCCGAGAAAAACATCTCTTTT 2378
QY 2137 CGGCAAGCCCTGAACCCCAAGGCTTACCAGCAGACTCTGGAGGCTGTGCTTGTCTGATG 2196
DB 2379 TGGATGTCAGCTGGAGGAACCATATTACAGGCTCCGTATACAGGCTGTGCCCTCTCCCTCC 2438
QY 2197 TGACCTTGGAGATGCTCCCTGGTGGGATCAGACAGAGATGGAGAGAGGCAATTAACCT 2456
DB 2439 AGACCTTGGAAATCTCTCCCGCAGTGGGATCGGACAGAGATTGGCGAAGGGCGTGAACCT 2498
QY 2257 GTCTGGGGCCAGCGCAGCGGCTCAGTCTGCTGAGCTGTTTACAGTGTATGCCGATAT 2316
DB 2499 GTCTGGGGCAGACAGCAGCGCTGAGCTTGGCCCGGCGTGTACTTCCAACCTGACAT 2558
QY 2317 TTTCTTGTGATGATCCCACTGCTCCCGGTGGACTCTCATGTGGCCCAAGCAGCATTTTGA 2376
DB 2559 TTACCTTCTGATGATCCCTCTCAGAGTGGATGCCATGTGGGAAAAACATCTTTGA 2618
QY 2377 CCAGCTCATCGGCCAAGAGGCTGCTGCGAGGCAAGACGCGAGTCTGTCAGCGCAGCG 2436
DB 2619 AAATGTGATTTGGCCCAAGGGATGCTGAAGACACAGACGCGATCTTGTTCAGCAGCAG 2678
QY 2437 CATTAGCTTCTGCCCCCAGACAGACTTATCATTTGTGTAGCTGTGAGAGAGTGTCTGA 2496
DB 2679 CATGAGTACTTTGCCGACAGTGGACGCTCATCTCATCTGATGAGTGGCGGAAGATCTCTGA 2738
QY 2497 GATGGCCGTACCCAGCCCTGCTGCGAGCGCAACGCTCTTTGCCAATTTCTCTGCAA 2556
DB 2739 GATGGCTCTTACCAGGAGCTGCTGGCTCAGACGCGGCTTTCGCTGAGTTCCTGGGTAC 2798
QY 2557 CTATCCCCCGATGAGGACCAAGGCACTTGGAGGACAGCTGGACCGCTTGGAAAGTGC 2616
DB 2799 CTATCCAGCAGACAGCAGGACGAGGATCCAGAGGAAGGGGTCCAGGGCGCTCAGCGG 2858
QY 2617 AGAGGATTAAGGAGCAGTCTGATTGAAGACACACTCAGCAACACACAGGATCTGACAGA 2676
DB 2859 TCCAGGGAAGGAAGCAAGCAAAATGGCAATGGCAT-----2894
QY 2677 CAATCATCCAGTCACTTGTGGTCCAGAGGAGTTTATGAGACAGCTGAGTGGCCCTGTC 2736
DB 2895 -----GCTGCTGAGCGAGTGCAGGGAAGCAACTGCAGAGACAGCTCAGCAGCTCTC 2948
QY 2737 CTCAGATGGGAGGACAGGCTCGCTCTACCCGGAGGACCTTGGGTCCATCAGAGAA 2796
DB 2949 CTCCTATAGTGGGACA-----TCAGAGGCAACCAACAGCAGCCGAGAACTGCAGAAA- 3003
QY 2797 GGTGCGAGGTGACAGAGGGGAGGCGCAGATGGGCGACTTGACCCAGGAGGAGAAAGCAGCAT 2856

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Db 3004 ----GCTGAGGCCAAGAAGGAGGAGACCTGGAAGCTGATGAGGCTGACAAGGGCGAGAC 3059
QY 2857 TGGCACTGTGGAGCTAGTGTGTTCTGGGATTAAGCAAGGCGTGGGGCTCTGTACCAAC 2916
Db 3060 AGGCGAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAGGCCATCGGACTCTTCATCTC 3119
QY 2917 GCTGGCCATCTGCTCTCTGTATCTGGGTCAAGCTGGGCTGCCATTGGAGCCCATGTGTG 2976
Db 3120 CTTCCTCAGCATCTTCTTTTCAATGTAACCAATGTGTCCCGCTGGCTTCCAACTATTG 3179
QY 2977 GCTCAGTGCTGGCAAAATGATCCCATGGCAGACAGTAGACAGAAACAACACTTCCCTCGAG 3036
Db 3180 GCTCAGCCTCTGGACTGATGACCCCATCGTCAACGGGACTCAGGAGCACAGAAAGTCCG 3239
QY 3037 GCTGGGGTCTAGTCTGCTTTAGGAATTCGAAGGGTCTTGGGTGATGCTGGCAGCCAT 3096
Db 3240 GCTGAGCGCTATGAGAGCCCTGGGCAATTCACAAGGATCGCGGTGTTTGGCTACTCCAT 3299
QY 3097 GGCATGGGACGGGTGGCATCCAGGCTGCCGTGTGTTGCACAGGCACTGCTGCACAA 3156
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QY 3157 CAAGATACGCTGCCACAGTCTCTTTTGACACACACCATCAGCGCGCATCCTGAACTG 3216
Db 3360 CATCTCGGCTACCCATGAGCTTCTTTGAGCGGACCCCGAGTGGAACTGCTGTAACCG 3419
QY 3217 CTTCCTCAAGGACATCTATGTCTGTATGAGGTTCGTGGCCCTGTCTATCTCATGTGCT 3276
Db 3420 CTTCCTCAAGGAGCTGGACAGTGGACTCCATGATCCCGGAGGTCTATCAAGATGTTTCA 3479
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Db 3480 GGCTCCCTGTTCAAGCTCATTTGGTGCCTGCATCGTATTCCTGCTGCCACGCCCAFCG 3539
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Db 3540 CGCCATCATCTCCCGCCCTTGGCCCTACTTACTTCTTCGTCCAGAGGTTCTACGTGG 3599
QY 3397 CACATCAGGCAACTAAGCGGTGGAATCAGTCAGCGGTCACTTATCTACTCCCACTT 3456
Db 3600 TTCTCTCCGGGAGCTGAAGCGCTCGAGTGGTCAAGCCGCTCCCGGTCTATTTCCTCAT 3659
QY 3457 TTCGGAGACAGTGTGCTGAGTGTCTATCGGGCTTACAACCGCAGCGGATTTGA 3516
Db 3660 CAACGAGACTTGTCTGGGGTCAAGCTCATTTGAGCTTCGAGGACAGAGGCGTTCAT 3719
QY 3517 GATCATCTAGTACTAAGTGGATGCCAACAGAGAAAGCTGTACCCCTACATCATCTC 3576
Db 3720 CCACAGAGTGACCTGAAGTGGACGAGAACAGAGGCTATTACCCAGCATCGTGC 3779
QY 3577 CAACCGGTGGCTGAGCATCGGAGTGGAGTTCTGTGGGAACCTGCGTGGTCTCTTTGCTGC 3636
Db 3780 CAACAGGTGGCTGGCGTGGCTGAGTGTGTGGCAACTGCATCGTCTGTCTGTCTGC 3839
QY 3637 ACTATTTCGCTCATCGGAGGAGCGCTGAACCGGGGCTGGTGGCTTCTCTGTCTGTC 3696
Db 3840 CTTGTTGGGTGATCTCCAGCACAGGCTCAGTGTGGTGGGCTCTCAAGTGTG 3899
QY 3697 CTACTCTTGCAGGTGACATTTGCTCTGAACCTGGATGATACGAATGATCTCAGATTGGA 3756
Db 3900 TTACTCATTTGAGGTCAACACCTACTTGAACCTGGCTGGTTCGATCTCATGAAATGGA 3959
QY 3757 ATCTACATCTGGTGTGGAGGCTGAAGGATCTCCAGACAGACAGACAGAGCGGC 3816
Db 3960 AACCAACATCTGGCGTGGAGGCTCAAGGAGTATTCAGAGACTGAGAAGGAGCGGC 4019
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Db 4080 CCGGAATCTACTGCTGCGCTACCGAGAGGACCTGGACTTCGTTCTCAGGCACATCATGT 4139
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QY 3937 GCATGTGCACCGTGGCGAGAAAGGTGGGATCGTGGGCGCACTGGGGTGGCAAGTCTTC 3996
Db 4140 CACGATCAATGGGGAGAAAAGTTCGGCATCGTGGGGCGGACGGGAGCTGGGAAGTCGTC 4199
QY 3997 CATCACCTTTTGGCTGTTCGCCATCTCGGAGCGGCAAGGTTGAAATCCGCATGTATGG 4056
Db 4200 CCTGACCTTGGCTTATTTCGGATCAACGAGTCTGCGGAAGAGAGATCATCATCGATGG 4259
QY 4057 CCTCAATGTGSCAGACATCGGCCCTCCATGACCTCGCTCTCAGCTGACCATCATCCCCA 4116
Db 4260 CATCAACATCGCAAGATCGGCCCTGCAGACTCCGCTTCAGATCACCATCATCCCCA 4319
QY 4117 GGACCCCATCTGTTCTCGGGGACCTGCGCATGAACCTGGACCCCTTCGGCAGCTACTC 4176
Db 4320 GGACCTGTTTGTTCGGGTTCCTCCGAATGAACCTGGACCCATTCAGCCAGTACTC 4379
QY 4177 AGAGGAGGACATTTGGTGGCTTTGGAGCTGCCACCTGCACAGCTTTGTGAGTCCCA 4236
Db 4380 GGATGAAGAAGTCTGGAGCTCCCTGGAGCTGGCCACCTGAAGGACTTCGTGTGAGCCCT 4439
QY 4237 GCGGCAAGGCTTGACTTCCAGTCTCAGAGGCGGGGAGAAATCTCAGCTGGGCGCAGAG 4296
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QY 4297 GCAGCTCGTGTGCTGCGCGAGCCCTGTCTCGCAAGAGCGCATCTCTGTTTGTAGACGA 4356
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QY 4357 GGCACAGCTGCCATCCAGCTGGAGACTGACAACCTCATCCAGGCTACCATCCGACCCA 4416
Db 4560 GGCACGCGAGCGTGGACCTGGAACGCGGACCTCATCCAGTCCACCATCCGACACA 4619
QY 4417 GTTGTATPACTGCACTGTCTCTGACCATCGCACCGGCTTAACACTATCATGGACTACAC 4476
Db 4620 GTTCGAGGACTGCACCTCTCTACCATCGCCACCGCTCAACACCATCATGGACTACAC 4679
QY 4477 CAGGTCCTCGTCTTGACAAAGAGTAGTAGTGAATTTGATTTCTCCAGCCAACTCAT 4536
Db 4680 AAGGTCGATCGTCTTGGACAAAGAGAAATCCAGGAGTACGCGGCCCATCGGACCTCT 4739
QY 4537 TGCAGCTAGAGGACATCTTCTACGGGTGGCAGAGATGCTGGACTTGCCTAAAATATTT 4596
Db 4740 GCAGCAGAGAGGTCTTTTCTACAGCTGGCCAAAGACGCGGCTTGGTGTGAGCCCCAGA 4799
QY 4597 CCTGAGATTTTC 4607
Db 4800 GCTGGCATATC 4810
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RESULT 11

AAx21976

ID AAx21976 standard; cDNA; 5011 BP.

XX AAX21976;

AC AAX21976;

XX DT 18-MAY-1999 (first entry)

XX Human multidrug resistance-associated protein coding sequence.

DE Multidrug resistance-associated protein; MDR; human; diagnosis;

XX MDR tumour cell identification; cancer therapy; ds.

OS Homo sapiens.

XX US5882875-A.

XX 16-MAR-1999.

XX 05-JUN-1995; 95US-0462109.

XX 05-JUN-1995; 95US-0462109.

XX 27-OCT-1992; 92US-0966923.

QY 2317 TTCTTGTGGATGACCACTGTCGGGTGGACTCTCATGTGCGCCAAAGACATCTTTGA 2376
DB 2559 TTACCTCTTGATGATCCCTCTCAGCAGTGGATGCCATGTGGGAAACACATCTTTGA 2618
QY 2377 CCACGTCATCGGSCCAAGAGCGGTGCGCAGCAAGACCGAGTGTGGTGACGACCGG 2436
DB 2619 AATGTGATTGGCCCAAGGGATGCTGAAGACACAGACGCGGATCTTGTGACGACAG 2678
QY 2437 CATTAGCTTCTGCGCCCAAGACAGACTTCATCATGTTGCTAGCTGATGGACAGGTGCTGA 2496
DB 2679 CATGAGCTACTTCCGACAGCTGAGCTCATCATGTCATGTCATGATGGCGGCAAGATCTCTGA 2738
QY 2497 GATGGCCGTCACCAAGCCCTGCTGACGACGACGCTCTTTGGCAACTTCTCTGCRA 2556
DB 2739 GATGGCTCTACCAAGAGCTGTGGCTCGAGACGGCGCTTCGCTGAGTTCCTGCTGATC 2798
QY 2557 CTATGCCCGGATGAGGACCAAGGCACTCTGGAGGACAGCTGGACCGCTTGGAAAGTGC 2616
DB 2799 CTATGCCACACAGCAGCAGCAGGATCGACAGGAGACGGGTACCGGGCTCAGCGG 2858
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DB 2859 TCCAGGAGGAGCAAGCAAAATGGAATGGCAT----- 2894
QY 2677 CAATGATCCAGTCACCTATGTGGTCCAGAGCAGTTTATGACAGCTGAGTCCCTGTC 2736
DB 2895 -----GCTGGTACGGGACAGTGCAGGGAAGCAACTGACAGACAGCTCAGCAGCTCCTC 2948
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DB 3004 -----GCTGAGGCCAAGAGGAGGACACCTGGAAGCTGATGAGGCTGACAAAGCGCAGAC 3059
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DB 3060 AGGGCAGGTCAAGCTTTCGGTACTGGGACTACATGAAGGCCATCGGACTCTTCATCTC 3119
QY 2917 GCTGCCCTCTCTCTGTATGTGGTCAAAAGTCGGCTGCCATTTGGAGCCAATGTGG 2976
DB 3120 CTTCCTCAGCATCTTCCTTTTCATGTATACCATGTGTCCGGCTGGCTTCCAACTATTG 3179
QY 2977 GCTCAGTGCCTGGCAAAATGATGCCATGGCAGACAGTAGACAGAAACAACTTCCCTGAG 3036
DB 3180 GCTCAGCCTCTGACTGATGACCCCATCTCAACGGGACTCAGGAGCAGCAACAAAGTCG 3239
QY 3037 GCTGGCGCTATGCTGCTTTAGGAATCTGCAAGGGTCTTGTGTGATGCTGGCAGCCAT 3096
DB 3240 GCTGAGCGCTATGAGAGCCCTGGGCATTTCAACAGGGATCGCCGTGTTGGCTACTCCAT 3299
QY 3097 GGCCATGGCAGCGGTGGCATCCAGGCTGCCGTGTGTACACAGGCACTGCTGCACAA 3156
DB 3300 GGCCGTGTCATCGGGGAACTTGGCTTCCGCTGTCTGACGTGGACCTGCTGCACAG 3359
QY 3157 CAAGATACGCTGGCACAGTCTCTTTGACACCACACCATCAGCCGCACTCCTGAATG 3216
DB 3360 CATCTGGGTCAACCATGAGCTCTTTGAGCGGACCCCACTGGGAACCTGGTGAACCG 3419
QY 3217 CTTCGCAAGGACATCTATGTGTTGATGAGGTCTTGGCCCTGTCATCTCTCATGCTGT 3276
DB 3420 CTTCGCAAGGAGCTGGACACAGTGGATCTCATGATCTCCGGAGTCAATCAAGATGTTAT 3479
QY 3277 CAATTCCTTCTCAACGCGCATCTCCACTCTTGTGTGTCATGTGGCCAGCAGCCGCTCT 3336
DB 3480 GGCTCCCTGTTCAAGCTCATTTGGTCCCTGTCATCTGCTTATCTGCTGGCCACGCCCATCC 3539
QY 3337 CACTGTGTCTATCTGCCCCCTGGCTGCTCTACACCTTAGTGACGCGCTCTCTATGACG 3396
DB 3540 GCGCATCATCATCGCGCCCTTGGCTCTACTTCTTCTGTCAGAGGTTCTACGTGCG 3599
QY 3397 CACATCGGCAATGAAGCGGCTGGAAATCAGTCAGCGCTCACCTATCTACTCCCATTT 3456

DB 3600 TTCTCCCGCAGCTGAAGCGCTCGAGTCGGTCAGCGCTCCCGGTCTATTCCCATTT 3659
QY 3457 TTCGAGACAGTGAAGTGGTCCAGTGTATCTCCGGCCCTACAAACCGCAGCCGGATTTGA 3516
DB 3560 CAACGAGACCTTGTGGGGTCAAGCTCATCTCGAGCCCTTCGAGGAGCAGGCGCTTCAT 3719
QY 3517 GATCATCAGTCATATAAGTGGATGCCAACACAGAGAAGCTGCTACCCCTCATCATCTC 3576
DB 3720 CCACGAGTGAACCTGAAGTGGAGAGACAGAACAGCCCTATTACCCACGATCGTGGC 3779
QY 3577 CAACCGTGGCTGAGCATCGAGTGGAGTGTGCTGGGAACCTGCTGCTTTTGTGTC 3636
DB 3780 CAACAGTGGCTGCGCTGCGCTGGAGTGTGCGCAACTGCTGCTTCTGTTTGTGTC 3839
QY 3637 ACTATTTCGCTCATCGGAGGACGCTGAACCCCGGGGTGTTGGCCCTTCTGTGTC 3696
DB 3840 CCTGTTTCCGCTGATCTCCAGGACAGCCCTCAGTCTGGCTTGGTGGCCCTCTCAGTGC 3899
QY 3697 CTACTCTTGCAGGTGACATTTGCTCTGAATGGATGATACGAATGATGTCAGATTTGA 3756
DB 3900 TTACTCATTCGAGTCAACAGTACTTGAATGCTGCTGCTGCGATGTCATCTGAATGGA 3959
QY 3757 ATCTAATCATGCTGCTGTGAGAGGTCAGAGGACTACTTCCAAAGACAGACAGAGCGCC 3816
DB 3960 AACCAACATCTGCGCTGAGAGGCTCAAGGACTATTACAGAGACTGAGAGGAGCGCC 4019
QY 3817 CTGGTGGTGGAGGACGCGCTCTCCGAAGGTTGGCCCCCAGCTGGGGAGTGGAGTT 3876
DB 4020 CTGGCAAAATCCAGGAGACAGCTCCGCCAGCAGCTGGCCCCAGGTGGGCCCTCAGTAAT 4079
QY 3877 CCGGAATATTCTGTGGCTACCGCGCGCTAGACTGCTGCTGAGAGACCTGACTCT 3936
DB 4080 CCGAATCTACTGCTGCGCTACCGAGAGGACTGGACTGCTGCTCAGGACATCAATGT 4139
QY 3937 GCATGTGACGCTGGGAGAAAGTGGGGTCTGTGGCGCGCACTGGGCTGGCAAGTCTTC 3996
DB 4140 CAGCATCAATGGGGAGAAAAGTTCGGCATCTGTGGGCGGACGGAGTGGGAAGTCGTC 4199
QY 3997 CATGACCTTTGCTGTTCCGATCTCTGGAGGGGCAAGGGTGAATTCGCAATGTATGG 4056
DB 4200 CCTGACCTTGGGCTTATTTCCGATCAACGAGTCTGCCAAGAGAGATCATCATCGATGG 4259
QY 4057 CTCAATGTGGCAGACATCGGCTTCCATGACTGCTGCTCAGCTGACCATCATCCCGCA 4116
DB 4260 CATCAACATCGCCAAAGTCCGCTGACGACTCCGCTTCAAGATCAACATCATCCCGCA 4319
QY 4117 GGACCCATCTCTTCTCGGGACCTTCCGATGAACCTGGACCCCTTCGGCAGCTACTC 4176
DB 4320 GGACCTGTTTGTGTTTCCGCTTCCCTCCGAATGAACCTGGACCATTCAGCCAGTACTC 4379
QY 4177 AGAGGAGGACATTTGTTGGCTTGGAGCTTCCACCTGCACACGTTTGTGAGCTCCCA 4236
DB 4380 GGATGAAGAGTCTGGACGCTTCCCTGGAGCTGGCCCTCAGGACTTCGTGTGACGCCCT 4439
QY 4237 GCGGAGGCTGGACTTCCAGTCTCAGAGGGCGGGGAGAACTCAGCTGGGCCAGAG 4296
DB 4440 TCCTGACAGCTAGACCATGAATGTGCAGAAAGGGGGAGAACCTCAGTGTGGGACAG 4499
QY 4297 GCAGCTGTGCTGCTGGCCGAGCCCTGCTTCCGCAAGAGCGCATCTGTTTGTAGACA 4356
DB 4500 CCAGCTTGTGCTGCTAGCCCGGCGCTGCTGAGAGAACGAAAGATCTTGTGTTGATGA 4559
QY 4357 GGCACAGCTGCCATCGACTGGAGACTGACAACTCATCCAGCTACCATTCGCGACCCA 4416
DB 4560 GGCACGCGCGCTGGACTTGGAAACGGAGCAGCTCATCCAGTCCACCATTCGCGACACA 4619
QY 4417 GTTTCATACCTGCACCTGCTGACCATCGCACACCGGCTTAAACACTATCATGACTACAC 4476
DB 4620 GTTCGAGGACTGCACCGCTCTCACCATCGCCGACCGGCTCAACACCATCATGAGCTACAC 4679
QY 4477 CAGGCTCTGCTGCTGGACAAAGGAGTAGTGTGAATTTGATTTCTCCAGCCCACTCAT 4536

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Db 4680 AAGGTGATGCTCTTGGNCAAGAGAGAAATCCAGAGTACGGCGCCCATCGGACCTCT 4739
Qy 4537 TGCAGCTAGAGCATCTTCTACGGGATGGCCAGAGATGCTGGACTTGCTTAAATATATT 4596
Db 4740 GCAGCAGAGAGGTCTTTTCTACAGCATGGCCAAAGACGCCGCTTGGTGTGAGCCCCAGA 4799
Qy 4597 CCTGAGATTTC 4607
Db 4800 GCTGGCATATC 4810

RESULT 13
ID AA294741 standard; cDNA; 5011 BP.
XX AC AA294741;
XX DT 01-AUG-2000 (first entry)
XX DE Human ATP binding cassette ABC1 (MRP1) cDNA.
XX KW ABC1; ATP binding cassette; human; cholesterol; lipid disorder;
XX KW atherosclerosis; lipid disorder; dyslipidemia; psoriasis;
XX KW lupus erythematosus; diagnosis; gene therapy; MRP1;
XX KW multidrug resistance associated protein; chromosome 16q13.12; ss.
XX OS Homo sapiens.
XX PN W0200018912-A2.
XX PD 06-APR-2000.
XX PF 21-SEP-1999; 99WO-EP06991.
XX PR 25-SEP-1998; 98US-0101706.
XX PA (FARB ) BAYER AG.
XX PI Schmitz G, Klucken J;
XX PS WPI; 2000-293151/25.
XX PT Adenosine triphosphate binding proteins useful for identifying agents
XX PT for treating atherosclerosis and other inflammatory disorders -
XX PS Claim 9; Page 115-117; 154pp; English.
XX CC The present sequence is that of human ATP binding cassette
XX CC subfamily C protein ABC1 cDNA. The cDNA was identified using a
XX CC differential display method in which monocytes from peripheral
XX CC blood were subjected to macrophage differentiation and cholesterol
XX CC loading with acetylated low density lipoproteins and subsequent
XX CC deloading with high density lipoprotein (HDL3) to identify
XX CC cholesterol sensitive genes. The gene maps to chromosome 16q13.12
XX CC and is also termed MRP1 (multidrug resistance associated protein).
XX CC The invention provides cholesterol-sensitive ABC genes (see
XX CC AA294734-63). These genes, and polypeptides encoded by them,
XX CC can be used for diagnostic and therapeutic applications, and for
XX CC biochemical or cell-based assays to screen for pharmacologically
XX CC active modulator compounds useful for the treatment of lipid
XX CC disorders, atherosclerosis or other inflammatory diseases such as
XX CC psoriasis and lupus erythematosus.
XX SQ Sequence 5011 BP; 1063 A; 1499 C; 1394 G; 1055 T; 0 other;

Query Match 34.2%; Score 1737.8; DB 21; Length 5011;
Best Local Similarity 62.2%; Pred. No. 0;
Matches 2882; Conservative 0; Mismatches 1662; Indels 87; Gaps 6;

Qy 25 CGGGAGCTCGGCTCCAGTCTTGGGACTCCAACTGCTGTGCACACAGAAACCCGGA 84
Db 220 CGCGATGGCTCCGACCCGCTCTGGGACTGGAATGTCACGTGGAATACCAACACCCGGA 279
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Qy 85 CTTCACTCCCTGCTTCCAGAACTCCCTGCTGGGCTTGGGCTTACCTATCTACCTGTGGGT 144
Db 280 CTTTCAACCAAGTCTTTCAGAACACAGCTCCTCGTGGTGGGTCCTTTTACCTCTGGGC 339
Qy 145 CGCCCTGCCCTGCTACTTCTTACCTCGGCACCACTTGTCTGGGTACATCATCTCTC 204
Db 340 CTGTTTCCCTTCTACTCTCTATCTCCCGACATGACCCGAGGCTACATTCAGATGAC 399
Qy 205 CCACCTGTCCAAAGCTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 264
Db 400 ACCTCTCAACAACCAAACTGCTTGGGATTTTGTCTGGATGCTGCTGCTGCTGCTGCTGCTG 459
Qy 265 CTTTCTTACTCTTCCATGGCTTGTCTTCCATGGCCGGGCCCCCTGCCCTCTGTTTCTTTGT 324
Db 460 CCTCTTCTACTCTTCTTGGGAAAGTCTGGGCATATTCTTGGCCCCAGTGTCTTCTGCT 519
Qy 325 CACCCCCCTGGTGGTGGGCTCACCATGCTGCTGGCCACCTGCTGCTGCTGCTGCTGCTGCTG 384
Db 520 CAGCCCAACTCTCTTGGGCATCACCACGCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 579
Qy 385 GCTGACGGCGTACAGTCTTGGGGGTCTCATATTCTTCTGCTTCTGCTGCTGCTGCTGCTGCTG 444
Db 580 GAGGAGGGAGTTCAGTCTTCAAGGATCATGCTCACTTCTTGGCTGTAGCCCTAGTGTG 639
Qy 445 CGCCATGCTCCATTCGCTCCCAAGATCCTTTTAGCCAAAGGAGAGGCTGAGATCTCAGA 504
Db 640 TGCCCTAGCCATCTCTGAGATCCAAATTTATGACAGCTTTAAAAGAGGATGCCCCAGTGA 699
Qy 505 CCCCTTCCGCTTCAACCACTTCTACATCCACTTGTGCCCTGGTACTCTCTGCTGCTGCTGCT 564
Db 700 CTTGTTTCTGCTGACATCACTTCTAGCTTACTTTTCCCTCTTACTCAATTCAGCTGCTGCT 759
Qy 565 GGCCTGCTTCAGGAGAAACCTCCATTTTCTCCGAAAAGATGTGACCCCTAACCCCTA 624
Db 760 GTCTGTTTCTCAGATCGCTCACCCCTGTCTCGGAACCATCCAGACCTTAATCCCTG 819
Qy 625 CCCTGAGACCAAGCGCTTCTTCTCCGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 684
Db 820 CCCAGAGTCCAGCGCTTCTTCTGCTGAGGATCACCTTCTGCTGCTGCTGCTGCTGCTGCTG 879
Qy 685 CATCTATGCTTACCGCATCCCTCGAGGAGAAAGGACCTCTGCTCCCTAAAGGAGAGGA 744
Db 880 TGTCCGGGCTACCCGCCAGCCCTGGAGGCGAGTACCTCTGCTGCTTAAACAAGGAGA 939
Qy 745 CAGATCCAGATGCTGCTGACGAGCTGCTGGAGGATGGAGGA----- 788
Db 940 CACGTCGGAACAGTCTGCTGCTGTTTGTAAAGAACTGGAAGAGGATGCCCAAGAC 999
Qy 789 -----AGCAGGAAAGCAGACGCGCAGCACACAGGCTTCAGCAGCACCTGGGAAAAA 840
Db 1000 TAGGAAGCAGCGGTGAAGTGTGTACTCTCCAAGGATCTGCTCCAGCGCGCAAGAGAG 1059
Qy 841 TGCCTCCGCGGAGGAGGCTGCTGCTGCTG-----CCCGGCCAGGCC 885
Db 1060 TTCCAAGTGGATGGAATGAGGAGTGGAGGCTTTGATCGTCAAGTCCCCACAGAGA 1119
Qy 886 CCGGAAGCCCTCTCTTCCCTGAAGCCCTGCTGCCACCTTCTGGCTCCAGCTTCTCTATCAG 945
Db 1120 GTGGAACCCCTCTCTGTTAAGTGTATACAGACCTTTGGGCCCTACTTCTCTATGAG 1179
Qy 946 TGCCTGCTTCAAGCTTATCCAGGACCTGCTCTCTTCAATCCACAGCTGCTCAGCAT 1005
Db 1180 CTTCTTCTTCAAGGCCATCCACGACCTGATGATGTTTCCGGGCCCGCAGATCTTAAAGTT 1239
Qy 1006 CTTGATCAGGTTTATCTCAACCCCATGGCCCCCTGCTGGTGGGGCTTCTGCTGGCTGG 1065
Db 1240 GCTCATCAAGTTCGTGGAATGACACGAAGGCCCCAGAGCTGCTTACACCTACAT 1299
Qy 1066 GCTGATGTTCTGCTCCATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1125
Db 1300 GCTGCTGTTTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1359
Qy 1126 CTTTGTGACTGGGTGAAGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1185
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Db	1360	CTTCGTCACTGGCATGAGATCAAGACCGCTGTCAATGGGGCTGTCTATCGGAAGGCCCT	1419
Qy	1186	GGTTATCACCAACTCAGTCAAACGTCGCTCCACTCTGGGGGAAATTTGTCAACCTCATGTC	1245
Db	1420	GGTGATCACCAATTCAGCCAGAAAACTCTCCACGCTGGGGAGATTTGTCAACCTCATGTC	1479
Qy	1246	AGTGGATGCCACGCTTCATGGACCTTGCCCCCTTCTCAATCTGCTGTGGTCAGCAC	1305
Db	1480	TGTGGAGCTCAGAGTTTTCATGGACTTGGCCACGTACAAATTAAACATGATCTGGTCAGCCCC	1539
Qy	1306	CCTGCAGATCATCTCGCGCATCTACTTCTCTGGCAGAACCTAGTCCCCTCTGTCCTGGC	1365
Db	1540	CCTGCAAGTATCCTTGTCTCTACTCTGTGGCTGAATCTGGGCCCTTCGGTCTGGC	1599
Qy	1366	TGGAGTCGCTTTCATGGTCTTGTGATTCCAATCAACGGAGCTCTGGCCGTGAAGATGCG	1425
Db	1600	TGGAGTGGCGGTGATGGTCTCTCATGGTCCCGTCAATGCTGTGATGGGATGAAGACAA	1659
Qy	1426	CGCTTCCAGGTAAAGCAAAATGAATTTGAAGACTTCGGGCATCAAGCTGATGATGAGAT	1485
Db	1660	GAGGTATCAGCTGGCCACATGAAGAGCAAAAGACAATCGGATCAAGCTGATGAACGAAAT	1719
Qy	1486	CTTGAAGGCATCAGGTGCTTGAAGCTGTAGCCCTGGGAGCCACGTTCTGAAGCAGGT	1545
Db	1720	TCTCAATGGGATCAAGTCTTAAGCTTTATGSCCTGGGAGCTTGCATCTCAAGGACAAGGT	1779
Qy	1546	GGAGGGCATCAGCAGGGTGAAGCTCCAGCTGTGGCAGCGCGCTTACCTCCACACCAC	1605
Db	1780	GCTGGCCATCAGCAGGAGGAGCTGAAGTGCTGANAAGTCTGCCCTTACCTGTACGCCGT	1839
Qy	1606	AACCACTTCACTGGATGTGCAGCCCTTCTCTGGTGACCTGTATCACCTCTGGGTGTA	1665
Db	1840	GGGACCTTTCACCTGGGTGTGCACGCCCTTTCTGTGGCCCTTGTGTCACATTTGCCGCTA	1899
Qy	1666	CGTGTACGTGGACCAACAATGTCTGAGCGCGAGAGGCCCTTTGTGTCCTGTGTCCTT	1725
Db	1900	CGTGACCATTGAGGAGAACACATCCTGGATGCCACAGACGCTTCTGTCTTTGGCCCTT	1959
Qy	1726	GTTTAATATCTTAAAGACTTCCCTCAACATGCTGCCACAGTTAATCAGCAACCTGACTCA	1785
Db	1960	GTTCAACATCTCCGGTTTCCCTCGAACATTTCCCATGGTATCAGAGCATCGTGCA	2019
Qy	1786	GGCCAGTGTCTCTGAACGGATCCACAAATCTCTGAGCCAGAGAGAACTTGACCCCCA	1845
Db	2020	GGCGATGTCTCCCTCAACGCTGAGATCTTTCTCTCCCATGAGGAGCTGGAACCTGA	2079
Qy	1846	GAGTGTGGAAGAAAGACCATCTCCCAAGGC-----TATGCCATCACCATACACAG	1896
Db	2080	CAGCATCGAGCAGCGGCTGTCAAAGCGCGGGGGACGAACAGCATCACCCTGAGGAA	2139
Qy	1897	TGSCACCTTCACTTGGGCCCAGGACCTGCCCCCACTCTGCACAGCCTAGACATCCAGGT	1956
Db	2140	TGSCACATTTCACTTGGCCAGGAGCGACCTCCACACTGAATGGCATCACTTCTCCAT	2199
Qy	1957	CCGGAAGGGGCATCTGTGGCGCTGTGGGCGCTGTGGGCTGTGGGAAGTCTCCTCGT	2016
Db	2200	CCCCAAGTGTCTTGTGTGGCGCTGTGGGCGAGTGGGCTGGGGAAGTCTGCTCTGCT	2259
Qy	2017	GTCTGCCCTGTGGGAGAGATGGAGAGCTAGAGGCAAGAGTGCATGAAGGGCTCCGT	2076
Db	2260	CTCAGGCCCTTTTGGCTGAGATGGACAAGTGGAGGGCAGCTGGCTATCAAGGGCTCCGT	2319
Qy	2077	GGCCTATGTGCCCCAGCAGGAGTGGATCCAGAAGCTGCACCTTTCAGGAACCTGCTTTT	2136
Db	2320	GGCCTATGTGCCACAGAGCGCTGGATTCAGATGATTTCTCTCCGAGAAACATCCTTTT	2379
Qy	2137	CGGCAAGCCCTTGAACCCCAAGCGCTACACAGACTCTTGGAGCGCTGTGCCCTGTAGC	2196
Db	2380	TGGATCTCAGCTGGAGGAACCATATATACAGTCCGTGATACAGGCTGTGCCCTCTCCC	2439
Qy	2197	TGACCTTGGAGATGCTTCCTTGGTGGGATCAGACAGATTTGGAGAGAGGGCATTAACCT	2256

Db	2440	AGACCTTGGAAATCCTTGCCCACTGGGGATCGGACAGAGATTGGCGAGAAGGGCGTGAACCT	2449
QY	2257	GTCTGGGGGCCAGCGCAGCGGGTCACTCTGGCTCGAGCTGTTTACAGTGATGCCGATAT	2316
Db	2500	GTCTGGGGCCAGAGCAGCGGTGAGCCTTGCCCGGGCGGTGTACTCCACGCTGACAT	2559
QY	2317	TTTCTTGCTGGATGACCCACTGTCCGCGGTGGACTCTCATGTGGCCCAAGCACATCTTTTGA	2376
Db	2560	TTACCTCTTCGATGATCCCTCTCAGCAGTGGATGCCCATGTGGGAAAAACACATCTTTGA	2619
QY	2377	CCAGCTCATCGGGCCAGAAGCGGTGTGGCAGGACGAGACGCGAGTGTGTGGAGCACAGG	2436
Db	2620	AAATGTGATTGGCCCCCAAGGGATGTGAAGAACAAGACGGCATCTTGGTCAACGCACAG	2679
QY	2437	CATTAGCTTCTGCCCCACAGACAGACTTCATCTATTGTCTAGCTGATGGACAGGTGCTGA	2496
Db	2680	CATGAGCTACTTCCCGCAGGTGAGCTCATCTGTCATGAGTGGCGGCAAGATCTCTGA	2739
QY	2497	GATGGGCCCGTACCAGCCCTGTGTCAGCGCAACGGCTCCTTTTGCCAACCTTTCTCTGCAA	2556
Db	2740	GATGGGCTCTACCAGGAGCTGTGCTCGAGACGGCGCTTCGCTCAGTTCCTGCGTAC	2799
QY	2557	CTATGCCCGGATGAGGACCAAGGCACTTGGAGGACAGCTGGACCGCGTTGGAAGTGC	2616
Db	2800	CTATGCCACACAGACAGGAGCAGGATGTCAGAGAGAACGGGTCAACGGCGGTCAACGG	2859
QY	2617	AGAGGATAGGAGGCACTGCTGATTGAAGACACACTCAGCAACCAACGATCTGACAGA	2676
Db	2860	TCAGGGAAGGAAGCAAGCAATGGAGATGCGAT-----	2895
QY	2677	CAATGATCCAGTCAACCTATGTGTGTCGAAGCAGTATTATGACAGAGCTGAGTGCCCTGTC	2736
Db	2896	-----GCTGGTGACGCAGATGTCAGGAGCAACTCGAGAGACAGCTCAGAGCTCCTC	2949
QY	2737	CTCAGATGGGGAGGACAGGTCGGCTGTACCCCGGAGGCACCTGGGTCCATCAGAGAA	2796
Db	2950	CTCCTATAGTGGGGACA---TCAGAGGCACCAACAACAGCAGCGGAGAACTGCAGAAA	3004
QY	2797	GGTGCAGGTGACAGAGCGGAAGCAGATGGGCACTGACCCAGAGGAGAAACGACCAT	2856
Db	3005	----GCTGAGGCCAAGAAGGAGAGACCTTGAAGCTGATGGAGGCTGCAAGGCGCAGAC	3060
QY	2857	TGGCACTTGGAGCTCAGTGTGTTTGGGATTATGCCAAGCGCGTGGGCTGTGTACCAC	2916
Db	3061	AGGGCAGGTCAAGCTTTCGCTGTACTGGGACTACATGAAGGCCATCGGACTCTTCATCTC	3120
QY	2917	GCTGGCCATCTGTCCTGTATGTGGGTCAAGTGGCGTGCATTTGGAGCCAAATGTGTG	2976
Db	3121	CTTCTCTCAGCATCTTCCCTTTTCATGTGTAAACCATGTGTCCGCGCTGGCTTCCAACATTTG	3180
QY	2977	GCTCAGTGCCTGCACAAATGATGCCATGTCAGACAGTATGACAGAAACAACACTTCCCTGAG	3036
Db	3181	GCTCAGCTCTGGACTGATGACCCCAATGTCACAGGGACTCAGGACACACGAAAGTCCG	3240
QY	3037	GCTGGCGCTTATGCTGCTTTTAGGAATTTGCAAGGGTTCTTGGTGATGTGTCGACGCCAT	3096
Db	3241	GCTGAGCGTCTATGGAGCCTTGGGCATTTCAAGGGAATTCACAAAGGATCGCGCTTTGGCTACTCCAT	3300
QY	3097	GGCCATGGCAGGGTGGCATCCAGGCTCCCGTGTGTTGACACAGGCACTGCTGCACAA	3156
Db	3301	GGCCGTGTCCATCGGGGGGATCTTGGCTTTCGCGTCTCTGCACGTGGACTGCTGCACAG	3360
QY	3157	CAAGATACGCTCGCCACAGCTCTCTTTCACACCACACCATCAGGCCGATCCTGAACCTG	3216
Db	3361	CATCTTCGCGTCACCCATGAGCTTCTTGAAGGACCCCAAGTGGGAACCTGGTGAACCG	3420
QY	3217	CTTCTCCAAGGACATCTATGTGTTGATGAGTTCTTGGGCCCTCTGTCATCTCATGCTGCT	3276
Db	3421	CTTCTCCAAGGAGCTGGACACAGTGGACTCCATGATCCCGGAGGTCACTCAAGATGTTCA	3480
QY	3277	CAATTCTCTTCAAGCCCATCTCCACTCTGTGGTTCATATGGCACAGCCGCTCTT	3336
Db	3481	GGGCTCCCTGTTCAAGTCTATTGGTGGCTTCGATCGTTATCTTCTTCTGGCCACCCCATCG	3540

QY 3337 CACTGTGGTCACTCCTGCCCTGGCTGTGCTCTACACCTTAGTGTAGAGGCTTCTATGACG 3396
D 3541 CGCCATCATCATCCGCCCTTGGCTCTACTTCTTCTCGTCCAGAGGTTCTACGTGGC 3600
QY 3397 CACATCACGGCACTCAAGCGCTGAAGTCAAGTCAAGCGCTCACCCTATCTACTCCCACTT 3456
D 3601 TTCTCCCGGAGCTGAAGCGCTCGAGTGGTCAAGCGCTCACCCTATCTACTCCCACTT 3660
QY 3457 TTCCGAGACAGTCACTGGTCCAGTGTCTATCCGGGCTTACAACCGGAGCGGATTTGA 3516
D 3661 CACAGAGACTTCTGGGGTCAAGTGTCTATCCAGGCTTCGAGGAGCAGAGCGCTTCAT 3720
QY 3517 GATCATCATGATCACTGAAGTGTGATGCCAACCAGAGAAAGTGTACCCCTACATCATCTC 3576
D 3721 CCACACAGAGTCACTGAAGTGTGATGCCAACCAGAGAAAGTGTATACCCAGCAGTGGC 3780
QY 3577 CAACCGTGGCTGAGCATCGAGTGGAGTGTGTTGGGAACTCGTGTCTCTTTGCTGC 3636
D 3781 CAACAGTGGCTGGCGTGGCTGGAGTGTGTTGGGAACTCGATCGTGTCTTTGCTGC 3840
QY 3637 ACTATTTCGGCTCATCGGAGGAGCAGCCTGAACCCGGGCTGGTGGGCTTCTGTGTGC 3696
D 3841 CCTGTTGGGCTGATCTCCAGGACAGCCTCAGTGTGGTGGGCTCTCACTGTGC 3900
QY 3697 CTACTCTTGCAGGTGACATTTGCTGTGAAGTGTGATGATGATGATGATGATGATGATGATG 3756
D 3901 TTACTACTTGCAGGTGACATTTGCTGTGAAGTGTGATGATGATGATGATGATGATGATGATG 3960
QY 3757 ATCTAACATCTGGCTGTGAGAGGTGAGAGTGTGATGATGATGATGATGATGATGATGATG 3816
D 3961 AACCAACATCTGGCTGTGAGAGGTGAGAGTGTGATGATGATGATGATGATGATGATGATGATG 4020
QY 3817 CTGGTGTGGAAGGAGCGGCTTCCGAAAGTGTGGGCTTGGGCTTGGGAGTGTGAGT 3876
D 4021 CTGGCAATCCAGGACAGCTCCGCCAGCAGCTGGCCCGGAGTGGGCTGGAAT 4080
QY 3877 CGGGAATTTCTGTGGCTACCGGCGGCTGTAGACTGTGGTGTGAGAGACCTGAGTCT 3936
D 4081 CGGGAATTTCTGTGGCTACCGGCGGCTGTAGACTGTGGTGTGAGAGACCTGAGTCT 4140
QY 3937 GCATGTGACAGTGGGAGAGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCT 3996
D 4141 CAGATCAATGGGGAGAGAGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGGCT 4200
QY 3997 CATGACCTTTCTGCTTCCGATCCTGGAGGCGGCAAGGCTGAATCCGATTCGATG 4056
D 4201 CCGTACCTTGGCTTATTTCCGATCAACAGTCTGCCGAGGAGATCATCATCATG 4260
QY 4057 CCTCAATGTGGAGACATCGGCTCCATGACCTGGCTCTCAGTCACTGACCATCATCCGCA 4116
D 4261 CATCAACATCGCAAGTGGCTTGCAGACCTGACCTGGACCTTCAAGATCACCATCATCCCCA 4320
QY 4117 GGACCCCATCTGTTCTGGGACCTTGGCATGACCTGGACCTTGGGCTTGGGCTTGGGCT 4176
D 4321 GGACCTTGTGTTCTGGTCCCTCGAATGACCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT 4380
QY 4177 AGAGGAGACATTTGGTGGCTTTGGAGTGTGCCACCTGTCACACGCTTGTGAGTCCCA 4236
D 4381 GGATGAAGAAGTCTGGAGCTTCCGAGTGTGCCACCTGAGGAGTCTGTGTGAGCTCC 4440
QY 4237 GCGGCGGCTTGGACTTCCATGCTCAGAGGCGGGGAGATCTCAGGTGGGCGGAGAG 4296
D 4441 TCCTGACAAGCTTAGACATGAATGTGCAAGCGGGGAGAACCTCAGTGTGGGCGAGC 4500
QY 4297 CGAGTGTGCTGCTGGCGGAGCTTGTCTCGCAAGAGCCGCTGCTGTTTGAACCA 4356
D 4501 CCAGCTTGTGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 4560
QY 4357 GCGCACAGTGCATCGCTGGAGCTGACAACTCTATCCAGGCTACCATCCGACCCA 4416
D 4561 GCGCACAGCTGGAGCTGGAACGAGCAGCCTATCCAGTCCACCATCCGACCCA 4620

QY 4417 GTTGTATACCTGCCTCTCTGACCATCGACACCGGCTTAACACTATCATGACTACAC 4476
D 4621 GTTCGAGGACTGCACCTCTCTGACCATCGACACCGGCTTAACACTATCATGACTACAC 4680
QY 4477 CAGGCTCTGCTCTGACAAAGAGTAGTAGTGAATTTGATTTCTCCAGCCCACTCAT 4536
D 4681 AAGGCTGATCTCTTGGACAAAGAGAAATCCAGAGTACGCGCCCATCGGACCTCT 4740
QY 4537 TGCAGCTAGAGGATCTTCTACGGGATGGCCAGAGATGCTGCTAAATATATATT 4596
D 4741 GCAGCAGAGAGTCTTTCTACAGCATGGCCAAAGACCGGCTTGGTGTGAGCCCCAGA 4800
QY 4597 CCTGAGATTTT 4607
D 4801 GCTGGCATATC 4811

RESULT 14
AAZ90192
ID AAZ90192 standard; cDNA; 5011 BP.
XX
AC AAZ90192;
XX
DT 19-MAY-2000 (first entry)
XX
DE Human multidrug resistance protein (MRP) nucleotide sequence.
XX
KW Multidrug resistance protein; MRP; human; anthracycline; Vinca alkaloid;
KW epipodophyllotoxin; cancer; leukaemia; ss.
XX Homo sapiens.
XX US6025473-A.
XX 15-FEB-2000.
XX
XX 05-JUN-1995; 95US-0461384.
XX 27-OCT-1992; 92US-0966923.
PR 08-MAR-1993; 93US-0029340.
PR 26-OCT-1993; 93US-0141893.
PR 20-MAR-1995; 95US-0407207.
XX
PA (TOOH) UNIV QUEENS KINGSTON.
XX
PI Cole SPC, Deeley RG;
XX
XX WPI; 2000-181838/16.
DR P-PSDB; AAY78872.
XX
PT Isolated protein conferring multidrug resistance, to at least two drugs
PT selected from anthracyclines, epipodophyllotoxins and Vinca alkaloids,
PT on a drug sensitive mammalian cell -
XX
PS Claim 1; Column 51-62; 78pp; English.
XX
CC This sequence represents a human multidrug resistance protein (MRP)
CC nucleotide sequence. The human MRP encoded by this sequence confers
CC multidrug resistance, including resistance to at least two drugs selected
CC from anthracyclines, epipodophyllotoxins and Vinca alkaloids, on a drug
CC sensitive mammalian cell, when the protein is expressed in the cell. The
CC multidrug resistance is not substantially reversed by chemosensitizers
CC which reverse P-glycoprotein-mediated multidrug resistance. The MRP
CC protein sequence can be used to generate antibodies against MRP. The MRP
CC protein and nucleotide sequences can be used in compositions which are
CC used to treat patients with tumours displaying multidrug resistance. The
CC compositions and methods of the invention can be used particularly to
CC treat breast cancer, leukaemias, fibrosarcomas, cervical cancer, gliomas,
CC thymomas, neuroblastomas, and lung cancer. Antibodies directed against
CC MRP can be used to inhibit the multidrug resistance of a multidrug
CC resistant cell.
XX
SQ Sequence 5011 BP; 1064 A; 1497 C; 1394 G; 1056 T; 0 other;

Query Match		34.2%;	Score 1737.8;	DB 21;	Length 5011;
Best Local Similarity		62.2%;	Pred. No. 0;		
Matches 2882;		Conservative 0;	Mismatches 1662;	Indels 87;	Gaps 6;
QY	25	CGGGAGCTCGGCTCCCAAGTCTGGGACCTCCAACTGTCTGTGCACACAGAAACCCGA	84		
DB	219	CGCCGATGGCTCGGACCCCTCTGGACTGGAAATGCAGTGAATACCAAGCAACCCGA	278		
QY	85	CCTCACTCCCTCCAGAACTCCCTGCTGGCCCTGGGTGCTGCTACCTCTGTGGGT	144		
DB	279	CTTACCAAGTCTTTCAGAACAGCTCTGCTGTGGGTGCTGTTTCTACCTCTGGGC	338		
QY	145	CGCCCTGCTCTACTGCTCTACTCTGCGGCACCAATGCTGTGGCTACATCATCTCFC	204		
DB	339	CTGTCTCCCTCTACTCTCTCTCTCTCTCTCCGACATACCCAGGCTACATCATGAC	398		
QY	205	CCACCTGTCCAGCTCAAGATGCTCTGGGTCTCTGCTGTGGTGGTCTCTGGCGGA	264		
DB	399	ACCTCTCAACAAACCAAACTGCCCTTGGGATTTTGTGTGGATCGTCTGTGGCGAGA	458		
QY	265	CTTTTTTACTCTTCCATGGCTGCTCCATGGCCGGCCCTGCTGCCCTGTTTCTTGT	324		
DB	459	CTCTTCTACTCTTCTGGGAAGAAGTCGGGCATATCTCTGGCCCACTGTTCTGT	518		
QY	325	CACCCCTTGTGGGGTACCACTGCTGTGGCCACCTGCTGTATACATATGAGCG	384		
DB	519	CAGCCCACTCTTGGGCATCACACGCTGCTTCTACCTTTTAAATTCAGCTGGAG	578		
QY	385	GCTGAGGGCTACAGTCTTGGGGTCTCATATATCTTCTGGTCTGTGTGGTCTG	444		
DB	579	GAGGAAGGAGTTCAGTCTTCAAGGATCATGCTCACTTCTTGGCTGGTAGCCCTAGTGT	638		
QY	445	CGCCATCTGCCATTCCTGCTCAAGATCTTACCAAGGAGAGGTGAGATCTCAGA	504		
DB	639	TGCCCTAGCATCTGAGATCCAAATTTATGACACCTTAAAGAGATGCCAGGTGA	698		
QY	505	CCCTTCGCTTACCACTCTTACATCACTTTCGCTGCTGTCTCTGCTGCTCATCTT	564		
DB	699	CTGTGCTGACATCACTTCTACGTCTACTTTTCCCTCTACTCACTCACTGCTCT	758		
QY	565	GGCTGCTTCAAGGAACTCCATTTCTCCCAAGATGTCGACCTTAACCCCTA	624		
DB	759	GTCTTCTTCAGATCGCTCACCCCTCTCTCGAAACCATTCACGACCTTAATCCCTG	818		
QY	625	CCCTGAGACAGCGCTCTCTCTCCGCTGTTTTTCTGGTGTTCACAAAGATGCG	684		
DB	819	CCAGAGTCCAGCGCTCTCTCTGCTGAGGATCACTTCTGGTGGATCAGAGGTGAT	878		
QY	685	CATCTATGGCTACCGGATCCCTGGAGGAGAGGACCTCTGGTCCCTTAAAGGAGGA	744		
DB	879	TGTCGGGGCTACCGCCAGCCCTGGAGGAGTGAACCTCTGGTCTTAAACAAGGAGGA	938		
QY	745	CAGATCCAGATGTGTGACAGCTGCTGGAGCATGGAGGA-----	788		
DB	939	CAGTGGGAACAAGTGTGCTGTTTTTGGTAAAGAACTGGAAGAAGGAATGCGCAAGAC	998		
QY	789	-----AGCAGGAAGACAGAGCGGACGACACAAAGGCTTCAGCAGCACCTGGGAAAA	840		
DB	999	TAGGAAGCAGCGGTGAAGTTGTGTACTCTCTCAAGGATCCTGCCAGCGGAAGAGAG	1058		
QY	841	TGCTTCGGGAGGAGAGGTGTGTGGTG-----CCCGGCCAGGCC	885		
DB	1059	TTCAAGGTGGATGCAATGAGAGGTGGAGGCTTTGATCTCAAGTCCCCACAGAAGGA	1118		
QY	886	CGGAAGCCCTCTCTGAGAGCCCTGCTGGCACCTTCCGCTCCAGCTTCTTCATCAG	945		
DB	1119	GTGAACCCCTCTGTGTAAAGGTGTATACAAGACCTTTGGGCCCTACTTCTTCATGAG	1178		
QY	946	TGCTGCTTCAAGCTTATCCAGGACCTGCTCTCTCTTCATCAATCCACAGCTGCTCAGAT	1005		
DB	1179	CTTCTTCAAGGCCATCCACAGCCTGATGATGTTTTTCCGGGCGGAGATCTTAAAGTT	1238		

QY	1006	CCTGATCAGGTTTATCTTCCAAACCCATGGCCCTCTCTGGTGGGCTTCTGTGGCTGG	1065		
DB	1239	GCTCATCAAGTCTGCTGAATCACAGGAGCCCGACAGCTGGCAGGCTTCTTACACCGT	1298		
QY	1066	GCTGATGTTCTGCTGCTCAATGATGAGTGCCTGATCTTACACACTATTACCACTACAT	1125		
DB	1299	GCTGCTGTTGTCTCACTGCTGCTGAGACCTCGTCTGACCCAGTACTTCCACATCTG	1358		
QY	1126	CTTGTGACTGGGTGAAGTTTCGTACTGGATCATGGGTGTCATCTACAGGAGGCTCT	1185		
DB	1359	CTTGTGACTGGGTGAAGTTTCGTACTGGATCATGGGTGTCATCTACAGGAGGCTCT	1418		
QY	1186	GTTTATCACCAACTCAGTCAAGCTGCTGCTCACTGTGGGGAAATTTGCAACCTCATGTC	1245		
DB	1419	GSTGATCACCAATTCAGCCAGAAATCTCCAGGTCGGGAGATTTGCAACCTCATGTC	1478		
QY	1246	AGTGGATGCCAGCGCTTCATGAGACCTTGGCCCTTCTCTCAATCTGCTGTGGTCAAGC	1305		
DB	1479	TGTGGACGCTCAGAGGTTTATGACTTGGCAGTACATTAACATGATCTGCTCAGCCCT	1538		
QY	1306	CCTGACAGATCATCTGCGATCTTCTCTGCGACAACTAGGTCCTCTCTCTGGC	1365		
DB	1539	CCTGCAAGTCACTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1598		
QY	1366	TGAGTGCCTTTTCATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1425		
DB	1599	TGAGTGCCTTTTCATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1658		
QY	1426	CGCTTCCAGGTAAAGCAATGAAATTTGAAGGACTCGCGCATCAAGCTGATGAGTGAAT	1485		
DB	1659	GAGCTATCAGGTGGCCACATGAAGCAAGCAATCGGATCAAGCTGATGAACGAAT	1718		
QY	1486	CCTGAAGCAGTCAAGGCTGCTGAGCTGCTGAGCTGCTGAGCTGCTGAGCAGGT	1545		
DB	1719	TTCAATGGATCAAGTCTTAAAGCTTATGCTGGAGCTGGCATTAAGGACAGGT	1778		
QY	1546	GGAGGATCAGGAGGCTGAGCTTCCAGCTGCTGCGACGCGGCGCTTACCTCACACCCAC	1605		
DB	1779	GCTGGCATCAGGAGGAGGCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGCAGGT	1838		
QY	1606	AGCCACTTCACTGATGTGAGCCCTTCTGCTGAGCCTTCTGCTGAGCCTTCTGCTGCT	1665		
DB	1839	GGGACCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1725		
QY	1666	CGTGTACGTGGACCCAAACAATGCTGCTGAGCGGAGAGGCTTGTGCTGTGCTT	1758		
DB	1899	CGTGACCTTGGAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1958		
QY	1726	GTTTAAATCTTAAAGACTTCCCTTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCT	1785		
DB	1959	GTTTAAATCTTAAAGACTTCCCTTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCT	2018		
QY	1786	GGCCAGTGTCTCTGAAACGATCCAGCAATCTCTGAGCCAGAGGAACTTGACCCCA	1845		
DB	2019	GCGAGTGTCTCTTCAACGCTTCAAGGCTTCTTCTCTCTCTCTCTCTCTCTCTCTCT	2078		
QY	1846	GAGTGTGGAAGAAAGACCATCTCCCGAGC-----TATGCCATCACCACACAG	1896		
DB	2079	CAGCATCGAGGAGGCTTCTCAAGACGCGGGGCGACGACAGCATCACCCTGAGGAA	2138		
QY	1897	TGGCACCTTCACTTGGGCGCAGGACCTGCCCCCTCTCTGACAGCCTAGACATCCAGGT	1956		
DB	2139	TGCCACATTCACCTGGCCAGGAGCGACCTTCCACACTGAATGGCATCACCTTCTCCAT	2198		
QY	1957	CCGAAAGGGGACTTGTGGCGCTGCTGGCGCTGCTGGCGCTGCTGGCGCTGCTGGCGCT	2016		
DB	2199	CCCGAAGGTGCTTGTGGCGCTGCTGGCGCTGCTGGCGCTGCTGGCGCTGCTGGCGCT	2258		
QY	2017	GTCCTGCTGCTGGGAGGATGAGAGCTAGAGCAAGTGCACATGAAGGGCTCCGT	2076		
DB	2259	CTCAGCCCTCTTGTGGCTGAGATGACAAAGTGGAGGGGCGACGTGGGCTTCAAGGGCTCCGT	2318		
QY	2077	GGCTCTGTGCCCCAGCAGGAGCATGGATCCAGAACTGCACCTTCTCAGAGAAACGTGCTTTT	2136		

||||| 2319 GGCATGTCACAGCAGCGCTGGATTCAAGATTGATCTCTCGAGAAACATCCCTTTT 2378
QY ||||| 2137 CGCAGAACCCCTGAACCCCAAGGCTACACAGCAGACTCTGAGGCCCTGTGCTTGTGCTAGC 2196
Db ||||| 2379 TGGATGTCAGCTGGAGGAACCATATTACAGTCCGTGATACAGGCCTGTGCCCTCCTCCC 2438
QY ||||| 2197 TGACCTGGAGATGCTGCTGTGGTGGGATCAGACAGAGATTGGAGGAAGGGCATTAACCT 2256
Db ||||| 2439 AGACCTGGAAATCCTGCCAGTGGGATCGGACAGAGATTGGGAGAAGGCGGTGAACCT 2498
QY ||||| 2257 GTCTGGGGCCAGCGCAGCGGTGCTGAGTGGCTCGAGCTGTTTACAGTGATGCGGATAT 2316
Db ||||| 2499 GTCTGGGGGACAGACAGCGCGCTGAGCCTGGCCCGGCGCTGACTCCACAGCTGACAT 2558
QY ||||| 2317 TTTCTTGCTGGATGACCCACTGTCCGGGTGAGCTCTCATGTGSCCAAGACACATCTTTGA 2376
Db ||||| 2559 TTACCTCTTCGATGATCCCTCTCAGCAGTGGATGCCATGTGGGAAAACACATCTTTGA 2618
QY ||||| 2377 CCAGTTCATCGGCCAGAGGCGTGTGGCAGGACGAGCGAGTGTGTTGAGCGG 2436
Db ||||| 2619 AATGTGATTGGGCCCAAGGGGATGGTGAAGAAACAGACCGGATCTGTGTCACGCACAG 2678
QY ||||| 2437 CATTAGCTTCTGCCACAGACACTTCATATTGCTAGCTGATGCAGAGTGCTGA 2496
Db ||||| 2679 CATGAGTACTTCCCGAGTGGAGCTCATCTGTCATGAGTGGCGGGAAGATCTGA 2738
QY ||||| 2497 GATGGGCCCTACCCAGCCCTGTGACGCCAACAGCGCTCTTTGCCAACTTTCTCTGCAA 2556
Db ||||| 2739 GATGGGCTCTACCAGGAGTGTGCTCGAGACGGCGCTTGCCTGAGTTCCTGCGTAC 2798
QY ||||| 2557 CTATGCCCCGATGAGACCAAGGACCTTGGAGACAGCTGGACGCCGTGGGAAGTGTC 2616
Db ||||| 2799 CTATGCCAGCACAGACGAGCAGGAGTGCAGAGAGAACGGGTGTCACGGCGCTCAGCGG 2858
QY ||||| 2617 AGAGGTAAGGAGGCGCTGCTGATTGAAGACACACTCAGCAACACACAGGATCTGACAGA 2676
Db ||||| 2859 TCAGGGAAGGAAGCAAGCAATGGAGATGGCAT----- 2894
QY ||||| 2677 CAATGATCCAGTCACTATGTGTGTCAGAGACAGTATTATGAGACAGCTGAGTGCCCTGTC 2736
Db ||||| 2895 -----GCTGGTGACGACAGTGCAGGGAAGCAACTGCAGAGACAGCTCAGCAGCTCCTC 2948
QY ||||| 2737 CTCAGATGGGAGGACAGGCTGGCTGTACCCCGGAGGACCTGGGTCCATCAGAGAA 2796
Db ||||| 2949 CTCCTATAGTGGGGACA---TCAGCAGGCAACCAACAGCAGCCGCAAGAACTGCAGAAA- 3003
QY ||||| 2797 GGTGCAAGGTGACAGAGCGGAAGGACAGATGGGCACCTCACCCAGGAGAGAAAGCAGCCAT 2856
Db ||||| 3004 -----GCTGAGGCCAAGAGGAGGAGACCTGGAAGCTGATGGAGGCTGACAAGGGCGAGAC 3059
QY ||||| 2857 TGGCATGTGGAGCTCAGTGTGTTCTGGGATATGCCAAGCCGCTGGGGCTCTGTATCCAC 2916
Db ||||| 3060 AGGCGAGGTCAAGCTTTCCGTGTACTGGGACTACATGAAGGCCATCGGACTTTCATCTC 3119
QY ||||| 2917 GCTGGCCATCTGCTCCTGTATGTGGTCAAAGTGGGCTGCCATTTGGAGCCCAATGTGTG 2976
Db ||||| 3120 CTTCCTCAGCATCTTCTCTTTTCAATGTGTAAACCATGTGTCCGCGCTGGCTTCCAACTATTG 3179
QY ||||| 2977 GCTCAGTGGCTGCAAAATGATGCCATGGCAGACAGTAGACAGCAACAACTCCCTGTAG 3036
Db ||||| 3180 GCTCAGCCTTGAGCTGATGACCCCACTGTCACGGGACTCAGGAGCACAGAAAGTCCG 3239
QY ||||| 3037 GCTGGGCGTCTATGCTGCTTTAGGAATTTCTGAAGGGTCTTGGTGATGCTGGCAGCCAT 3096
Db ||||| 3240 GCTGAGCGTCTATGAGCCCTTGGGCATTTTCAAGGATGCGCGTGTGGCTACTCCAT 3299
QY ||||| 3097 GGCATGAGCAGGGGTGGCATTCAGCGCTGCCCGTGTGTGTCACAGCAGCATGTGTGCACAA 3156
Db ||||| 3300 GGCCGTGTCCATCGGGGGATCTGTGGCTTCCCGCTGTCTGCACGTGGACCTGCTGTGCACAG 3359
QY ||||| 3157 CAAGATACGCTGCCACAGTCCCTTTTGTGACACCAACACCATACGCGGCTGCTGACTG 3216

Db ||||| 3360 CATCTGCGGTCACCATGAGCTTCTTTGAGCGGACCCCCAGTGGGAACCTCGTGAACCG 3419
QY ||||| 3217 CTTCTCAAGGACATCTATGCTGTTGATGAGGTTCTGGCCCCCTGATCCTCTCATGCTGCT 3276
Db ||||| 3420 CTTCTCAAGGAGCTGGACACAGTGAATCCATGATCCGGAGGTTCATCAAGATGTTCA 3479
QY ||||| 3277 CAATTCCTTCTCAAGCCATCTCCACTCTTGTGTGTCATCATGAGCCAGCAGCCGCTCT 3336
Db ||||| 3480 GGGCTCCTGTTCAACGTCATTTGGTGCCTGATCTCTTATCTGCTGGCCACGCCCATCG 3539
QY ||||| 3337 CACTGTGTCTATCTGCCCTGGCTGCTCTACACCTTAGTGCAGCGCTTCTATTCACG 3396
Db ||||| 3540 CCGCATCATATCCCGCCCTTGGCTCATCTACTCTTCTGTCAGAGGTTCTACTGTGCG 3599
QY ||||| 3397 CACATCAGCGCAACTGAAGCGCTGGAAATCAGTCAGCGCTCACCTATCTACTCCACTT 3456
Db ||||| 3600 TTCTCCCGCGCAGCTGAAGCGCTCGAGTCTGTCAGCGCTCCCGCTTATTTCCCAATT 3659
QY ||||| 3457 TTCGAGACAGTGAATGGTGCAGTGTCTCCGGGCTTACAAACCGCAGCCGGATTTTGA 3516
Db ||||| 3660 CAACGAGACCTTGTGGGGTTCAGCGTCAATTCGAGCTTCGAGGAGCAGGAGCGCTTCA 3719
QY ||||| 3517 GATCATCAGTCACTAGGTGGATGCCAACAGAGAAGCTCTACCCCTACATCATCTC 3576
Db ||||| 3720 CCACAGAGTCACTGAAGTGGAGAGAGCAAGAGGCTTATTACCCAGCATCTGGC 3779
QY ||||| 3577 CAACCGGTGGCTGAGCATCGGAGTGGAGTGTGTTGGGAACCTGCTGCTTTTCTGCTG 3636
Db ||||| 3780 CAACAGTGGCTGGCGCTGCGGCTGGAGTGTGGGCAACTGCATCTGCTCTTTGCTGTC 3839
QY ||||| 3637 ACTATTGCGCTCATCGGGAGGAGCAGCTTGAACCCGGGGCTGTGGGCTTTCTGTGTC 3696
Db ||||| 3840 CCTGTTGGGCTGATCTCCAGGACAGCTCAGTCTGGCTGGTGGGCTCTCAGTGTG 3899
QY ||||| 3697 CTACTCTTGCAGTGACATTTGCTCTGAACCTGGATGATCAAGATGATGTCAGATTTGA 3756
Db ||||| 3900 TTACTCATTTGAGGTCAACCTGATTTGATGCTGGATGCTCATCTGAAATGGA 3959
QY ||||| 3757 ATCTAACATCTGCTGTGGAGAGGTTCAAGAGTACTTCAAGACAGACAGAGAGCGCC 3816
Db ||||| 3960 AACCAACATCTGCGCTGGAGAGGCTCAAGAGTATTTCAGAGACTGAGAGAGGCGCC 4019
QY ||||| 3817 CTGGGTGGTGAAGGACGCGCCCTCCGAAGGTTGGCCCCACGCTGGGAGGTGGAGTT 3876
Db ||||| 4020 TTGCAATCCAGGAGACACGTCGCCAGCAGCTGGCGCCAGGTGGCGCGAGTGAAT 4079
QY ||||| 3877 CCGGAATTAATCTGCTGCTACCGCGCGGCTAGACCTGTGCTGAGAGACTCTGAGTCT 3936
Db ||||| 4080 CCGGAATCTGCTGCTGCTACCGAGAGGACTGGACTTCTCTCAGGACATCAATGT 4139
QY ||||| 3937 GCATGTGACGGTGGCGAGAAAGTGGGATCTGSGGCCCACTGGGGCTGGCAAGTCTTC 3996
Db ||||| 4140 CACGATCAATGGGAGAAAAGTTCGGCATCTGSGGGCGGACGGGAGCTGGGAAGTCTC 4199
QY ||||| 3997 CATGACCTTTGCTGTTCCGATCTCTGGAGGCGGCAAGGTTGAATCCGATTTGATGG 4056
Db ||||| 4200 CTTGACCTGGGCTTATTTCCGATCAAGCTCTGCCGAAGGAGATCATCATGATGG 4259
QY ||||| 4057 CCTCAATGTGGCAGACATCGGCTTCCATGCTGCGCTCTCAGCTGACCATCATCCCCA 4116
Db ||||| 4260 CATCAATCGCAGAGTGGCTTCCGATCTGCGCTTCAAGATCACCATCATCCCCCA 4319
QY ||||| 4117 GGACCCCATCTGTTCTCGGGGACCTGCGCATGAACCTGGACCCCTTCGCGAGTACTC 4176
Db ||||| 4320 GGACCTGTTTGTGTTTTCGGGTTCCCTCCGAATGAACCTGGACCCATTCAGCCAGTCTC 4379
QY ||||| 4177 AGAGGAGCATTTGTTGGGCTTTGGAGCTGTGCCACTGTCACACAGTTTGTGAGTCCCA 4236
Db ||||| 4380 GGATGAAGAAGTCTGGAGCTCCCTGGAGCTGCCCACTGAAGGACTTCGTTGTACGCCCT 4439
QY ||||| 4237 GCGGCGAGGCTGACATCTCAGTGTCTCAGAGGGGGGAGAACTCAGCTGTGGGCGACG 4296
Db ||||| 4440 TCCTGCAAGCTAGACCATGAATGTCAGAGAGGGGGGAGAACTCAGTGTGGGCGACG 4499

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1179 CTTCTTCTTCAAGGCCATCCACGACCTGATGATGTTTTCGGGCCGCGAGATCTTAAAGTT 1238
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1006 CTTGATCAGGTTTATCTCCAAACCCATGGCCCGCTCTCTGGGGGCTTCTGGTGGCTGG 1065
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1239 GCTCATCAAGTTCTGTAATGACACGAAGGCCCGAGACTGGCAGGGCTACTTCTACACCGT 1298
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1299 GCTGCTGTTTGTACCTGCTGCGCTGCAGACCTCTGCTGCTACACAGTACTTCCACATCTG 1358
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1126 CTTTGTGACTGGGGTGAAGTTTCTGCTACTGGGATCATGGGTGCTCATCTACAGGAAGGCTCT 1185
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1186 GGTATACCAACTCAGTCAAAAGCTGGTCCACTGTGGGGGAATTTCTCAACCTCATGTC 1245
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1246 AGTGGATGGCCAGCGCTTCATGACACCTTGCCCTCTCTCAATCTGCTGTGGTCAGCACCC 1305
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1539 CTTGCAAGTCACTCTGCTCTACCTCTGCTGGCTGCTGAATCTGGGCCCTTCCGTCCTGGC 1598
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1366 TGGAGTCGCTTTCATGGTCTGCTGATTCACATCAAGGAGCTGTGGCCGTGAAGATGGC 1425
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1599 TGGAGTGGGGGTGATGGTCTCATGTGTGCTGCTCAATGCTGTGATGGCGATGAAGACAA 1658
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1426 CGCTTCCAGTTAAAGCAATGAATGAAGGACTCGCGATCAAGCTGATGATGATGATGAT 1485
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1659 GAGTATCAGTGGGCCCATGAAAGCAAGACATCGGATCAAGCTGATGACGAAT 1718
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1486 CTTGAACGGCATCAAGGTGCTGAAGCTGTACGCTGGGAGCCAGCTTCTTGAAGCAGGT 1545
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1719 TCTCAATGGGATCAAAAGTCTAAAGCTTTATGCTGGGAGCTGGCATTAAGGACAAAGT 1778
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1546 GGGAGGCATCAGCAGGCTGAGCTCCAGCTGTGCGCAGCGGCCCTACTCCACACCAC 1605
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1779 GCTGGCCATCAGCAGGAGCTGAAGGTGCTGAAGAGTCTGCTTACCTGCTGACGCGCT 1838
1200
1606 AACCACTTCACTGATGTGACGCCCTTCTCTGCTGAGCCCTGATCAACCCTCTGGGTGA 1665
1201
1839 GGGCACCTTCACTGGGCTGCGACGCCCTTCTGCTGGGCTTGTGACATTTGCCGCTTA 1898
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1666 CGTGTACGTGGACCCAAACATGTGCTGGACCGCGAGAGGCCCTTGTGCTGTGCTCTT 1725
1203
1899 CTTGACCATTTGACGAGAACAACTCTGATGGATGCCAGACAGCTTGGTGTCTTTGGCCTT 1958
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1726 GTTAAATATCTTAAGACTTCCCTCAACATGCTGCCCCAGTTAATCAGCAACCTGACTCA 1785
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1959 GTTCAACATCTCCGGTTTCCCTTGAACATTTCCCCATGCTGATCAGCAGCATCCGTGCA 2018
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1786 GGCAGTGTGCTCTGAAACGGATCCAGCAATCTCTGAGCCCAAGAGAGAACTTGACCCCA 1845
1207
2019 GGGCAGTGTCTCCCTCAACGCTGAGGATCTTCTCTCCCATGAGGAGCTGGAACCTGA 2078
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1846 GAGTGTGGAAGAAAGACATCTCCCGAGC-----TATGCCATCACCACATACAG 1896
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1897 TGGACCTTCACTGGGCCAGGACTGCCCCCAGCTTGCACAGCCTAGACAGCTTCCAGGT 1956
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2139 TGGCACAATTCACCTGGGCGAGGAGGACCTCCCACTGAATGGCATCACCTTCTCCAT 2198
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1957 CCGGAAAGGGGACTGTTGGCGTGTGGGGCTGTGGGCTGTGGGAAGTCTCTCCCTGGT 2016
1213

2199 CCCGAAGGTCTCTTTGGTGGCCGTGGTGGGCCAGGTGGGCTCGGAAAAGTTGTCTCCTGCT 2258
2017 GTTCCCTGCTGGGAGAGATGGAGAACTAGAAAGCAAAAGTGCACATGAAGGGCTCCGT 2076
2259 CTCAGCCCTCTTGGCTGAGATGGACAAAGTGGAGGGCAGCTGGCTATCAAGGGCTCCGT 2318
2077 GGCCTATGTGCCCCCAGCAGGAGCATGGATCCAGAACTGCACTCTTCAGGAAAAGCTGCTTTT 2136
2319 GGCCTATGTGCCCAGCAGAGGCTGGATTCAGAAATGATTCTCTCCGAGAAAACATCTTTT 2378
2137 CGGCAAGGCCCTGAACCCCAAGCGCTACACAGACTCTGGAGGCCCTGTGCTCTGCTAGC 2196
2379 TGGATGTCAAGTGGAGGAACCATATTACAGGTCCGTGATACAGGCCCTGTGCCCTCTCC 2438
2197 TGACCTGGAGATGCTGCTGCTGGGATCAGACAGAGATTGGAGAAAGGCAATTAACCT 2256
2439 AGACCTGSAATCTTGCCTGAGTGGGATCGGACAGAGATTGGCAGAGAGGCGTGAACCT 2498
2257 GTCTGGGGCCAGCGGACAGCGGCTGAGTCTGGCTGAGCTGTTTACAGTGTGCGGATAT 2316
2499 GTCTGGGGGACAGAGAGCGCGTGAAGCTGGCCCGGCGCTGTACTCCAAAGCTGACAT 2558
2317 TTTCTTCTGATGACCACTGCTCCGCGTGGACTCTCATGTGGCCAAAGACATCTTTGA 2376
2559 TTACTCTTCTGATGATCCCTCTCAGCAGTGGATGCCCATGTGGGAAAACACATCTTTGA 2618
2377 CCAGCTCATCGGGCCAGAAAGCGCTGCTGGAGGCAAGACGAGTGTGCTGACGACGAG 2436
2619 AATGTGATTGGCCCCAAGGGAGTCTGAAGAACAAAGCGGATCTTGGTCCAGCAGAG 2678
2437 CATTAGCTTCTGCCCCAGACAGACTTTCATGCTGTAGCTGATGATGACAGCTGTCTGA 2496
2679 CATGAGCTTCTGCGCAGGTGGAGCTCATCATGCTCATGATGAGTGGCGCAAGATCTCTGA 2738
2497 GATGGGCCCTTACCCAGCCCTGCTGACGCAAGCGCTCTTGGCCAACTTCTCTGCA 2556
2739 GATGGGCTCTTACCCAGAGCTGCTGCTGAGACGGCCCTTCTGCTGAGTCTCTCGCTAC 2798
2557 CTATGCCCCGATGAGGACCAAGGGCACCTTGGAGGACAGCTGGACCGCTTGGAAAGTGC 2616
2799 CTATGCCAGCACAGCAGGAGGAGGATGAGAGAGAAAGCGGCTACGGGCGTACGCGG 2858
2617 AGAGGATAAGGAGCAGCTGCTGATTTGAAGACACACTCAGCAACACACAGGATCTGACAGA 2676
2859 TCCAGGGAAGGAAGCAAAATGGAGATGGCAT----- 2894
2677 CAATGATCCAGTACCTATGTGGTCCAGAACAGTATTATGAGACAGCTGAGTGGCCCTGTC 2736
2895 -----GCTGCTGACGGACAGTGCAGGGAAGCAACTGCAGAGACAGCTCAGCAGCTCCTC 2948
2737 CTCAGATGGGAGGACAGGCTCGGCTGTACCCCGAGGACCTTGGGTCCATCAGAGAA 2796
2949 CTCCTATAGTGGGACA---TCAGCAGGACCAACACAGCAGCCGCAACTGCAGAAA- 3003
2797 GGTGCAAGTGCACAGAGCGGAGGAGGAGTGGGCACTGACCCAGGAGGAGAAAGCAGCAT 2856
3004 -----GCTGAGGCCAAGAAAGGAGAGCCTTGAAGCTGATGAGGCTGACAAAGGCGAGAC 3059
2857 TGGCACTGTGGAGTCAAGTGTGCTGGGATTTGCCAAGGCCGTGGGCTCTGTACAC 2916
3060 AGGCAGGTCAAGCTTTCGCTGACTGGGACTACATGAGGCCATCGGACTCTCATCTC 3119
2917 GCTGGCCATCTGCTCTCTGATGTGGGTCAAAGTGGGCTGCCATTTGAGGCAATGTGTG 2976
3120 CTTCTCTCAGCATCTTCTCTTTCATGTGTAAACATGTGTCCGCGCTGGCTTCCAACTATTG 3179
2977 GCTCAGTGCCTGCACAAATGATGCCATGGCAGACAGTAGACAGAACACACTTCCCTGAG 3036
3180 GCTCAGCCTCTGAGATGATCCCTCATCGCAAGCGGACTCAGGAGCAGACAGAAAGTCCG 3239
3037 GCTGGGCGTCTATGCTCTTTAGGAATTTCTCAAGGGTCTTGTGGTGTGCTGGCAGCAT 3096
3240 GCTGAGGCTCTATGGAGCCCTTGGGCAATTTTCAAGGGATGCCGCTGTTGGCTACTCCAT 3299

QY 3097 GGCCATGGCAGCGGTGGCATCCAGGCTGCCCGTGTGCTTGCACACAGGCACTGCTGCACAA 3156
DB 3300 GGCCGTGTGCATCGGGGGATTTGGCTTCCCGCTGTCTGCACGTGGACCTGTCTGCACAG 3359
QY 3157 CAAGATACGCTGCCACAGTCCCTTCTTTGACACACACACATCAGCGCGCATCTGGAACG 3216
DB 3360 CATCTCGCGTCACCATGAGCTTCTTTGAGCGGACCCCGAGTGGAACTGCTGGAACCG 3419
QY 3217 CTTTCTCAAGAGACATCTATGTCTGTTGATGAGGTTCTGGGCCCTGTCACTCCTCATGCTGCT 3276
DB 3420 CTTTCTCAAGAGACATCTGAGCTTCTTTGAGCGGACCCCGAGTGGAACTGCTGGAACCG 3479
QY 3277 CAATTCCTTCTCAAGAGACATCTGAGCTTCTTTGACACACACATCAGCGCGCATCTGGAACG 3336
DB 3480 GGGTCCCTTCTCAAGAGACATCTGAGCTTCTTTGACACACACATCAGCGCGCATCTGGAACG 3539
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DB 3540 CGCCATCATATCCCGCCCTTGGCTCATCTACTTCTTCTGTCACAGGTTCTACGTGGC 3599
QY 3397 CACATCAGCGCACTGAAGCGCTGGAATCAGTCAAGCGCTCACCCTTACTTACTTCCCACTT 3456
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:04:10 ; Search time 8364.83 Seconds
(without alignments)
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Title: US-09-647-140A-5

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	5073.2	99.9	5117	9	AF083552	AF083552 Homo sapi
3	5071.6	99.9	5117	9	AB010887	AB010887 Homo sapi
4	5071.6	99.9	5193	6	AX443141	AX443141 Sequence
5	5056	99.5	5142	9	AF085690	AF085690 Homo sapi
6	4895.4	96.4	5291	9	AF085691	AF085691 Homo sapi
7	4892.4	96.3	4948	9	HSY17151	Y17151 Homo sapien
8	4828.8	95.1	5346	9	AF085692	AF085692 Homo sapi
9	4636.4	91.3	4762	9	AF009670	AF009670 Homo sapi
10	4586.8	90.3	4762	6	A64692	A64692 Sequence 58
11	3186.4	62.7	5174	10	AB010467	AB010467 Rattus no
12	3152.4	62.1	5107	10	AF072816	AF072816 Rattus no
13	1749.4	34.4	1977	6	AX333322	AX333322 Sequence
14	1749.4	34.4	1977	6	AX335826	AX335826 Sequence
15	1749.4	34.4	1977	6	AX410761	AX410761 Sequence
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18	1737.8	34.2	5011	6	AR093439	AR093439 Sequence
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23	1612.6	31.8	4587	10	AF022908	AF022908 Mus muscu
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28	1209.2	23.8	5817	5	AF486830	AF486830 Raja erin
29	1207.8	23.8	5473	3	AY069827	AY069827 Drosophil
30	1173.8	23.1	182222	2	AC123374	AC123374 Rattus no
31	1109	21.8	5407	4	OC249144	Z49144 O. cuniculus
32	1096.4	21.6	4864	9	HSCMRP	X96395 H.sapiens m
33	1096.4	21.6	4868	9	HSU63970	U63970 Human canal
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44	1042	20.5	4632	10	AF282773	AF282773 Mus muscu
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ALIGNMENTS

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LOCUS AF104943
DEFINITION Homo sapiens ABC transporter MOAT-D (MOAT-D) mRNA, complete cds.
ACCESSION AF104943
VERSION AF104943.1 GI:4140699
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 5079)
REFERENCE
AUTHORS Belinsky,M.G., Bain,L.J., Balsara,B., Testa,J.R. and Kruh,G.D.
TITLE Characterization of MOAT-C and MOAT-D, new members of the MRP/CMOAT subfamily of transporter proteins

J. Natl. Cancer Inst. 90 (22), 1735-1741 (1998)
99043202
MEDLINE
PUBMED
9827529
REFERENCE
2 (bases 1 to 5079)
Belinsky M.G., Bain L.J. and Kruh G.D.
AUTHORS
Direct Submission
TITLE
Submitted (04-NOV-1998) Medical Oncology, Fox Chase Cancer Center,
JOURNAL
7701 Burholme Avenue, Philadelphia, PA 19111, USA
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ORIGIN

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ACCESSION	ABO10887		
VERSION	ABO10887.1 GI:3132269		
KEYWORDS	multidrug resistance-associated protein(MRP)-like protein-2 (MLP-2).		
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AUTHORS	1 (sites)		
TITLE	Kiuchi,Y., Suzuki,H., Hirohashi,T., Tyson,C.A. and Sugiyama,Y. CDNA cloning and inducible expression of human multidrug resistance associated protein 3 (MRP3) FEBS Lett. 433 (1-2), 149-152 (1998)		
JOURNAL	98409330		
MEDLINE	2 (bases 1 to 5117)		
REFERENCES	Kiuchi,Y., Suzuki,H., Hirohashi,T. and Sugiyama,Y.		
AUTHORS	Direct Submission		
TITLE	Submitted (02-FEB-1998) Yuichi Sugiyama, Graduate School of Pharmaceutical Sci., The University of Tokyo, Department of Pharmaceutics; Hongo 7-3-1, Bunkyo-ku, Tokyo 113, Japan (E-mail:BXG0543@niftyserve.or.jp, Tel:+81-3-3812-2111, Fax:+81-3-5800-6949)		
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ORIGIN

Query Match		99.9%;	Score 5071.6;	DB 9;	Length 5117;
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Qy	361	CACCTGCTGATACAGTATGAGCGCTCAGGGCTACAGTCTTCCGGGGTCCCTCATAT	420		
Db	371	CACCTGCTGATACAGTATGAGCGCTCAGGGCTACAGTCTTCCGGGGTCCCTCATAT	430		
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Db	431	CTTCTGCTGCTGTGTGCTGTGCGCATGTCCTCCATTCGCTCCAGATCCTTTTAGC	490		
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Db	491	CAAGCAGAGGGTGAGATCTCAGACCCCTTCCGCTTCCACCTTCTACATCCACTTTGC	550		
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Db	551	CCTGTACTCTTGCCCTCATCTTGGCTGCTTTCAGGAGAAACCTCCATTTTCTCCGC	610		
Qy	601	AAAGATCTGACCCCTAACCCCTACCTTGAGACACGCTGCTTCTCTCCGCTGTT	660		
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Qy	661	TTTCTGCTGTTCAAAAGATGGCCATCTATGGTACCGGATCCCTCCGAGGAGAA	720		
Db	671	TTTCTGCTGTTCAAAAGATGGCCATCTATGGTACCGGATCCCTCCGAGGAGAA	730		
Qy	721	CCTCTGCTTCCCTAAAGGAGAGGACAGATCCAGATGGTGGTGCAGAGCTGCTGGAGC	780		
Db	731	CCTCTGCTTCCCTAAAGGAGAGGACAGATCCAGATGGTGGTGCAGAGCTGCTGGAGC	790		
Qy	781	ATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	840		
Db	791	ATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	850		
Qy	841	TGCTTCCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	900		
Db	851	TGCTTCCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	910		

Qy	901	CTGAAAGGCCCTGCTGGCCACCTTCGGCTCCAGCTTCTCATCAGTGCCTGCTTCAAGCT	960
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Db	1151	GAAGTTTCTGCTGCTGATCATGGTGTCTATCAGGAAGGCTCTGGTTATCACAACCT	1210
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Db	1691	AAACAATGCTGAGCGCGGAGAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1750
Qy	1741	ACTTCCCTTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1800
Db	1751	ACTTCCCTTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1810
Qy	1801	GAAAGGATCCAGCAATTCCTGAGGCAAGGAACTTGAACCCCTGAGTGTGGAAGAAA	1860
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RESULT 5
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LOCUS
DEFINITION Homo sapiens multidrug resistance-associated protein 3 (MRP3) mRNA,
complete cds.

5142 bp mRNA linear PRI 11-JAN-2000

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TITLE      Human MRP3 transporter: identification of the 5'-flanking region,
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JOURNAL     Biochim. Biophys. Acta 1415 (2), 369-374 (1999)
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PUBMED      9889399
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TITLE      Direct Submission
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 5078; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
QY 1 CCCCATGAGCGCCTGTGCGGTTCGGGGAGCTCGGCTCCAAAGTTCTGGGACTCCAAACCT 60
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DB 33 CCCCATGAGCGCCTGTGCGGTTCGGGGAGCTCGGCTCCAAAGTTCTGGGACTCCAAACCT 92
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QY 61 GTCTGTGCACAGAAAACCCGGACCTCACCTCCCTGCTTCCAGAACTCCCTGCTGCCTG 120
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Db 93 GTCTGTGCACAGAAAACCCGGACCTCACCTCCCTGCTTCCAGAACTCCCTGCTGCCTG 152
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QY 121 GGTGCGCTGCATCTACCTGTGGGTGCGCTGCCCTGCTACTTGTCTTACCTACCTGCGGACCA 180
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DB 153 GGTGCGCTGCATCTACCTGTGGGTGCGCTGCCCTGCTACTTGTCTTACCTACCTGCGGACCA 212
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QY 181 TTGTGCTGGCTACATCATCTCTCCACCTGTCCAAAGCTCAAGATGGTCTCTGGGTGTCTCT 240
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DB 213 TTGTGCTGGCTACATCATCTCTCCACCTGTCCAAAGCTCAAGATGGTCTCTGGGTGTCTCT 272
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QY 241 GCTGTGGTGGCTCTCTCTGGGCGGACCTTTTCTTACTCTTCCATGCGCTGGTCCATGGCG 300
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DB 273 GCTGTGGTGGCTCTCTCTGGGCGGACCTTTTCTTACTCTTCCATGCGCTGGTCCATGGCG 332
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QY 301 GGGCCCTGCGCTCTCTCTGGTCTTGTTCACCCCTTGTGTGGTGGGCTACCATGCTGCTGGC 360
    |||||||
DB 333 GGGCCCTGCGCTCTCTCTGGTCTTGTTCACCCCTTGTGTGGTGGGCTACCATGCTGCTGGC 392
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QY 361 CACCTGTGTATACAGTATGAGCGGCTGACGGGCTACAGTCTTCTGGGGGTCTCTCATTTAT 420
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DB 393 CACCTGTGTATACAGTATGAGCGGCTGACGGGCTACAGTCTTCTGGGGGTCTCTCATTTAT 452
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QY 421 CTTCTGTGTCTCTGTGTGTGTCTGCGCATCGTCCCATTCGCTCCAAAGATCTCTTTAGC 480
    |||||||
DB 453 CTTCTGTGTCTCTGTGTGTGTCTGCGCATCGTCCCATTCGCTCCAAAGATCTCTTTAGC 512
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QY 541 CCTGCTACTCTCTCCCTCTCATTTGGCTGTCTCAGGAGAGAACTCCATTTTCTCCGC 600
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DB 633 AAGAATGTGACACCTTAACCCCTACCTGTAGACACGCGCTGGCTTTCTCTCCGCGCTTT 692
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DB 1053 CTCCAACCCCATGGCCCCCTCTCTGGGTGGGCTTCCCTGGGTGGGCTGATGTCCTGTG 1112
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DB 1113 CTCCTATGATGACGCTGCTGATCTTACAACTATTTACCACTACATCTTTCTGACTGGGT 1172
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QY 1141 GAAGTTTCTGCTGGGATCATGGGTGTCTATCTACAGGAAGGCTGTGTTATACCAACTC 1200
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Db 1713 AAACAATGTGTGGACGCCGAGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1772
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Db 1953 CCTGCCCCCACTCTGCACACCTTAGACATCCAGTCCCGAAGGGGCACTGGTGGCCGT 2012
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Db 2133 GATCCAGACTGCACTTTCAGGAAAAGCTGCTTTTGGGAAAAGCCCTGAAACCCCAAGCG 2192
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Db 2193 CTACACAGACTCTGGAGGCTGTGCTTGTAGTGAACCTGGAGATGCTGCTGTGG 2252
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QY 3585 - 3584
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DB 3693 CTTTCCCTTAAGCAGAAAACTGGCCCTGCCCCCTGCCCATTTCTCTCTCATCTG 3752
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DB 3753 ATCCCCATAGGGGCTGAGCATCGGAGTGGAGTTCGTGGGAACTGCGTGGTCTCTT 3812
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Db 5193 CTCAGTCTCTACTCTGGGTGCTGCTGAATCCATTAAATGGGAGTACTGATGAAAT 5252
Qy 5070 AAAACTACA 5078
Db 5253 AAAACTACA 5261

RESULT 7
HSV17151
LOCUS HSV17151 Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3). 4948 bp mRNA linear PRI 12-MAY-1999
DEFINITION Y17151.2 GI:4826562
ACCESSION Y17151
VERSION Y17151.2
KEYWORDS ABC3 protein; MRP3 gene; multidrug resistance protein 3.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4948)
AUTHORS Konig, J., Rost, D., Cui, Y. and Keppler, D.
TITLE Characterization of the human multidrug resistance protein isoform
MRP3 localized to the basolateral hepatocyte membrane
JOURNAL Hepatology 29 (4), 1156-1163 (1999)
MEDLINE 99197095
PUBMED 10094960
REFERENCE 2 (bases 1 to 4948)
AUTHORS Koenig, J.
TITLE Direct Submission
JOURNAL Submitted (21-APR-1998) J. Koenig, DKFZ Heidelberg, Abteilung
Tumorbiochemie, Im Neuenheimer Feld, 280 D-69120 Heidelberg, FRG
COMMENT On May 13, 1999 this sequence version replaced gi:3087793.
FEATURES
Location/Qualifiers
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BASE COUNT 1011 a 1453 c 1364 g 1120 t

ORIGIN

Query Match 96.3%; Score 4892.4; DB 9; Length 4948;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4893; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 10

A64692

LOCUS

A64692

DEFINITION

Sequence 58 from Patent WO97/3111.

ACCESSION

A64692

VERSION

A64692.1

KEYWORDS

GI:4530758

SOURCE

unidentified.

ORGANISM

unidentified.

4762 bp

DNA

linear

PAT 29-MAR-1999

REFERENCE AUTHORS	TITLE	JOURNAL	COMMENT FEATURES	source
unclassified. 1 (bases 1 to 4762) Oude, E., Paulusma, C.C., Bosma, P.J., Borst, P., Evers, R., Kool and Marzel.	A FAMILY OF ORGANIC ANION TRANSPORTERS, NUCLEIC ACIDS ENCODING THEM, CELLS COMPRISING THEM AND METHODS FOR USING THEM	Patent: WO 9731111-A 58 28-AUG-1997; INTROGENE BV (NL)	Other publication AU 1736697 19970910.	
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(MRP)-like protein-2 (MLP-2), complete cds.
ACCESSION AB010467
VERSION AB010467.1 GI:3242459
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Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (sites)
AUTHORS Hirohashi,T., Suzuki,H., Ito,K., Ogawa,K., Kume,K., Shimizu,T. and
Sudiyama,Y.
TITLE Hepatic expression of multidrug resistance-associated protein-like
proteins maintained in eisel hyperbilirubinemic rats
Mol. Pharmacol. 53 (6), 1068-1075 (1998)
JOURNAL 9879126
MEDLINE 2 (bases 1 to 5174)
REFERENCE Hirohashi,T.
AUTHORS Direct Submission
TITLE Submitted (14-JAN-1998) Tomoko Hirohashi, Faculty of Pharmaceutical
Sciences, Tokyo University, Department of Pharmaceutics; Hongo
7-3-1, Bunkyo-ku, Tokyo 113, Japan
JOURNAL (E-mail:hirohashi@seizai.f.u-tokyo.ac.jp, Tel:81-3-5802-2045,
Fax:81-3-5800-6949)
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VERSION AX333322.1 GI:18123956
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REFERENCE 1
AUTHORS Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D. R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 3831 13-DEC-2001;
Avalon Pharmaceuticals (US)
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1		
JOURNAL	Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,		
FEATURES	Horrikan, S., Soppet, D.R. and Weaver, Z.		
SOURCE	Cancer gene determination and therapeutic screening using signature		
	gene sets		
	Patent: WO 0194629-A 6335 13-DEC-2001;		
	Avalon Pharmaceuticals (US)		
	Location/Qualifiers		
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	/db_xref="taxon:9606"		
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ORIGIN			8 others

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Search completed: December 18, 2002, 17:17:03
Job time : 8422.83 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:04:25 ; Search time 3824.06 Seconds
(without alignments)
19096.316 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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- 3: em_estin.*
- 4: em_estmu.*
- 5: em_estov.*
- 6: em_estpl.*
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- 8: em_htc.*
- 9: gb_estl.*
- 10: gb_est2.*
- 11: gb_htc.*
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- 15: em_estfun.*
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- 22: em_gss_fun.*
- 23: em_gss_mam.*
- 24: em_gss_mus.*
- 25: em_gss_other.*
- 26: em_gss_pro.*
- 27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	434.4	9.6	566	12	BG834418
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5	395.6	8.8	701	13	B1147240
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13	327.8	7.3	518	14	BM826384
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16	312	6.9	1080	13	BI221221
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AGENCY: 8414907 NIH_MGC_100 Homo sapiens cdna clone IMAGE:6271971
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BQ645685
AGENCY: 8414907 NIH_MGC_100 Homo sapiens cdna clone IMAGE:6271971
5', mRNA sequence.
ACCESSION
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SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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BQ920393 AGENCOURT
BI664268 603289021
BM626308 170006874
BC205053 RST24472
EC026509 Mus muscu
BI843062 fr02f04.y
AW013471 pc071KS.W
BJ001995 BJ001995

Human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 947)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2449 row: j column: 04
High quality sequence start: 18
High quality sequence stop: 645.
Location/Qualifiers

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ACCESSION AL596779
VERSION AL596779
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 655)
AUTHORS Poustka, A., Wellenreuther, R., Mewes, H.W., Well, B. and Wiemann, S.).
TITLE EST (Poustka, A., Wellenreuther, R., Mewes, H.W., Well, B. and Wiemann, S.).
JOURNAL Unpublished (1999)
COMMENT Contact: Poustka A.J.
Department Leirach
Max-Planck-Institute for Molecular Genetics
Innestrasse 73, 14195 Berlin, Germany
Tel: +49-30-84131623
Fax: +49-30-84131128
Email: poustka@mpimg-berlin-dahlem.mpg.de
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZp451H201) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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Location/Qualifiers
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VERSION BG834418.1 GI:14199678
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 566)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keeler,J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACACGCTATGACCAT
BACKWARD: GTTTTCCAGTCACGAGC
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Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
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Query Match 9.6%; Score 434.4; DB 12; Length 566;
Best Local Similarity 85.6%; Pred. No. 7.4e-91;
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QY 3072 CCTGTGGATGTGGTGGGATCTCCCATCAGCTTCTTTTGGAGCGGACACCATGGTCACT 3131
D 302 CCTGTGGACGTGGCGCGGTCTCTTATCGGCTTCTTTGAGCAGACGCCATCGGAACCT 361
QY 3132 GCTAAACCGCTTCTCAAGAGACACAGCGTGTGAGCTTGGAGCTTCCAGACAATCCG 3191
D 362 GCTGAACCGCTTCTCGAAGAGACAGACATAGTGGATGGGATCCACAGACAGATGG 421
QY 3192 GTCCCTGTGATGTACGCTTTGGACTCTCTGGAGGTGACGCTGGTGGCTGGCAGTGGCTAC 3251
D 422 GTCTTTGTGATGTATGCTTCCGGCTCTCTGGAAGTGGCTGGTGTGACAGTGGCCAC 481
QY 3252 CCCACTGGCCACTTGGCCATCTCCGCACTGTTTCTCTCTAGCTGGGTTCAGAGCCCT 3311
D 482 CCCACTGGCTGTGTGGCGCGTCTGCTCTGCTCTATGCTGGTGGTGGTTCAGGCGCT 541
QY 3312 GTATGTGTTAGCTCATGCCAGCT 3335
D 542 GTATGTGGCCAGCTGTGCCAGCT 565

RESULT 4
BG610482 558 bp mRNA linear EST 17-APR-2001
LOCUS 326419 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
DEFINITION BG610482
ACCESSION BG610482
VERSION BG610482.1 GI:13660461
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 558)
AUTHORS Stone,R.T., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Fahrenkrug,S.C., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keeler,J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACACGCTATGACCAT
BACKWARD: GTTTTCCAGTCACGAGC
Plate: 113 row: H column: 23
Seq primer: ATTTAGTGACATATAG.
FEATURES
Location/Qualifiers
1..558
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10p"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT 83 a 185 c 166 g 132 t
ORIGIN
```



```

602054722F1 NCI_CGAP_SC2 Mus musculus cDNA clone IMAGE:4193812 5',
mRNA sequence.
DEFINITION BF539254
ACCESSION BF539254.1 GI:11626635
VERSION EST
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 838)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rga@pds-rcmail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9526 row: 1 column: 05
High quality sequence stop: 563.
FEATURES
    source
        location/Qualifiers
            1..838
                /organism="Mus musculus"
                /strain="FVB/N"
                /db_xref="taxon:10090"
                /clone="IMAGE:4193812"
                /clone_lib="NCI_CGAP_SC2"
                /lab_host="DH10B (TI phage-resistant)"
                /note="Organ: salivary gland; Vector: pcMV-SPORT6; Site:1:
                NotI; Site:2: SalI; Cloned unidirectionally. Primer: Oligo
                dt. Average insert size 1.3 kb. Constructed by Life
                Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 160 a 236 c 252 g 170 t
ORIGIN

Query Match 8.7%; Score 393.4; DB 12; Length 838;
Best Local Similarity 76.5%; Pred. No. 3.7e-81;
Matches 559; Conservative 0; Mismatches 166; Indels 6; Gaps 6;

QY 1 ATGCCCGCGCTGCTGAGCCCTGGCGGGGAGGGGCTGTGGAACACAGACAGCCCTGAA 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 32 ATGCCACGCTGGAGAGACAGTGGCGGGCTGTGAGGCTGTGGAACACAGACAGCAGG 91
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 CCTGCCCGCCACAGCCTGTGAGCCTGTCTCTGTGAGACAGCAGGGTGTGGTACCC 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 92 CCTGCGGCGCTATCATTGCTCAGCCTGTGCTT-GTGAGACCGCGCAGCTGGGTGCC 150
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 CCCATGTACCTCTGGTCTTGGTCCCATCTACTCTCTCTTCATCCACACCATGCGCGG 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 151 CCCATGTACCTCTGGTCTTGGTCCCATCTACTCTCTCTATCCATCGCCATGCGCGG 210
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 GGCTACTCCGGATGCCACCTCTTCAAGCAAGATGTGTGTGATTGCGCCTCAT 240
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 211 TGCTACTCCGGATGTCCACCTCTTCAAAACCAAAATGTGTGGCTTGGCCCTCATC 270
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 GTCTGTGTACCTCCAGCGTGGCTGTCTTTGGAAATCCACAGGAAACCCCTGAG 300
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 271 CTCTGTGTATACCTTCAACGTGGCGGCTGTCTGTGAGGATCCACCGCGGTGCCCCAG 330
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 GCCCGAGATTCCTATTCATCTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 331 GCCCGAGAGCTTCTATTCACCTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 389
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 CTGATTTCACCGAGAGAAAGGAGTCCAGTCTATCTGTGTGTGTGTGTGTGTGTGT 420
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 390 CTGATCCACATGAGAGAGAGAGAGAGTCCGTGTATCCGGGTG-TGTTCCGGTACTGG 448
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 421 CTCTCTGTCTTCTCTGTGCGAGTACCAAGCTGTGCCAGCAGCGCTCCGAGCGGGTTC 480
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 449 CTGCTCTGCTGCTATCTTCCAGGAATCAACACTGTGCAGCAGCCCTCTGCAGGAACTTC 508
QY 481 CAGAGCGACCTGTGCGCCACCTGTCTACCTACCTATGCTGTCTCTGTGTGGCAGCAG 540
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 509 CGTCAGGAGCCCTCCACCA-CTGGCCACTACCTGTGCTGTGCTGTGCTGTGCTGTG 566
QY 541 TTGTGCTGTCTGCTGCGGATCAACCCCTCTTCTCCCTGAAGACCCCGCAGCAGTCT 600
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 567 CTGGTGTCTGCTGTCTGTGTGACGACGAGCAGCTTCTTCTCGGAAGACTCCAGCAGCAT-G 625
QY 601 AACCCCTTCCAGAGACTGGGCGAGCCTTCCCTTCCAAAGCCACGTTCTGTGGTGGTTC 660
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 626 AATCCGTGTCCAGAGGCTGAGGCTCTTCTCCCTCCAGGGCATGTACTGTGGTGGCTCT 685
QY 661 GCCTTGGTGTGAGGGGATACAGAGGACCTGAGACCAAAAGACCTCTGTGCTGTGGG 720
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 686 GGACTGTATGGAAGGCTACAAAAGGCTGTGGGACCAAGACCCCGTCACTTTGGGG 745
QY 721 AGAGAAACTC 731
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 746 AGAGAAACTC 756

RESULT 7
LOCUS BI338028 603 bp mRNA linear EST 30-JUL-2001
DEFINITION 361675 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BI338028
VERSION BI338028.1 GI:15031311
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 603)
AUTHORS Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
and Keele, J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCAGTCAGCAGC
Plate: 129 row: N column: 14
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
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        /db_xref="taxon:9823"
        /clone_lib="MARC 1P1G"
        /tissue_type="pooled"
        /lab_host="DH10B"
        /note="vector: pcMV SPORT6; Site:1: NotI; Site:2: SalI;
        Library made from pooled tissue from day 11, 13, 15, 20,
        and 30 embryos."
BASE COUNT 94 a 206 c 173 g 130 t
ORIGIN

Query Match 8.7%; Score 392.8; DB 13; Length 603;
Best Local Similarity 82.9%; Pred. No. 4.3e-81;
Matches 461; Conservative 0; Mismatches 92; Indels 3; Gaps 1;

QY 1 ATGCCCGCGCTGCTGAGCCCTGCGGGGCGAGGGGTCTGGAACACAGACAGCCTCAA 60

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|||||
51 ATGGCGCGCGCGCGAGCCCTCGCGGGCC---CGGCTGTGAACACAGACGAGCGCTGG 107
Db

|||||
61 CTTGGCGCCACACAGCTGCTGAGCCCTGTGCTTCTGAGAACACAGAGGCTGTGGTACC 120
QY

|||||
108 CTTGGCGCGCGCGCGAGCTGCTGAGCTGTGCTTCTGAAAACGCGAGGGTGTGGTGCC 167
Db

|||||
121 CCATGTAATCTCTGGTCTCTGGTCCCATCTACCTCTCTTCCATCCACACACATGGCCGG 180
QY

|||||
168 CCATGTAATCTCTGGTCTCTGGTCCCATCTACCTCTCTTCCATCCACACACATGGCCGG 227
Db

|||||
181 GGCTACCTCCGATGTCGCCACTCTTCAAGCAAGATGCTGTGATGCTGTGATGCTGTGATG 240
QY

|||||
228 GGCTACCTCCAGATGTCGCCACTCTTCAAGCAAGATGCTGTGATGCTGTGATGCTGTGATG 287
Db

|||||
241 GTCTGTGTACCTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY

|||||
288 GTCTGTGTACCTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 347
Db

|||||
301 GCGCCAGAAATCTCTATCTACTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY

|||||
348 GCGCTGAGTCTCTATATACCCACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 407
Db

|||||
361 CTGATTCACACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
QY

|||||
408 CTGATCCACTTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 467
Db

|||||
421 CTTCTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY

|||||
468 CTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 527
Db

|||||
481 CAGAGGAGCCCTGCTGCGCCACCTGCTCCACTACCTATGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY

|||||
528 CAGGAGGAGCCCTGCTGCGCCACCTGCTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 587
Db

|||||
541 TTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 556
QY

|||||
588 TTTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 603
Db

RESULT 8
U66674
LOCUS U66674 Homo sapiens clone EST90757 mRNA sequence. HTC 23-JUL-2001
DEFINITION Homo sapiens clone EST90757 mRNA sequence.
ACCESSION U66674
VERSION U66674.1 GI:1906559
KEYWORDS HTC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 1977)
AUTHORS Allikmets R., Gerrard, B., and Dean, M.
TITLE Characterization of the human ABC superfamily: isolation and
JOURNAL mapping of 21 new genes using the expressed sequence tags database
MEDLINE Hum. Mol. Genet. 5 (10), 1649-1655 (1996)
PUBMED 97049974
8894702
REFERENCE 2 (bases 1 to 1977)
AUTHORS Allikmets R., Gerrard, B., and Dean, M.
TITLE Direct Submission
JOURNAL Submitted (12-AUG-1996) Human Genetics Section, National Cancer
INSTITUTE, NCI-FCRDC, Frederick, MD 21702, USA
FEATURES
source
Location/Qualifiers
1..1977
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="EST90757"
/note="similar to ATP-binding cassette transporter"
BASE COUNT 450 a 537 c 513 g 469 t 8 others
ORIGIN
Query Match 8.5%; Score 384.6; DB 11; Length 1977;

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Best Local Similarity 55.8%; Pred. No. 6.6e-79;
Matches 811; Conservative 0; Mismatches 631; Indels 12; Gaps 4;
QY 3063 CCAGAGGCTCTCTGGGATGTGTGGATCTCCCATCAGCTTCTTTGAGCGGACACACCAT 3122
Db
6 CCAGGCACTGCTGCACAAACAGATACGCTGCCACAGCTCTCTTTGACACACACACATC 65
QY 3123 TGGTCACTCTGTAACCGCTTCTCAAGAGACAGACACAGGTTGACGTTGGACATTCACGA 3182
Db
66 AGCGCGATCTGTAACCTGCTTCTCAAGAGACATCTATGTGCGCTTGATGAGGTCTTGCGC 125
QY 3183 CAAACTCCGCTCCCTGCTGATGATGAGCTTTGGACTCTCTGAGGTGACGCTTGGTGGC 3242
Db
126 CTTGTCACCTTCAACGCGCTCAATTTCTTCAAGGCCATCTCCACTCTTTGGTGCAT 185
QY 3243 AGTGGCTTACCCCACTGG-----CCACTGTGGCCATCTTCCCACTGTTTCTCTCTACG 3295
Db
186 CATGGCCAGCAGCAGCGATCTTNACTTGTGGTNANTGTCCTTGGTNGTGTCTTACA 245
QY 3296 CTGGGTTTACAGCCTGTATGTGTTAGCTCATGCCAGCTGAGACGCTTGGAGTCAAGCCA 3355
Db
246 CTTAGTGTGACGCTTCTATGACGCCACATCAAGCAACTGAAGCGGCTGGAATCAGTCA 305
QY 3356 GCTACTGCTGTGCTGCTCCACATGCTGAGAGCTTCCAGGGGAGCAGACGTGTCGGG 3415
Db
306 GCGG-TCACTTCTACTCTCCACTTTTGGAGACAGTGAAGTGTGCGGCTGTCATCGGG 364
QY 3416 CATTCCGAACCCAGGCGCCCTTTGTGGCTCAGAAACATGTCGCGTAGATCAAAAGCCAGA 3475
Db
365 CTTACAAACCCAGCGGGATTTGAGATCATCATGATGATTAAGTGTGATGCCAACAGA 424
QY 3476 GGATCAGTTTCCGCGACTGCTGGCTGACAGGTGGCTTGGCGGCAATGTGGAGCTCTCTGG 3535
Db
425 GAAAGTGTCTACCCCTACATCATCTCAACCGTGGCTGAGCATCGGAGTGTGCTGG 484
QY 3536 GGAATGCGCTGCTGTTGACAGCGCCACAGTGTGCTGCTGAGCAAAAGCCACCTCAGTG 3595
Db
485 GGAATGCGCTGCTGCTTGTGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 544
QY 3596 CTGGCTGCTGGGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3655
Db
545 CGGGCTGCTGGGCTT-CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 603
QY 3656 TTGTTCCGAACCTGACAGACCTAGAGAACAGATCTGCTGCTGCTGCTGCTGCTGCTGCTG 3715
Db
604 TGATACGAATGATGTCAGATTTGGAATCTAACTCGTGGCTGTGGAGAGGCTCAAGGAGT 663
QY 3716 ATGCTTGGAGCGCCCAAGGAGCTCCCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3775
Db
664 ACTCCAAGACAGACAGAGAGGCGCCCTTGGTGGTG---GAACAGCGCCCTCCCGAAGGT 720
QY 3776 GGCTCAGGCGCGGACAGATCGAGTTCGGGACTTTGGGCTAAGATGCGGACCTGAGCTCC 3835
Db
721 TGGCCCCACGTGGGAGGTGGAGTTCGGGAATTAATCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 3836 CGCTGCTGTGACGGGCTGCTTCAAGATCCACGAGGAGAGAGTGGGCTGCTGCTGCTGCTG 3895
Db
781 ACCTGCTGTGAGAGACCTGAGTCTGATGTCACGTGTCAGGAGAGGAGTGGGATCTGG 840
QY 3896 GCAGGACCGGCGGAGGAGTCTCCCTGCGCAGTGGGCTGCTGCGGCTCCAGGAGGAGCAG 3955
Db
841 GCGGCACTGGGCTGCAAGTCTTCCATGACCTTTTGGCTTTCGCGGAGGAGGAGGAGGAGG 900
QY 3956 CTGAGGCTGGGATCTGATCGAGGCTGCTCCCATTCGCCAGTGGGCTGCTGCTGCTGCTGCTG 4015
Db
901 CAAAGGCTGAATCCCATTTGAGGCTCAATGTGACAGACATCGGCTCCATGAGCTGC 960
QY 4016 GCTCCAGGATCAGCATCATCCCCAGGAGGCCATCTCTGTTCCCTGCTGCTGCTGCTGCTGCTG 4075
Db
961 GCTCTCAGCTGACCATCATCCCCAGGAGGCCATCTGTTCTCGGGGAGGAGGAGGAGGAGG 1020
QY 4076 ACCTGCACTGCTGACGAGGAGCTCGGAGAGGCTATCTGCGGAGGAGGAGGAGGAGGAGG 4135

```


No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions.*

BASE COUNT 52 a 105 c 79 g 78 t

ORIGIN

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Query Match . . . . . 7.0%; Score 314; DB 13; Length 314;
Best Local Similarity 100.0%; Pred. No. 8.9e-63;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TTCATCCTACTGTGTGGCTACACGATGAGCTTCGAGTGTCTCTGATTCCACACCGAGA 376
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 TTCATCCTACTGTGTGGCTACACGATGAGCTTCGAGTGTCTCTGATTCCACACCGAGA 60

QY 377 GGAAAAAGGGAGTCCAGTCATCTGGAGTGTGTTGGTTACTGGCTTCTCTGCTTTGTCT 436
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 GGAAAAAGGGAGTCCAGTCATCTGGAGTGTGTTGGTTACTGGCTTCTCTGCTTTGTCT 120

QY 437 TGCCAGCTACCAAGCTGCCCGAGCGCTCCGAGCGGGCTTCCAGAGCGACCTGTCC 496
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 TGCCAGCTACCAAGCTGCCCGAGCGCTCCGAGCGGGCTTCCAGAGCGACCTGTCC 180

QY 497 GCCACCTGTCCACCTAGCTATGCTGTCTGTGTGGTGGCACAGTTTGTGCTGCTGCC 556
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 GCCACCTGTCCACCTAGCTATGCTGTCTGTGTGGTGGCACAGTTTGTGCTGCTGCC 240

QY 557 TGGCGGATCAACCCCTTCTTCCCTGAAGACCCCGACAGTCTTAACCCCTGTCCAGAGA 616
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 TGGCGGATCAACCCCTTCTTCCCTGAAGACCCCGACAGTCTTAACCCCTGTCCAGAGA 300

QY 617 CTGGGGCAGCCTTC 630
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Db 301 CTGGGGCAGCCTTC 314
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Search completed: December 18, 2002, 21:26:58
Job time : 3852.31 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:49:35 ; Search time 109.187 Seconds
(without alignments)
16388.716 Million cell updates/sec

Title: US-09-647-140A-7

Perfect score: 4509

Sequence: 1 atggccgcgcctgctgagcc.....cccagagtcagcctggctc 4509

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 356696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 713392

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA.*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
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- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
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- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3030	67.2	5728	10	US-09-917-800A-479
2	1076.8	23.9	1936	10	US-09-880-107-3832
3	713	15.8	5300	10	US-09-880-107-3373
4	693	15.4	4918	10	US-09-917-800A-1578
5	384.6	8.5	1977	10	US-09-954-456-804
6	384.6	8.5	1977	10	US-09-880-107-3407
7	384.6	8.5	1977	10	US-09-967-768A-190
8	350.2	7.8	1448	10	US-09-925-299-157
9	336.6	7.5	4551	9	US-09-938-842A-1674
10	271.4	6.0	3786	9	US-10-012-896-1006
11	271.4	6.0	4395	9	US-10-012-896-1007
12	271.4	6.0	6140	9	US-10-012-896-536
13	271.4	6.0	6140	10	US-09-759-143-536
14	271.4	6.0	6140	10	US-09-780-669-536
15	271.4	6.0	6140	10	US-09-822-827-536
16	264.2	5.9	6082	9	US-10-012-896-535
17	264.2	5.9	6082	10	US-09-759-143-535
18	264.2	5.9	6082	10	US-09-780-669-535
19	264.2	5.9	6082	10	US-09-822-827-535

20	262.4	5.8	4872	9	US-09-938-842A-436
21	246.6	5.5	4869	9	US-09-938-842A-1392
22	229	5.1	1019	10	US-09-925-297-247
23	196.8	4.4	4545	9	US-09-938-842A-55
24	161.6	3.6	1812	10	US-09-815-242-4147
25	158.6	3.5	744	10	US-09-833-381-293
26	156	3.5	88421	9	US-09-976-059-1
27	133.4	3.0	2298	10	US-09-795-693-16
28	133.4	3.0	3408	10	US-09-795-693-16
29	133.4	3.0	3512	9	US-10-072-621-1
30	130.4	2.9	2172	10	US-09-815-242-4038
31	128.2	2.8	1074	9	US-10-012-896-824
32	128.2	2.8	1074	10	US-09-759-143-824
33	128.2	2.8	1074	10	US-09-780-669-824
34	128.2	2.8	1074	10	US-09-822-827-824
35	125.8	2.8	1427	10	US-09-925-300-613
36	121.6	2.7	3289	10	US-09-739-254-11
37	121.6	2.7	3289	10	US-09-904-615-11
38	118.4	2.6	4189	10	US-09-866-866A-5
39	113.2	2.5	3912	10	US-09-917-800A-1560
40	112.8	2.5	4369	10	US-09-769-097-1
41	112.8	2.5	4425	10	US-09-769-097-3
42	110.8	2.5	4254	10	US-09-917-800A-1424
43	110.2	2.4	1076	9	US-09-764-884-13
44	108	2.4	4788	10	US-09-866-866A-7
45	107.8	2.4	3069	10	US-09-756-095-105

ALIGNMENTS

RESULT 1

US-09-917-800A-479
; Sequence 479, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 479
; LENGTH: 5728
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 AB010466
US-09-917-800A-479

Sequence 436, App
Sequence 1392, Ap
Sequence 247, App
Sequence 55, Appl
Sequence 4147, Ap
Sequence 293, App
Sequence 1, Appli
Sequence 18, Appl
Sequence 16, Appl
Sequence 1, Appli
Sequence 4038, Ap
Sequence 824, App
Sequence 824, App
Sequence 824, App
Sequence 824, App
Sequence 613, App
Sequence 11, Appl
Sequence 11, Appl
Sequence 5, Appli
Sequence 1560, Ap
Sequence 1, Appli
Sequence 3, Appli
Sequence 1424, Ap
Sequence 13, Appl
Sequence 7, Appli
Sequence 105, App

Query Match					
Best Local Similarity		67.2%	Score 3030;	DB 10;	Length 5728;
Matches 3629; Conservative		80.3%;	Pred. No. 0;	Mismatches 850;	Indels 39; Gaps
Qy	1	ATGCGCGGCTGCTGAGCCCTGGCGGGCAGGGGTCTGAACACAGACAGAGCTCAA	60		
Db	43	ATGCCACGGCTGAGAGTCTCTGGCAGGCCTGAGGGTCTGGAACACAGAACAGGAG	102		
Qy	61	CCTGCGCCACCAGCCTGCTGAGCCCTGTCTTCCTGAGAACAGCAGGGTCTGGGTACCC	120		
Db	103	CCTGTGCGCTATCACATTGCTCAACCTGTCTCTCGAGCCGCCGGAGCTGGGTGCC	162		
Qy	121	CCCATGTACTCTGGGTCTTGTTGGTTCCTTACCTCTCTTCATCCACACATAGCCGG	180		
Db	163	CCAATGTACCTCTGGGTCTTGCGCCCATCTACCTCTCTAGCATCATCGCATGCTGC	222		
Qy	181	GGCTACCTCCGGATGCCCCACTCTTCAAGCCAAGATGGTCTTGGATTGCCCTCAT	240		
Db	223	TGCTACCTCCGGATGCCC GCCCTCTTCAAAATCAAAATGGTCTCGGTCTTGCCCTCATC	282		
Qy	241	GTCCTGTGTACCTCCAGCGTGGCTGTGCTCTTTTGGAAAATCCAAACAGGAACGCTCAG	300		
Db	283	CTTCTCTACACCTTCACGGCGCGTGCCTCTCTGAGGATCCACGGGGCATGCCCCAG	342		
Qy	301	GCCCCAAGTAATCTCATPTCATCTACTGTGTGGCTCAACCAGATGAGCTTCGCATGTTC	360		
Db	343	GCCCCAGAGCTTCTCATTTCACTACCTGACCGTGTGGCTCAACCACCATGAGCTTCGCCACCTTC	402		
Qy	361	CTGATTACACCGAGAGAAAAAGGAGTCCAGTATCTGGCTCAACCAGATGAGCTTCGCATGTTC	420		
Db	403	CTGATCACATGAGAGAAGAAAGGGGGTCCGTGTCATCTGGGTCTTGTCTCGGTACTGG	462		
Qy	421	CTTCTCTGCTTTGCTTGTGCCAGCTACCAAGCTGCCAGAGCGCTCCGGAGCGSGTTC	480		
Db	463	CTGCTCTGCTCTGTGTGCGCGCATCGACTGTCCAGAGCGCTCCGAGAGGAGCTTC	522		
Qy	481	CAGAGCAGCCCTCTGCGCCACCTGTCCACCTACCTATGCCCTGTCTGCTGGTGGTACTGG	540		
Db	523	CGCAGGAGCGCCCTCCACACCTTGGCCACTACCTGTGCTTCTCCCTGGTGGTGGCAGAG	582		
Qy	541	TTTGTGCTGTCTGCTTGGCGGATCAACCCCTCTTCTCCCTGAAGACCCCGCAGAGCTCT	600		
Db	583	CTGGTGTCTGTCTGTGTGATGACCAAGCACCCCTTCTTCTCGGAAGACTCCAAGCCATTTG	642		
Qy	601	AACCCCTGTCCAGAGACTGGGGCAGCTTCCCTCCAAAGCCACGCTCTGCTGGGTCTTCT	660		
Db	643	ANTCCATGTCAGAGCGCAGGCTCTTTCCCTCCAGGCCATGTTCTGCTGGGCTCTCT	702		
Qy	661	GGCCTGGTCTGGAGGGATACAGGAGGCCACTGAGACAAAGACCTCTGCTCGCTTGGG	720		
Db	703	GGACTGTATGGAAGGCTTACAGAAACTGCTGGGGCCAAAGACCTCTGCTCACTTTGAG	762		
Qy	721	AGAGAAATCTCTCAGAAACTTGTITTCGGCTTGTAAGAGGAGTGGATGAGGAACCGC	780		
Db	763	AGAGAAATCTCTCAGAAACTTGTITTCAGCTGGAAGAGAGATGAGGAGGAACCTTC	822		
Qy	781	AGTGACGCCGAGGACACAACAGGCAATAGCATTTAAAGGAAGGCGCAGTGGCATG	840		
Db	823	AGTGAGCTGCGGGGGCAC-----AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	858		
Qy	841	AAGGCTCCAGAGACCGAGCCCTCTCTACGGCAAGAGGAGCGCAGTGGCGCCACTGCTG	900		
Db	859	GGGACCCCGAGACAGAGGCTTCTCTGACGCCAGAGAGAGGCCAGCGGGCCGCTGCTC	918		
Qy	901	AAGGCCATGCGAGGTGTTCATTTACTTCTCTCTCTGGGAGCCCTCAGCCTCATCATC	960		
Db	919	AGGGTATCTGGCGTGTGTTCGGTCCACTTTCTCTGCTGGGGACCCCTCAGCCTGTGCTATT	978		
Qy	961	AGTGTATGCTTTCAGTGTCACTGTCCCAAGCTGCTCAGCCTTTCTCTGGAGTATTATGGT	1020		
Db	979	AGGGATGCTTTCAGTGTGCTGTTCAGAGCTCTCAGTCTGTTCTGGAGTTCATGGC	1038		

Db 2116 GCTTGGTCCACAATACCTCTCTGTGTGGAGAAATGTGTCTTCAGGACGAGCTGGATCTG 2175
QY 2158 CCTGGCTGGAGAGAGTACTAGAACCTCTGTGCCCTGCAGCCAGATGTGTGACAGCTTCCCT 2217
Db 2176 CAAATGTTGCGAGAAATTTCTAGAACCTCTGTGCTTGGGTCTGTATGTGGCCAGCTTCCCT 2235
QY 2218 GAGGAAATCCACACTTCAATTTGGGAGCAGGCGCATGAATCTCTCGGAGGCCAGAGCAG 2277
Db 2236 CGAGAGTTACACCCAGTAGGGAGGAGGAGGCATGAATCTTCTGGGGGCCAGAGCAG 2295
QY 2278 CGGCTGAGCCTTGGCCGGGCTGTATACAGAAAGCAGCTGTGTACTCTGTGATGACCCC 2337
Db 2296 CGGCTGAGCTTGGCTCGGCTGTGTACAGAGGCTGTGTGTACTGTGATGATGACCCC 2355
QY 2338 CTGGGGGCCCTGGATGGCCACAGTTGGCCAGCATGTCTTCAACACAGGTCAATGGGCTGTGT 2397
Db 2356 CTAGCAGCCCTGGATGCGCATGTACGCCAGGAAGTCTTCAACACAGGTCAATGGCCCACT 2415
QY 2398 GGGCTACTCCAGGGAACACAGGATTTCTGTGACGACGCACTCCACATCTGTGCCCAG 2457
Db 2416 GGACTTCTCCAAAGTACGACTCGGATCTGTGAACACACACGCTGCATGTCTGCCCCAA 2475
QY 2458 GCTGATTTGGATCATAGTCTGCAAAATGGGCCATCGCAGAGATGGTTCTTACCAGGAG 2517
Db 2476 GCTGACAGATCTGCTGTGCTGCCAATGGGACCATCGCAGAGATGGGCTCTTACCAGAC 2535
QY 2518 CTCTGACAGAGAAAGGGGCCCTCTGTGTCTTCTGATCAAGCAGACAGCAGCAGAGAT 2577
Db 2536 CTCTGACATAGGAAGGAGCCCTGTGTGTCTTCTGGATGGAGCCAGCAGCAGCTCAGGC 2595
QY 2578 AGAGGAGAGAGAAACAGACCTTGGGACACAGCACCAGGACCCAGAGGCACTCTGA 2637
Db 2596 GAAGGAGAGAGAAAGCACTGTCTGACACCACAGTAGTATGATGACCTTGGAGGCTTTCTGA 2655
QY 2638 GGCAGAGGCCCGAGCTTAGACGCGAGAGG-----TCCATCAAGTCACTCTCTCAGAGAG 2691
Db 2656 GGTGGAGGCCCGAGCAGACAGAGAGAGGAGCCAGACCCAGTGCAGGAGCCCTGTGAAG 2715
QY 2692 GACCGTACCACTCTCAGAAAGCCAGACAGAGTGTCTCTGATGACCCCTGACAGGCGCAGGA 2751
Db 2716 GGCAGT---ACTTCAGAGGCAAGATGAGGAGGCTCTCTGTGATGACCTTGGAGGCTACTGA 2772
QY 2752 TGGCAGCAGAAAGGACAGCATCCAATACGCGAGGTTGAAGGCCACAGTGCACCTGGCC 2811
Db 2773 CTGACAGCAGAGAGAGCAGTGTGCGATGTGGCGGGTGAAGAGCGCCACATACCTGAGC 2832
QY 2812 TACCTGGCTGCGGTGGGCACCCCTCTGTCTCTACGCACTTCTCTCTCTCTCTGCGCAG 2871
Db 2833 TACCTGGCGGGTGGGCACACCCCTCTGCACTTACACCTGTCTCTCTCTCTGCGCAG 2892
QY 2872 CAACTGGCTCTCTCTGCGGGGTACTGTGCTGAGCCTGTGGGGGAGCAGCCCTGCAGTA 2931
Db 2893 CAACTGGCGCTCTCTGCAAGAGCTACTGTGCTGAGCCTCTGGGCGAGCAGCCCGTCTGT 2952
QY 2932 GGTGGCAGCAGACGAGGAGCCCTCGTGGCGGGATCTTTCGGGCTCTCTGCGCTGTCTC 2991
Db 2953 GATGGGAGCAGATGCAATTCAGCCCTCGTGGGCTCCATCTTGGACTCTCTGGCTGTGTG 3012
QY 2992 CAAAGCAATGGGCTGTCT 3051
Db 3013 CAAAGCAATGGGCTGTCT 3072
QY 3052 AGTTGTCTTCTCAGAGGCTCTCTCTGAGATGTGGTGGATCTCCCATCAGCTTCTTTGAG 3111
Db 3073 TGCCTGTCTTCTCAGGAGCTCTCTCTGAGAGCTGTCTCTCTCTCTCTCTCTCTCTCTCT 3132
QY 3112 CGGACACCAATGTGTCT 3171
Db 3133 CGCACACAGTCTGGGAACT 3192
QY 3172 GACATTCAGACAACTCCGCT 3231
Db 3192 GCGGAAACCCAGATCT 3252

Db 3193 GACATCCACAGACAGATGAGGACCCCTGCTGACCTATGCTTGGACTCTCTGGAGTTGGC 3252
QY 3232 CTGGTGGTGGCAGTGGCTACCCCACTGGCCACTGTGGCCACTCTCTGGCCACTGTCTCTCTCT 3291
Db 3253 CTGGCAGTGTGATGGCCACACCACTGGCTATTTGTGGCCACTCTCTCTCTCTCTCTCTCTCT 3312
QY 3292 TAGGCTGGGTTTCAGAGCCCTGTATGTGTGTAGCTCATGCCAGCTGAGACAGCTTGGAGTCA 3351
Db 3313 TATGCTGGGTTTCAGAGCCCTTACGTGGCCACATGTGGCCAGCTGAGACGCTGGAGTCG 3372
QY 3352 GCAGCTACTCTGCTCTGCTCCACATGGCTGAGAGCTTCCAGGCGCAGCAGACAGTGTCT 3411
Db 3373 GCCAGTACTCTCTCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3432
QY 3412 CGGGCAATCCGAACCCAGGCCCCCTTTTGTGGCTCAGAAACAATGCTCCGCTAGATGAAGC 3471
Db 3433 AGGGCCCTCCAGCCGCCAGGGGCCCTTACAGCTCAGCAGCATGCCCTCATGGATGAGAAC 3492
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QY 3532 CTGGGAATGGCTGTGTGTCAGCGCCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3591
Db 3553 CTGGGAATGGCTGTGTGTCAGCGCTTACATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3612
QY 3592 AGTGTGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3651
Db 3613 AGTGTGGGCTCTGCGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3672
QY 3652 TGGGTTGTTGCAATGTCAGACACTTAGAACAAGCATGTGTGCTGCTGCTGCTGCTGCTGCT 3711
Db 3673 TGGGTTGCTCGGAGCTGTCAGATCTGGAGAACAGCATGGTGGCGCTGGAGCGAGTACAG 3732
QY 3712 GACTATGCTGGAGCCCAAGAGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3771
Db 3733 GACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3792
QY 3772 CCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3831
Db 3793 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3852
QY 3832 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3891
Db 3853 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3912
QY 3892 GTTGGCAGACCGGGCAGGGAAGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3951
Db 3913 GTGGCAGACAGGCGCGGAGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3972
QY 3952 GCAGCTGAGGGTGGATCTGATCGAGGGGCTCCCATTTGCCACCTGGGGCTTCCACACA 4011
Db 3973 GCCACTGAGGGTGGATTTGGATCGATGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4032
QY 4012 CTGCGCTCCAGATCAGATCATATCCCGCAGAGCCCATCTCTGCTGCTGCTGCTGCTGCT 4071
Db 4033 CTGCGGTTCCAGATCAGATCATATCCCGCAGAGCCCTGCTGCTGCTGCTGCTGCTGCT 4092
QY 4072 ATGAACCTGACCTCTGTCAGGAGCAGCTCGGAGGCTATCTGGGCGAGCCCTTGGAGAC 4131
Db 4093 ATGAACCTGAGCCTGCTTCCAGGAGAACAGATGAGGGCATCTGGGCGAGCGCTTGGAGAC 4152
QY 4132 GTGAGCTCAAAGCTTGGTGGCCAGCCTTGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 4191
Db 4153 GTGAGCTCAAAGCCTTCTGTCAGGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4212
QY 4192 CGAGGCGGAGCCTGAGCCTGGGCGCAGAAACAGCTCTCTGCTGCTGCTGCTGCTGCTGCT 4251
Db 4213 CAGGAGAGATGACCTGAGTGTGGGTGAGAAAGCAGCTCTCTGCTGCTGCTGCTGCTGCT 4272
QY 4252 CGGAGACCCAGATCTCTATCTGTCAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4311
Db 4273 CGGAAACCCAGATCTCTATCTGATGAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4332

Db 1261 GACCCCTGGAGGAGCTCAGATGAGGCCATGCTCGGAGCTGGTTTGCACAGTGCAC 1320
QY 4356 TGTGCTGCCATGTCACCGCTCGCTCCGCTGATGAGTGTGCCCGGGTTCCTGCTCAT 4415
Db 1321 TGTGCTGCTCATTTGCCCGCTCGCTCCGCTGATGAGTGTGCCCGGGTTCCTGCTCAT 1380
QY 4416 GGACAGGGGAGGTGGGAGAGGCGGAGCGGCCCGGCCAGCTGCTGGCCAGAGGGCCT 4475
Db 1381 GGACAGGGGAGGTGGGAGAGGCGGAGCGGCCCGGCCAGCTGCTGGCCAGAGGGCCT 1440
QY 4476 GTTTTACAGCTGGCCAGGAGTCAAGCTGGTC 4509
Db 1441 GTTTTACAGCTGGCCAGGAGTCAAGCTGGTC 1474

RESULT 3

US-09-880-107-3373

; Sequence 3373, Application US/09880107

; Patent No. US20020142981A1

; GENERAL INFORMATION:

; APPLICANT: Horne, Darci T.

; APPLICANT: Vockley, Joseph G.

; APPLICANT: Scherf, Uwe

; APPLICANT: Gene Logic, Inc.

; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

; FILE REFERENCE: 44921-5028-WO

; CURRENT APPLICATION NUMBER: US/09/880,107

; CURRENT FILING DATE: 2001-06-14

; PRIOR APPLICATION NUMBER: US 60/211,379

; PRIOR FILING DATE: 2000-06-14

; PRIOR APPLICATION NUMBER: US 60/237,054

; PRIOR FILING DATE: 2000-10-02

; NUMBER OF SEQ ID NOS: 3950

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3373

; LENGTH: 5300

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U49248

US-09-880-107-3373

Query Match 15.8%; Score 713; DB 10; Length 5300;
Best local Similarity 51.4%; Pred. No. 8e-166;
Matches 1902; Conservative 0; Mismatches 1695; Indels 102; Gaps 7;

QY 896 TGCTGAAGGCATCTGGCAGGTGTTCCATTCTACCTTCTCTCTGGGACCCCTCAGCCTCA 955
Db 1030 TGATGAAGGCTCTGTTCAAACTTTCTACATGGTGTCTCTGAAATCAFTTCTACTGAAGC 1089
QY 956 TCATCAGTGTGCTTTCAGGTTCCTACTGTCCCAAGCTGCTCAGGCTTTTCTCGAGTTTA 1015
Db 1090 TAGTGAATGACATCTTCAGGTTTGTGAGTCTCAGTGTCTGAATGCTGATCTCCTTTG 1149
QY 1016 TTGFGATGCCAAGCCTCCAGCTCCAGGAGGCTACCTCTCTCGCGTGTGATGTCTCT 1075
Db 1150 CAAGTGACCGGTGACACATATTTGGGATTTGGATATCTCTGTGCAATCTCTTATTCACTG 1209
QY 1076 CAGCTGCCTGCAAAAGCTGTTTTCAGCAGCAGACATCTACAGCTCAAGGTGCGGCAGA 1135
Db 1210 CGGCTCTCATTCAGTCTTTCTGCGCTTCAGTGTATTTTCCAACTGTGCTTCAAGCTGGGTG 1269
QY 1136 TGAGGTTTCGGCTCGGCATCACTGGCTGTTGTACAGAAAGGCTCTGGCTCTGTCCAGCG 1195
Db 1270 TAAAGTACGACAGCTATCATGCTTCTGTATATAGAGGCAATTCACCTATCCAACT 1329
QY 1196 GCTCCAGAAAGGCGAGTGGGCTGATGTGTCATATCTGGTTCGCTCGGACGTGTCAGC 1255
Db 1330 TGGCCAGGAAGGAGTACACCGTTTGGAGAAACAGTGAACCTGTATCTCTGTGGATGCCAGA 1389
QY 1256 GGCTGACCGAGAGGCTCTCTACCTCAACGGGCTGTGGCTCTCGTCTGGATCGTGG 1315
Db 1315

Db 1390 AGCTCATGATGTGACCAACTTTCATGCACATGCTGTGGTCAAGTGTCTTACAGATTCTCT 1449
QY 1316 TCTGCTTCGCTCTATCTCTGCGACCTCTCTGGGGCCCTCCGCCCTCAGTCGCCATCGCTGCTCT 1375
Db 1450 TATCTATCTTCTTCCCTATGAGAGAGTGTGGACCCCTCAGTCTTAGCAGGTGTTGGGGTGA 1509
QY 1376 TCTGAGCCCTCCCTCCCTCTGAAATTTCTTCATCTCCAAGAAAAGAACACCATCAGAGG 1435
Db 1510 TGGTCTGTGAATCCCAATTAATGCGATCTGTCCCAAGAGTAAGAACCATTCAGGTCA 1569
QY 1436 AGCAATAGGCGAAGAGTCAACGGCGACGCTCACCAGCTCTATCTCTCAGGAACTCGA 1495
Db 1570 AAAATATGAAGATAAAGACAAACGTTTAAAGATCATGATGAGATCTTAGTGGATCA 1629
QY 1496 AGACCATCAAGTTCATGCTGGGAGGAGCCCTTTTGGACAGAGTCTGGGCGATCCGAG 1555
Db 1630 AGATCTGAAATATTTTGGCTGGGAACCTTCATTCAGAGACCAAGTACAAAACCTCCGGA 1689
QY 1556 GCCAGGAGCTGGGCGCTTTCGGACCTCCGGCCCTCTCTCTCTGCTGTGCTGCTGCTCT 1615
Db 1690 AGAAGAGCTCAAGAACCTGTGGCCCTTAGTCAACTACAGTGTGTAGTAATATTCGTCT 1749
QY 1616 TCCAACTGTCTACATTTCTGTCGCACCTGCTGTGCTGTGCTGCCACACTCTCTGGTGG --- 1672
Db 1750 TCCAGTTAACTCCAGTCTGTTATCTGTGTCACATTTCTGTTATGCTCTGTTGGATA 1809
QY 1673 CCGAGATCTATGATGACAGAAAGCCTTTGTGACTCTCAGAGTCTCAACATCTCTCA 1732
Db 1810 GCAACAATATTTTGGATGCACAAAGGCGCTTCACCTCCATTAACCTCTTCAATATCTCTG 1869
QY 1733 ACAAGGCCCGAGGCTTTCCTCGCCCTTCTCCATCCACCTCCGTCGTCGAGGCCGCTGCTCT 1792
Db 1870 GCTTTCCCTGAGCATGCTTCCCATGATCTCTCTCCATGCTGCCAGGCGAGTGTTCCTCA 1929
QY 1793 TTGACCGTGTGTCACCTTCTCTGCTGCGTGGAAAGTGTGACCGTGTGCTGTAAGTCAA 1852
Db 1930 CAGAGCGGTAGAGAAGTACTTTGGGAGGGATGACTTGGACACATCTGCCATTCGACATG 1989
QY 1853 GTTCTCTGGAAGCGCTGCCGGAGAGGATTCATACCATACACATGACAGTGCACCTTCGCCCT 1912
Db 1990 ACTGCAATTTTGACAAAGCCATGCAGTTTCTG -----AGGCCCTCTTTACCT 2037
QY 1913 GTTCCAGGAAAGCCCTTCCCTGCTCCACAGAAATAAACCTCAGGTGCCCCAGGCTGTC 1972
Db 2038 GGAACATGATTCCGAGCCAGCCAGATGTGAACCTTGACATATATGGAGGCCAAC 2097
QY 1973 TCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2032
Db 2098 TTGTGCTGTGATAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2157
QY 2033 GGGAGCTGTCAAGCTGGAGGGGTTGCTGAGCATCGAGGCTGTGCTGCTGCTGCTGCTGCTG 2092
Db 2158 GAGAAATGGAATGTCCACGGGCACATACCATCAAGGGCCACCTGCTGCTATGCTCCAC 2217
QY 2093 AGGAGCCTGGGTGAGAACACCTCTGCTGTAGAGAAATGCTGCTGCTGCTGCTGCTGCTGCTG 2152
Db 2218 AGCAGTCTCGATTGAGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 2277
QY 2153 ACCACCTGCTGGAGAGAGTACTAGAGCCTGTGCGCTGCGCCAGCATGTGGACAGCT 2212
Db 2278 ATGAAAGAGGTACCAAGTACTGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2337
QY 2213 TCCCTGAGGGAATCCACACTTCAATTTGGGAGCAGGCGATGAATCTCTCCGAGGCCAGA 2272
Db 2338 TGCCTGGAGGAGATTTGCTGAGATTTGGAGAGAGGGGTATAAATCTTAGTGGGGGTCA 2397
QY 2273 AGCAGCGCTGAGCCTGGCCGGGCTGTATACAGAAAGCAGCTGTGTACCTGCTGGATG 2332
Db 2398 AGCAGCGATCAGCTGCGCAGAGCTACTACCAAAATTTAGACATCTATCTTCTAGATG 2457
QY 2333 ACCCCCTGGGCGCTGTGATGCCCGCAGCTGTGGCCAGCATGTCTTCAACACCATTCATTGGGC 2392
Db 2458 ACCCCCTGCTGCACTGCTATGATAGGAAACATATTTTATAAGGCTCTTGGGCC 2517

Db 4675 CTGGACCCCTTTACTTTATGCGCTAAGGAGCTGGCATTTG 4713

RESULT 4

US-09-917-800A-1578

; Sequence 1578, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917, 800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1578
; LENGTH: 4918
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_012833
US-09-917-800A-1578

Query Match 15.4%; Score 693; DB 10; Length 4918;
Best Local Similarity 51.3%; Pred. No. 6.6e-161;
Matches 1867; Conservative 0; Mismatches 1670; Indels 102; Gaps 7;

QY 956 TCATCAGTGTGCTTTCAGGTTCACTGTCCCAAGCTGCTCAGCGCTTTTCTCGGAGTTTA 1015
Db 1071 TAATACATGACCTTTTGGTGTCTGTAATCCTCAGCTGCTCAAGTGTCTGATCGTTTCG 1130
QY 1016 TTGGTGTATCCAGCCTTCAGCTGGAAGGCTACCTCGCGCTGCTGATGTTCCTCT 1075
Db 1131 TGAAGAGCTCTAATCATACGTGTGGTGTGGCTATATCTGTGCAATCCTATATGTTGCTG 1190
QY 1076 CAGCTCCCTGCAACCTGCTTTTCAGCAGCAGCAATGTACAGCTCAAGCTGCGCAGA 1135
Db 1191 TGACTCTATCCCAATCTTTCTGCTTCAGTCTTACATATGTTTGTGTGGAA 1250
QY 1136 TGAGTTGCGGTGCGGCATCACTGGCTGTGTACAGAAAGGTCTGCTGCTGTCACGCG 1195
Db 1251 TGTGCGTACGCAACACCGTCTATGCTTCGATATATAGAGGCATTGACCTATCTACT 1310
QY 1196 GCTCCAGAAAGGCGAGTGGGCTGATGTGTCATATCTGGTGTGGCTGGACGTGCGAGC 1255
Db 1311 TGGCTAGGAAGCAGTACACCATTTGGAGAGCGGTGAATGTGCTGTAGATCCCA 1370
QY 1256 GGCTGACCGAGAGGCTCTCTACCTCAACGGGCTGTGGCTGCTGCTGTGGATCGTGG 1315

Db 1371 ACCTAATGATCGGACCAACTACATGCGAGTGTGGTGTGCTCAAGTGTATACAGATTACTT 1430
QY 1316 TCTGCTTCTCTATCTCTGGCAGCTCCTGGGCGCTCCTCCGCTCACTGCGATCGTGTCT 1375
Db 1431 TGTCCATCTCTCTCTGGAGAGATTGGACCGTCCATCTTAGCAGGTGTGGGTTA 1490
QY 1376 TCCTGAGGCTCCTCCTCTGAAATTTCTCATCTCCAAGAAAAGAACACCAATCAGGAGG 1435
Db 1491 TGGTTCCTCTAATCCAGTTAATGGAGTTCTGGCTACCAAGATCAAAAATATTCAGCTCC 1550
QY 1436 AGCAATGAGGAGAGGACTCAGCGGACGCTCACCAGCTCTATCTCCTCAGCAACTCGA 1495
Db 1551 AAATATGAAGAAATAAGACAAACGTTTAAATCATGAATGAGATTCTCAGTGGAAATCA 1610
QY 1496 AGACCATCAAGTTCCATGGCTGGGAGAGCCTTTGTGACAGAGTCTTGGGAGCTCCGAG 1555
Db 1611 AGATCCTGAATATCTTGGCTGGGAACCTTCATTTCAAGAGCAGTCCAGGAGCTCGGA 1670
QY 1556 GCCAGGAGTGGGCGCTTGGGAGCTCCTGGGCTCCTCTCTCTGCTGCTGCTGCTGCT 1615
Db 1671 AGAAAGAACTCAAGAACTTGTCTGGCTTGGGAGCTGCGAGTCTGCTGATCTTCATTT 1730
QY 1616 TCCAAAGTGTCTACATTTCTGGTGGCAGCTGGTGTGTTCTGCTGCCACACTCTGGTGG --- 1672
Db 1731 TACAGATAACTCCAATCCTGGTGTCTGTTGTTTCTGTTATGCTTCTGTTGTTGTTGATA 1790
QY 1673 CCGAGAATGCTATGAATGAGAGAAAGCCTTTGTGACTCTCAGTCTTCAACACTCTCA 1732
Db 1791 GCGCAATGTTTGAATGCGGAGAGGCAATTTACCTCCATCACCCTCTTCAATATCTTAC 1850
QY 1733 ACAAGGCCAGGCTTTCCTGCTCCTCTCCTCATCCACTCCTCTGCTGCTGCTGCTGCT 1792
Db 1851 GCTTCCCTCTGCTCCATGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1910
QY 1793 TTGACCGTCTGCTCAGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1852
Db 1911 TGGACCGCTGAGAGAGTATTTGGGAGGAGCAGATTTAGACACATCTGCCATTCGCGCGG 1970
QY 1853 GTTCTCTGGAAGCCTGCGGGAAGGATTGCTATCACCATACACATGCTGCTGCTGCTGCT 1912
Db 1971 TCAGCAATTTTGAATAAGCTGTGAAGTTTCA -----GAGGCTCTTTACTT 2018
QY 1913 GGTCCAGGAAAGCCTCCTCCTGCTCCAGAAATAAACCTCAGGTCGCTGCTGCTGCTGCT 1972
Db 2019 GGGACCGGACTTGAAGGCAACAATCCAGATGTGAACATGGAACATAAAGCAGGCAAC 2078
QY 1973 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2032
Db 2079 TGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2138
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Db 2139 GAGAAATGAAACCTTCCAGGAGCAGATCACCATCCAGGATCCAGGCTATGCTGCTGCT 2198
QY 2093 AGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2152
Db 2199 AGCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2258
QY 2153 ACCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2212
Db 2259 ATGAAGAAGTACAGCAAGTTCTCAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2318
QY 2213 TCCCTGAGGAAATCCACACTTCAATTTGGGAGCAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 2272
Db 2319 TGCCTGAGGAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2378
QY 2273 AGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2332
Db 2379 AGCAGGAGTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2438
QY 2333 ACCCCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2392
Db 2439 ATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2498

QY 2393 CTGGTGGCTACTCCAGGGAACACAGGATTTCTCGTGACGACGCACTCCACATCTCTGC 2452
Db 2499 CCAACGGCTGTTGGCTGCAAGACAGAGATCTTTGTACTATGTTATTTCACTTCTCTC 2558
QY 2453 CCAGGCTGATTTGGATCATAGTCTGGCAATGGGCGATCGCAGAGATGGTTCCTTACC 2512
Db 2559 CCAAGTGGATGAGATTTAGTTCTCGGGAAGGCCACCTCTTAGAGAAAGGATCTTATC 2618
QY 2513 AGGAGCTTCTGCAGAGAAAGG----- 2533
Db 2619 GTGACCTGTTGGACAAAGAGGAGTGTGCTAGGAACCTGGAAGACCTTTCATGAAGCAT 2678
QY 2534 --GGGCCCCCTGCTGCTCTGTGATCAAGCCACAGACGACGAGATAGAGGAAGAGA 2591
Db 2679 CAGGGCTTGAAGGAGAGGCCACAGTCAATTAATGACAGTGGAGCGAAGACGATGATG 2738
QY 2592 AACAGAACCTGGGACACGACCAAGGACCCAGAGGACCTCTGCAGGACGAGGCGCGA 2651
Db 2739 GGCTGATTTCCACCATTGGAGGAATCCCTGAGGATCGAGTTCCTTTGGCCATGAGAGAG 2798
QY 2652 GCTTAGACGCGAGAGTCCATCAAGTCACTAGTCCCTGAGAAGGCCGTAACACTTTCAGAAGC 2711
Db 2799 AAAATAGTCTTCGCCGTACACTGAGCGCGAGCTCTAGGTCCAGCAGCGGAGTGGGAAGT 2858
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QY 2760 AGGA-----AAGGACAGCATCAATACGCGAGGGTGAAGGCCACAG 2800
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QY 2969 TCTTGGGCTCTCTCGCTCTCCAGCAATTTGGGCTGTTTGGCTCCATGGCTGGCGTGC 3028
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QY 3209 CTTTGGACTCTCGAGGTGACGCTTGGTGGGCGAGTGGCTACCCACCTGGCCACTGTGG 3268
Db 3399 TCTTTGGCATCTGGCACTCTGTGATGATCTGATGGCCACCTGCTTCGCTATCA 3458
QY 3269 COATCTCGCACTGTTCTCTCTACCTAGCTGGTTCAGAGCCTGTATGTTAGTCTAT 3328
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QY 3329 GCCAGTGAGCGCTTGGAGTCAAGCAGTACTCTGCTCTGCTGCTCCACATGGCTGAGA 3388
Db 3519 GCCAGTGAGCGGTTGGATTTCTGCACCAATCTCCGATCTATTCTCACTTCACTGAGTGA 3578

QY 3389 CGTTCCAGGCGACGACAGTGGTCCGGGCATTTCCGAACCCAGGCCCTTTTGTGGCTCAGA 3448
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QY 3449 ACATGCTCCGCTAGATGAAGCCAGGAGTCACTTTCCCGCAGTGTGTGCTGACAGGT 3508
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QY 3509 GGCTTGGCGCAATGTGGAGCTCTCTGGGAATGGCTTGGTTCGACGCGCCACGCTGTG 3568
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QY 3629 TCAGGTTGACCCAGACACTGCAGTGGGTGTGTCGAACCTGACAGACTAGAGACAGCA 3688
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QY 3689 TCCTGTGCTGAGCGGATGACGAGCTATGCTGGACGCCCAAGGAGCTCCCTGGAGGC 3748
Db 3879 TTCTGGCAGTTGACGAATAAGTGAATACATAAATGTAGAGATGAGCGCCCTGGGTGA 3938
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Db 3939 CTGACAAAG--GCCTCCGCGAGACTGGCCAGACATGGTGAGATCCAGTTTAACT 3995
QY 3809 TTGGGCTTAAGATCCGACCTGAGCTCCCGCTGCTGTCAGGCGCTCTCTTCAAGATCC 3868
Db 3996 ATCAAGTCCGATTCGCGCGAGCTGGATCTGGTACTGAAAGGATCACTTGTAACTCA 4055
QY 3869 ACCAGGAGAAAGTGGGCATCTTTGGAGAGCCGCGGCGAGGAACTCTCTCCCTGGCCA 3928
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QY 3929 GTGGGCTGCGGCTCCAGGAGGACGCTGAGGTGGGATCTGATCGAGCGGGTCCCCA 3988
Db 4116 ACTGCTCTTCAGAACTTTAGAGTCTGCGGGGGCCAGATCATCATTTGATGGGATAGT 4175
QY 3989 TTCCCACTGGGCGCTGCACACACTGCGCTCCAGAGATCAGCATCATCCCCAGGACCCCA 4048
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Db 4236 TTTTGTCTCGGGAGTCTGAGGATGAATCTCGACCTTTCAACAAATATTCAGATGAGG 4295
QY 4109 CTATCTGGGCGCTTCGAGACGCTCAAGGCTTGGTGGCCAGGCTGCCCCGCC 4168
Db 4296 AGTTTGGAGGGCCCTGGAGTTGGCTCACCTCAGATCTCTTGTGCTGCTGCTACAGTTG 4355
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Db 4356 GGTGTTATCCGAAGTGACAGAGGTTGGTCAACAACCTGACCATAGGCGAGGAGTCC 4415
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Db 4596 TGTCTCTAGACAAACGGAAGATTTGCGAGTATGCGAGTATGCGAGTCTCTGAAGAACTGCTGTCCAACA 4655
QY 4469 AGGGCTGTTTTACAGACTGGGCCAGGAGTCAAGCCCTGG 4507

QY	4496	AGTCAGGCCTGGTC	4509
Db	1441	ATGCTGGACTTGCC	1454

RESULT 6

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US-09-880-107-3407
; Sequence 3407, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Barci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression P
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,3
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,0
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3407
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession
; NAME/KEY: unsure
; LOCATION: (1)..(1968)
; OTHER INFORMATION: n = a o r g o
US-09-880-107-3407

```

	Query Match	8.5%;	Score 384.6;	DB 10;	Length 1977;
	Best Local Similarity	55.8%;	Pred. No. 4.1e-85;		
	Matches 811;	Conservative 0;	Mismatches 631;	Indels 12;	Gaps 4;
QY	3063	CCAGAGGCTCCTGTGGGATGTGGTGGCATCTCCCATCAGCTCTTTTTCAGCGGACACCCAT	3122		
Db	6	CCAGGCACTGCTGCACAAACAGATACGCTGCCACAGTCTCTTTTGACACACACCATC	65		
QY	3123	TGCTACCTGCTAAACCGCTTCTCCAAAGAGACAGACACGGTTGACGTGGACATCTCCAGA	3182		
Db	66	AGCGCGATCCTGAACGTCTTCCAAAGACATCTATGTGCGCTTGAYAGAGTTCTGGCC	125		
QY	3183	CAAACTCCGGTCCCTGCTGATGTACGCTTTTGGACTCCTGGAGGTCAAGCTGGTGGTGGC	3242		
Db	126	CCTGTCAACNTCAACGCGCTCAATTACTTCTCAACGCCATCTCCACTCTTGCGGTCTAT	185		
QY	3243	AGTGGCTACCCCACTGG-----CCACTGTGGCCATCTCTGGCCACTCTTCTCCTCTACG	3295		
Db	186	CATGGCCAGCAGCAGCGATCTTNACTTGTGGTNNANTGCCCTGGTNGTGTCTTTACA	245		
QY	3296	CTGGGTTTCAGAGCGGTATGTGGTTAGTTCATGCCAGCTGAGACGCTTGGAGTCAGCCA	3355		
Db	246	CCTTAGTGAGCGCTTCTATGACGCCACATCAGCGCACTGAAGCGGCTGGAATCAGTCA	305		
QY	3356	GCTACTCGTCTGTGCTGCCATGCTCAGACGTTCCAGGAGCAGCAGTGTGTCCGGG	3415		
Db	306	GCGG-TCACTCTACTCTCCACTTTTCGGAGACAGTGAAGTGGTGCACAGTGTCTATCCGGG	364		
QY	3416	CATTCCGAACCCAGGCCCCCTTTGTGGCTCAGAACAAATGCTCGCGTAGATGAAGCCAGA	3475		
Db	365	CCTACACCCGACCGGGATTTTGAGATCATCATAGTATAGGTGGATGCCAACAGA	424		
QY	3476	GGATCAGTTTTCCGCGACTGGTGGCTGACAGGTGGCTTGGCGGCAATGTGGAGCTCCTGG	3535		
Db	425	GAAGCTCTACCCCTACATCATCTCCAACCGGTGGCTGAGCATCGGAGTGGAGTTCTGTG	484		
QY	3536	GGATGCGCTGTGTTTGGACCGCCACAGTGTGCTGTGTGAGCAAGCCACACTCAGTG	3595		

[illegible]

RESULT 7
US-09-967-768A-190
; Sequence 190. Application US/09967768A
; Patent No. US20020150877A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena

; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE OF INVENTION: Sets
; FILE REFERENCE: 689290-72
; CURRENT APPLICATION NUMBER: US/09/967,768A
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/60/236,109
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,034
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,111
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 190
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1977)
; OTHER INFORMATION: n=a,t,g or c
US-09-967-768A-190

Query Match 8.5%; Score 384.6; DB 10; Length 1977;
Best Local Similarity 55.8%; Pred. No. 4,1e-85;
Matches 811; Conservative 0; Mismatches 631; Indels 12; Gaps 4;

QY 3063 CCAGAGGCTCCTGTGGATGTGGTGGATCTCCATCAGCTCTTTCAGCGGACACCCAT 3122
DB 6 CCAGGCACTGCTGCACAAAGATAGCTCGCCACAGTCTCTTTTGACACCAACCATC 65

QY 3123 TGGTCACTGCTAAACCGCTCTCCAGGAGACAGACACAGGTGAGCTGACATTCAGA 3182
DB 66 AGCGCCATCCTGAATGCTCTCCAGGACATCTATGCGCTTGATGAGGTCTTGGCC 125

QY 3183 CAAACTCCGCTCCTGCTGATGTACGCTTTGGACTCTCTGGAGGTGAGCTGTGGTGGC 3242
DB 126 CCGTGCACCTCAGCCCTCAATTAATCTTTCACAGCCATCTCCACATCTTGTGTAT 185

QY 3243 AGTGGTACCCCACTGG-----CAACTGTGGCCATCTGCGACATCTGTTCTCTCTACG 3295
DB 186 CATGCCAGCAGCGAGTCTTNACTTGTGGTNNANTGCCCTGGGTNGTCTCTTACA 245

QY 3296 CTGGGTTTCAGAGCTGTATGTTAGTCTATGCGAGCTGAGACCTTGGATCAGCCA 3355
DB 246 CTTAGTGAGCGCTTCTATGAGCCACATCAGGCAACTGAAGCGGCTGGAATCAGTCA 305

QY 3356 GCTACTCTGCTCTGCTCCCATGCTGAGACGTTCCAGGCGCAGCACAGTGGTCCGG 3415
DB 306 GCCG-TCACCTATCTACCTTTTCGGAGACAGTGAAGTGGTCCATCCGG 364

QY 3416 CATTCGGAACCCAGGCCCCCTTTGTTGGCTCAGAACAAATGCTGCGGTAGATGAAGCCAGA 3475
DB 365 CCTAACCCGACGCGGGATTTTGAATCATAGTACTAAGTGGATGTCACCAACCA 424

QY 3476 GATCAGTTTCCCGAGCTGTGGTGTGAGAGTGGTCTCGGCCAATGTGGAGCTCCTGG 3535
DB 425 GAAGCTGTACCCCTTACATCTCTCAACCGGTGGCTGAGCATCGGAGTGGAGTTCGTGG 484

QY 3536 GGAATGGCTGTGTGTTGAGCGCGCCACGCTGTGCTGTGAGCAAAAGCCCACTCAGTG 3595
DB 485 GGAATGGCTGTGTCTTTGTGCTACTATTTGCCGTATCGGGAGGAGCAGCTGAACC 544

QY 3596 CTGGGCTCGTGGGCTCTCTGCTCTGCTGCTCCCTCCAGGTGACCCACACACTGCAGTGG 3655
DB 545 CGGGCTGTGGGCTT-TCGTGTCTCTACTCTCTGAGTGCATTTGCTCTGAACCTGA 603

QY 3656 TGTTCGCAACTGACAGACACCTAGAACAGCATGCTGTGATGAGCGGATGACAGTACT 3715
DB 604 TGATACGAATGATGTCAGATTTTGAATCTAATCATGCTGTGCTGTGGAGAGGTCAGGAGT 663

QY 3716 ATGCTGAGCGCCCAAGAGGCTCCTGGAGGTGCTGCCACATGTGCCAGTCAAGCCCCCT 3775

Db 664 ACTCAAGACAGACAGACAGAGCGCCCTGGGTGGTG---GAACAGCGCCCTCCCAAGGT 720
QY 3776 GGCTTCAGGGCGGCGAGATCGAGTTCGGGACTTTGGGCTAAGATCCGACCTGAGCTCC 3835
Db 721 TGGCCCCACGTGGGAGGTGGAGTTCGGGAATTAATCTGTGGCTACCGCGCGGCTTAG 780
QY 3836 CGCTGGCTGTCCAGGGCTGTCTTCAAGATCCAGCAGGAGAGAGGTGGCATCTGTG 3895
Db 781 ACCTGGTGTCTGAGAGACCTGATGTGACAGTGGCGAGAGAGGTGGGATCTGTGG 840
QY 3896 GCAGGACCGGGCAGGGAAGTCTCCCTGGCAGTGGGCTGTCTGGGCTCCAGGAGGAG 3955
Db 841 GCCCACTGGGCTGGCAAGTCTTCCATGACCTTTGCTGTTCGCAATCTTGGAGGCG 900
QY 3956 CTGAGGTGGATCTGGATCGACGGGTGCCCATTTGCCACGTGGGGCTGCACACATGTC 4015
Db 901 CAAAGGCTGAATCCGATTCATGGCTCAATGTGGCAGACATCGGCTCCATGACCTGC 960
QY 4016 GCTCCAGATCAGCATCATCCCCCAGGACCCCATCTGTTCCCTGGCTCTTGGGATGA 4075
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QY 4076 ACCTCGACCTGCTCGAGGACACTCGGAGAGGCTATCTGGGCGAGCCCTGGAGAGGTGC 4135
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QY 4136 AGCTCAAGGCTTTGGTGGCCAGCCTGGCCGCGCAGCTGCAGTACAACTGTGTGACCCGAG 4195
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QY 4196 GCGAGGACCTGAGGCTGGGCGCAGAAACAGTCTGTGTGTGGCAGTCCCTTCTCCGGA 4255
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Db 1381 AGTTGATCTCCAGCCAACTCATTCGAGCTAGAGGCACTTCTACGGGATGGCCAGAG 1440
QY 4496 AGTCAGGCTGTGC 4509
Db 1441 ATGCTGGACTTGC 1454

RESULT 8

US-09-925-299-157
; Sequence 157, Application US/09925299
; Patent No. US2002055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 157
; LENGTH: 1448

QY 2596 GAACCTGGGACGACCAAGACCCAGAGCCACCTCTGCAGGAGGAGGCGCCGAGCTT 2655
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 Db 1982 ACTTCAGAGGTGGTGCCTACATGGATTTGCTTCAATTTTCTTATTTCTCTAAACACATCGAG 2041
 QY 2836 CTCTGCTCTACGACACTTCTCTCTCTCTGCGCAGCAAGTGGCTCTCTCTGCGCGGGC 2895
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 Db 2758 GTTGGCTTTGGTTCCTGATCTGGCAAAACTCTCGATGCGGCGAGGTGGTGTGGGA 2817
 QY 3616 GTCTGTGCTGCTCCAGGTCAGCCAGACACTGCACTGAGTGGTGTGTTCCGCAACTGGACAG 3675
 Db 2818 CTGTCTATGCTCCTCAGCTCATGGGATGTTTCACTGGTGTGTTCCAGCAAAAGTGTGAA 2877

QY 3676 CTAGAGAACAGCATCGTGTCTAGTGGAGCGGATGCAGGACTATGCTTGGACGCCCAAGGAG 3735
 Db 2878 GTTGAATAATGATGATCTCAGTAGAAAGGCTATTGAATACACAGACCTTTGAAAAAGAA 2937
 QY 3736 GCTCCCTGGAGCTGCCACATGTGCAGCTCAGCCCCCTGGCCTCAGGGCGGCGAGATC 3795
 Db 2938 GCACCTTTGGGAATATCAGAAAGCCCA--CCAGCCTGGCCCCCATGAAGAGTGTATA 2994
 QY 3796 GAGTTCCGGGACTTTGGGCTAAGATGCCACCTGAGCTCCCGCTGCTGTCAGGCGCGTG 3855
 Db 2995 ATCTTTGCAATGTGAACTTCATGTACATCAGGTGGCCCTCTGGTACTGAAGCATCTG 3054
 QY 3856 TCCTTCAAGATCCACGAGGAGAGAGTGGCATCTGTTGGCAGGACCCGGGCGAGGAAG 3915
 Db 3055 ACAGCACTCATTAATCAAGAAAAAGTTGGCATTTGGGAAGAACCAGGACCTGGAAAA 3114
 QY 3916 TCCCTCCCTGGGAGTGGGCTGCTGCGCTCAGGAGGAGCTGAGGTGGGATCTGGATC 3975
 Db 3115 AGTTCCCTCATCTCAGCCCTTTTATAGATT--GTCAAGAACCCGAAGGTAAAAATTTGGATT 3171
 QY 3976 GACGGGTGCCCATTTGCCACGTGGGCTGTCACACACTGCGCTCCAGGATCAGCATC 4035
 Db 3172 GATAAGATCTTGACAACTGAAATTTGACATTCACGATTTAAGGAAGAAATGTCAATCAT 4231
 QY 4036 CCCAGGACCCCATCTCTTCCCTGGCTCTCTGCGGATGAACCTCGACCTGCTGCGAGGAG 4095
 Db 3232 CCTCAGGAACCTGTTTGTCTCAGTGAACAAATGAGGAAAAACCTGATCCCTTTTATGAG 3291
 QY 4096 CACTCGGAGGAGGCTATCTGGCAGCCCTTGGAGAGCGTGCAGCTCAAGACCTTGTGGGCC 4155
 Db 3292 CACAGGATGAGGAACCTGTGAAATGCCCTTACAAGAGGTACAACTTTAAAGAAACCATTTGAA 3351
 QY 4156 AGCCTGCCGCGCCAGCTGCAGTACAAGTGTGCTGACCGAGGCGAGCTGAGCCTGGGC 4215
 Db 3352 GATCTCTCTGTAATAATGATGACTCAATTAGCAGATCAGGATCAATTTAGTGTGGA 3411
 QY 4216 CAGAAACAGCTCTGTGTCTGGCAGTGCCTTCTCCGGAAGACCCAGATCCTCATCTG 4275
 Db 3412 CAAAGACAACCTGGTGTGCTTGGCCAGGCAATTTCTCAGGAAAAATCAGATATTGATTAT 3471
 QY 4276 GACCAAGCTACTGCTGCGTGGAGCCCTGSCAGGAGCTGCAGATGCAGGCCATGCTCGGG 4335
 Db 3472 GATGAGGCGAGCAATATGTGGATCCAAAGAACTGATGAGTTAATACAAAAAATCCGG 3531
 QY 4336 AGCTGGTTTGCACAGTGCACCTGTGCTGCCATTTGCCCTGCCCTGCGCTGCGTGCAGC 4395
 Db 3532 GAGAAATTTGGCCACTGCACCGTGTACCATTTGCACACAGATTGAACACCATTTATTCAC 3591
 QY 4396 TGTCCCGGTTCTGTGTCATGGAACAGGCGAGGTGGCGAGAGCGGCGAGCCG--GCC 4452
 Db 3592 AGCGACAAGATAATGGTTTATAGATTCAGGAAGACTGAAAGAAATATGATGAGCCGTATGTT 3651
 QY 4453 CAGCTGCTGCGCCAGAGAGGCTCTTTTACAGACTGGCCCGAGGAGTCAAGGCTGG 4507
 Db 3652 TTGCTGCAAAATAAGAGAGCTTATTTTACAAGATGGTGTCAACAACTGGGCAAGG 3706

RESULT 11

US-10-012-896-1007

; Sequence 1007, Application US/10012896

; Publication No. US20020183251A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillion, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqiu

; APPLICANT: Kalos, Michael D.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

QY	3676	CTAGAGAACAGCATCTGTCACTGGAGGGATGCAAGGACTATGCTTGACGCCCAAGGAG	3735
Db	3487	GTTGGAATATGATGATCTTCAGTAGAAAGGGTCATTGAATACACAGACCTTTGAAAAGAA	3546
QY	3736	GCTCCCTGGAGGCTGCCACATGTGCAGCTACGCCCCCTTGGCCTCAGGGCGGCAGATC	3795
Db	3547	GCACCTTGGGAATATCAGAAACGCCACCA---CCAGCCTGGCCCCATGAAGAGGAGTGATA	3603
QY	3796	GAGTTCGGGACCTTTGGGCTTAAGATCGCGACCTGAGCTCCCGCTGGCTGTGCAGGGCTG	3855
Db	3604	ATCTTTGACAATGTGAACCTTCATGTACAGTCCAGGTGGGCTCTGGTACTGAACATCTG	3663
QY	3856	TCCTTCAAGATCCAGCAGGAGAGAAGTGGGCATCTGTTGCGACGACCGGGCAGGGAAG	3915
Db	3664	ACAGCACTCATTTAAATACAGAAAAGGTTGGCATTTGGGAAACACGGAGCTGGAAAA	3723
QY	3916	TCCTCCCTGGCAGTGGCTGCTGCGGCTCCAGGAGGCAGCTGAGGGTGGGATCTGGATC	3975
Db	3724	AGTTCCCTCATCTCAGCCCTTTTTAGATT---GTCAGAACCCGAAGGTAAATTTTGGATT	3780
QY	3976	GACGGGGTCCCATTTGCCACAGCTGGGGCTGACACACTGCGCTCCAGGATCAGCATCATC	4035
Db	3781	GATAAGATCTTGACAACTGAAATTTGCACTTCACGATTTAAGGAAGAAAACTCAATCATA	3840
QY	4036	CCCCAGGACCCCATCCTGTTCCCTGGCTCTCTGGGGATGAACCTCGACCTGCTGTCAGGAG	4095
Db	3841	CCTCAGGAACCTGTTTTGTTTCTACCTGGAACAATGAGGAAAAACCTTGGATCCTTTAATGAG	3900
QY	4096	CACCTCGGACGAGGCTATCTGGCAGCCCTGGAGAGCGGTGACAGTCAAGGCTTGGTGCC	4155
Db	3901	CACACGGATGAGGAACCTGTGGAATGCCCTTACAGAGGTACAACTTAAAGAAACCATTTGAA	3960
QY	4156	AGCTGCCCGGCCAGCTGCAGTACAAGTGTGCTGACGAGCGGAGGACCTGAGCGTGGCC	4215
Db	3961	GATCTTCTCTGTTAAATGGATCTGAATTAGCAGAACTCAGGATCCAATTTTAGTGTGGA	4020
QY	4216	CAGAAACAGCTCCTGTGTCGTGACGTCCCTCTCCGGAGACCCAGGATCCCTCATCTCTG	4275
Db	4021	CAAAGCAACTGGTGTGCTTCCAGGGCAATTTCTCAGGAAAAATCAGATATTGATTATT	4080
QY	4276	GACGAGGCTACTGCTGCGCTGGACCCCTGGCAGGAGCTGCAGATGCAGGCCATGCTCGGG	4335
Db	4081	GATGAAGCAGCGCAAAATGTGGATCCAAAGAACTGATGAGTTAATACAAAAAAAATCCCG	4140
QY	4336	AGCTGGTTTGACAGATGCACATGTGCTGCCAATTCGCCACCGCTCGCCTCCGTGATGGAC	4395
Db	4141	GAGAAATTTGGCCACTGCACCGTCTAACCAATTCCACACAGATTGAACACCATATTGAC	4200
QY	4396	TGTGCCGGGTCTTGCTCATGGACAAGGGCAGGTGCGAGAGCGCGCACGCCG---GCC	4452
Db	4201	ACGGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAGAAATATGATGAGCCGTATGTT	4260
QY	4453	CAGCTGTGCCCGAAGAGGGCCTGTTTTACAGACTGCGCCAGGAGTCAAGCCCTGG	4507
Db	4261	TTTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGTGCAACAACTGGGCAAGG	4315

RESULT 12

US-10-012-896-536
; Sequence 536, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:

QY	2356	CACGTTGGCCAGCATGCTTTCACACGAGTCATTGGGCCCTCGTGGCTACTCCAGGCAACA	2415
APPLICANT:	Xu, Jiangchun		
APPLICANT:	Dillon, Davin C.		
APPLICANT:	Mitcham, Jennifer L.		
APPLICANT:	Harlocker, Susan L.		
APPLICANT:	Jiang, Yugu		
APPLICANT:	Kalos, Michael D.		
APPLICANT:	Retter, Marc W.		
APPLICANT:	Stolk, John A.		
APPLICANT:	Day, Craig H.		
APPLICANT:	Vedvick, Thomas S.		
APPLICANT:	Carter, Darrick		
QY	1861	GAAGTTAGCAGACACTTGTTCGAACCTGTGTAATTTGCAAAATTTTGCATGAGAAGATCACA	1920
QY	2416	ACACGGATTCTCGTGACGACGCGACCTCCACATCCTGCCCCAGGCTCATTTGGATCATAGTG	2475
QY	1921	-----ATTTTAGTACTCATCAGTTGCAGTACCTCAAGCTCAAGTCAGATCTTGATA	1974
QY	2476	CTGGCAAAATGGGGCCATCGCAGAGATGGGTTCTACAGAGAGTTCTCGCAGAGGAAGGGG	2535
QY	1975	TTGCAAGATGTAATAATGCTGCAGAGCGGCACCTTACACATCTCTCAATAAAGACTCCATA	2024

QY 2536 GCCTCGTGTCTTCTGATCAGCCACACACCCAGGAGATAGAGAGAGAGAAACA 2595
Db 2035 GATTTGGGTCCCTTTTAAAGAGGATAATGAGNAAGTGAACAACCTCCAGGTCCAGGA 2094
QY 2596 GAACCTGGACAGACACCAAGGACCCAGAGCACCTCTGACGAGGAGGCCGAGCTT 2655
Db 2095 ACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTG-----GTCTCAACAAT 2149
QY 2656 AGACGGAGAGGTCCATCAAGTACGCTCCTGAGAAGACCGTACCACCTTCAGAAGCCAG 2715
Db 2150 CTCTAGACCCCTCTTGAAGATGGTCTCTGGAGAGCCAAAGATACAGAGAATGTCCAG 2209
QY 2716 ACAGAGGTTCTCTGATCACCCTGACAGGAGGAGTGGCCAGCAAGAGACAGATC 2775
Db 2210 TTACACTATCAGAGGAGAACCGTCTGGAAGAAAGTTGGTTTCAGGCTATTAAGAAAT 2269
QY 2776 CAATACGGCAGGTTGAAGGCCACAGTGCACCTTGGCCCTACTCGCTGCCGTGGCACCCCC 2835
Db 2270 ACTTCAGAGCTGGTCTCACTGATGTGCTTCAATTTTCCTTATTCCTTAACACTGCGAG 2329
QY 2836 CTCGCTCTACGCACCTCTTCTCTCTCTGCCAGCAAGTGGCCCTCTCTGCCGGGGC 2895
Db 2330 CTCAGGTTGCCCTATGTGCTTCAAGATTGCTGGCTTTTCATACCTGGGCAACAACAAAGTA 2389
QY 2896 TACTGCTCAGCCTGTGGCGGACGACGCCCTGCAGTAGTGGGAGCAGAGCAGGAGGCC 2955
Db 2390 TGTAAATGTCACTGTAAATGAGGAGGAGAAATGTAAACGAGAGCTAGATCTTTAACTG-- 2447
QY 2956 CTGCGTGGCGGATCTTTCGGCTCTCTCGCTGCTCAAGGCCATTTGGCTGTGTTGCTCTC 3015
Db 2448 GTACTTAGGAATTTATCAGTTTAACTGTAGTACCGTTCTTTTGGGATAGCAAGATC 2507
QY 3016 ATGCGTGGCGTCTCCTAGGTGGGCGCCGGGCATCCAGGTGCTCTTCCAGAGGCTCCTG 3075
Db 2508 TCTAATGTGATTTCTACGTCTTGTAACTCTTCACAAACT--TGCAACAACAAATGTTT 2565
QY 3076 TGGGATGTGGTGGATCTCCCATCAGCTTTCTTGGCGGACACCCCATTTGGTCACTGCTA 3135
Db 2566 GAGTCAATTTCTGAAAGCTCCGGTATTTATTTCTTGTAGAAATCCAATAGAGAAATTTTA 2625
QY 3136 AACCGCTTCTCAAGGAGACAGACAGGTGTGAGTGGACATTCAGACAAACTCCCGTCC 3195
Db 2626 AATCGTTTCTCCAAAGACATTTGACACTTTGGATGATTTGCTGCCGTGAGCTTTTAGAT 2685
QY 3196 CTGCTGATAGCCTTTGGACTCTCGAGGTGAGCCTGCTGGTGGCGATGGCTACCCCA 3255
Db 2686 TTATCCAGACATTTGTACAAAGTGGTTGGTGGTCTCTGTGGCTGTGGCCGTGATTCTCT 2745
QY 3256 CTGGCCACTGTGGCCATCTGCGCACTGTTTCTCTCTAGCTGGGTTTCAGAGCCTGTAT 3315
Db 2746 TGGATGCGCAATACCTTGTGTTCCCTTTGGAATCAATTTTCATTTTCTCGGCGATATTTT 2805
QY 3316 GTGGTTAGCTATCCAGCTGAGACGCTTGGAGTCAAGCAGCTACTCTGCTGTCTGCTCC 3375
Db 2806 TTGGAAACCTCAAGAGATGTGAGCGCTTGGAAATCTACAACTCGGAGTCCAGTGTGTTCC 2865
QY 3376 CACATGGCTGAGACGTTCCAGGGCAGCACAGTGGTCCGGGCAATTCGAAACCCAGGCCCC 3435
Db 2866 CACTTGTCTATCTTCTCCAGGGGCTCTGGACCATCCCGGCGATACAAAGCAGAGAAGAGG 2925
QY 3436 TTTTGGCTCAGACAAATGCTCGCTAGATGAAGCCAGGATCAGTTTCCCGCCACTG 3495
Db 2926 TGTAGGAACTCTTTGATCAGACACCCAGGATTTTACATTCAGAGGCTTGGTCTGTTGTTTTG 2985
QY 3496 GTGGCTGACAGTGGCTTCCGCGCAATGTGGAGCTCTCTGGGAATGGCCTGGTGTGTTGCA 3555
Db 2986 ACAACCTCCGCTGGTTCCCGCTCGCTGTGGATGCCATCTGTGCCATGTTTGTFCATCATC 3045
QY 3556 GCGGCCACGCTGTGCTGTGAGCAAGCCCACTCAGTGTGGCTCGTGGGCTCTCTCT 3615
Db 3046 GTTGCCCTTTGGGTCCCTGATTTGCGCAAAACTCTGGATGCCGGGAGGTTGGTTTGGCA 3105

QY 3616 GTCTCTGCTGCCCTCCAGGTGACCCAGACACTGCAGTGGGTTGTTCCCAACTGGACAGAC 3675
Db 3106 CTGTCTTATGCCCTCAGCTCATGCGGATGTTTCAGTGGTGTGTTCGACAAAGTGTCTGAA 3165
QY 3676 CTAGAACACAGCATCTGTCTAGTGGAGCGGATGCAGACTATGCTGTGACGCCCAAGAG 3735
Db 3166 GTTGAGAAATATGATGATCTCAGTAGAAGGTCTATTAATACACAGACCTTTGAAAAAGAA 3225
QY 3736 GTCTCCCTGGAGGTGCCCATGTGCAGCTCAGCCCCCTGGCCTCAGGGCGGCAGATC 3795
Db 3226 GCACCTTTGGGAATATCAGAAACGCCCACTA---CCAGCCTGGCCCCATGAAGGAGTGATA 3282
QY 3796 GAGTTCCGGGACITTTGGGCTAAGATGCCGACCTCAGCTCCGCTGGCTGTGTCAGGGGCGTG 3855
Db 3283 ATCTTTGACAATGTGAACCTTCATGTACAGTCCAGGTGGGCTCTGGTACTGAAGCATCTG 3342
QY 3856 TCCTTCAAGATCCACGAGGAGGAGGTGGCATCTGTGGCAGGACCGGGGCGAGGGAAG 3915
Db 3343 ACAGCACTCATTAATCACAAGAAAGGTGGCATTTGGGAAGAACCGGAGCTGGAAAAA 3402
QY 3916 TCCTCCCTGGCCAGTGGGCTGCTGCGCTCCAGAGGACGCTGAGGTTGGATCTGGATC 3975
Db 3403 AGTTCCCTCATCTCAGCCCTTTTAGATT---GTCAGAACCCGAAGGTAAAAATTTGGATT 3459
QY 3976 GACGGGTCCCATTTGCCAGCTGGGCTGCACACACTGCGCTCCAGGATCAGCATATC 4035
Db 3460 GATAAGATCTTGACAACCTGAAATTTGGACTTCACGATTTAAGGAAGAAATGCAATCATA 3519
QY 4036 CCCAGGACCCCATCTCTGCTGCGCTCTCTGCGGATGAACCTCGACCTCTCGCAGGAG 4095
Db 3520 CTTCAGGAACCTGTTTGTTCAGTGGAAACAATGAGGAAAAACCTGGATCCCTTTAATGAG 3579
QY 4096 CACTCGACAGAGCTATCTGGGCGCCCTGGAGACGCTGACAGCTCAAAGCCTTGGTGGCC 4155
Db 3580 CACACGGATGAGAACTGTGGAATGCCCTTACAGAGGTACAACTTAAAGAAACCATTTCAA 3639
QY 4156 AGCTGCCCGCCGACGTCAGTACAAGTGTGCTGACCGAGCGGAGACCTGAGCGTGGGC 4215
Db 3640 GATCTCTCTGGTAAATGGATCTGAATTAGCAAAATCAGGATCCAATTTTAGTGTGGGA 3699
QY 4216 CAGAAACAGCTCTGTCTGCGACGCTGCCCTTCTCGGAGAGCCAGATCCTCATCTG 4275
Db 3700 CAAAGACAACCTGCTGCTGCTTCCAGGSCAATCTCAGGAAAAATCAGATTTGATTAT 3759
QY 4276 GACAGCTACTGCTGCTGCGCTGGACCTCGGCAGCGAGCTGCAGATGCGAGGCCATGCTCGG 4335
Db 3760 GATGAAGCGACGCAATGTGGATCCAAAGAACTGATGAGTTAATACAAAAAAATCCGG 3819
QY 4336 AGCTGTTTGCACAGTGCCTGCTGCCATTTGCCACCGCTCGCTCCGCTGATGGAC 4395
Db 3820 GAGAAATTTGCCCACTGCACCGCTGAACCATTCGACACAGATTTGAACACCATTTATGAC 3879
QY 4396 TGTGCCCGGGTCTCTGCTATGGACAAGGCGAGGTGCGACAGAGCGGCGAGCCCG---GCC 4452
Db 3880 AGCAACAAGATATGTTTGTAGTTTTCAGGAAGACTGAAGAATATGATGACCGCTGATT 3939
QY 4453 CAGCTGCTGGCCCAAGAGGCCCTGTTTTCAGACTGCCCCAGGAGTCAAGGCGCTGG 4507
Db 3940 TTGCTGCAAAATAAGAGAGAGCTATTTTACAAAGATGTTGCAACAACTTGGCAAGG 3994

RESULT 13

US-09-759-143-536
; Sequence 536, Application US/09759143
; Patent No. US200202248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.


```
QY 3676 CTAGAGAACAGCATCGTGTCACTGGAGCGGATGCAGGACTATCCCTGGACGCCCAAGGAG 3735
Db 3166 GTTGAGAAATATGATCTCACTAGAGAGGGTCAATTGAATACACAGACCTTTGAAAAGAA 3225
QY 3736 GCTCCCTGGAGGCTGCCACATGTGCAGCTCAGCCGCCCTGGCTCAGGCGCGGAGATC 3795
Db 3226 GCACCTTGGGAATATCAGAAAGCCCAACA---CGAGCTTGGCCCATGAGAGAGTGATA 3282
QY 3796 GAGTTCGGGACTTTGGGTAAAGATCCGACCTAGAGCTCCCGCTGCTGTGCAGGCGGTG 3855
Db 3283 ATCTTTGACAATGTGAATCTCATGTACAGTCCAGGTGGGCTCTGTACTGAAGCATCTG 3342
QY 3856 TCCTTCAAGATCCACGACGAGAGAGTGGCATGCTTTGGCAGGACCGGGGAGGAG 3915
Db 3343 ACAGCACTCATTAATACAGAAAGGTGGCAITTTGGGAAGAACCAGGAGCTGGAATA 3402
QY 3916 TCCTCCCTGGCAGTGGGTGCTGCGGCTCCAGGAGGACGCTGAGGTGGGATCTGGATC 3975
Db 3403 AGTTCCCTCATCTCAGCCCTTTTAGATT---GTCAGAACCCGAGGTAAATTTGGATT 3459
QY 3976 GACGGGGTCCCATATGCCACGCTGGGGCTGCACACACTGGCTCCAGGATCAGCATCATC 4035
Db 3460 GATAAGATCTTGACAACTGAATTTGACTTACAGTTCAGATTTAAGGAAGAAATGTCAATCATA 3519
QY 4036 CCCCAGGACCCCATCTGTGCTGCTGCTCTGCGGATGAACCTCAGCTGCTGCAGGAG 4095
Db 3520 CCTCAGGAACCTGTTTGTCTCACTGGAACTGAGGAAACCTTGATCCCTTTTAATGAG 3579
QY 4096 CACTCGGACGAGCTATCTGGGACGCTGGAGCGCTCAGCTCAAGCCCTTGGTGGCC 4155
Db 3580 CACAGGATGAGGAATCTGGATGGCTTACAGAGGTACAACTTAAAGAAACCATTTGAA 3639
QY 4156 AGCTTCCCGGCGAGCTGCAGTACAGTGTGTGACCGGAGGAGACCTGAGCGTGGGC 4215
Db 3640 GATCTTCTCTGGTAAATAGGATACAGTAAATAGCAGATCAGGATCCAAATTTTAGTGTGA 3699
QY 4216 CAGAAACGCTCTGTGCTGCGACGTGCTTCCCGAAGACCCAGATCCTCATCTG 4275
Db 3700 CAAGAACAACTGGTGGCTTCCAGGCGCAATCTCAGGAAATACAGATATTGATTATT 3759
QY 4276 GACGAGCTACTGCTGCCCTGGACCTTGGCAGGAGCTCAGATGAGCGCATGCTCGGG 4335
Db 3760 GATGAAGCAGCGCAATGTGGATCCAAAGACTGATGAGTTAATACAAAAAANTCCGG 3819
QY 4336 AGCTGTTTGCACAGTGCATGTGTGCTGCCATTTGCCACCGCTGCGCTCCGCTGATGGAC 4395
Db 3820 GAGAAATTTGCCCACTGCACCGCTGTAACTTTGCACACAGATTTGAACACCATTTATGAC 3879
QY 4396 TGTGCCGGTCTGCTCATGACAGGCGAGGTGGCAGAGCGGCAGCCG---GCC 4452
Db 3880 AGCGACAAGATATGTTTGTAGTACGAGAGCTGAAAGATATATGATGAGCGGTATGTT 3939
QY 4453 CAGCTGCTGGCCGAGAGGCGCTGTTTACAGACTGGCCCGAGGATCAGGCGCTGG 4507
Db 3940 TTGCTGCAAAATAAGAGAGCCATTTTACAGATGGTCCACAACTGGGCGAAGG 3994
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RESULT 14

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US-09-780-669-536
; Sequence 536, Application US/09780669
; Patent No. US2002005197A1
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GENERAL INFORMATION:

```
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
```

```
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 536
; LENGTH: 6140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(6140)
; OTHER INFORMATION: n=A,T,C or G
US-09-780-669-536
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Query Match 6.0%; Score 271.4; DB 10; Length 6140;
Best Local Similarity 46.0%; Pred. No. 5.3e-57;
Matches 1185; Conservative 0; Mismatches 1366; Indels 24; Gaps 7;
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```
QY 1936 CTCACAGATAAACCTCAGGTGCCCCAGGGTGTCTGTGGTGTGTGGTGTCCAGTG 1995
Db 1441 CTACAAGGCTTTCTCTTACTGTACAGACCTGGCGAATTTGTAGCTGTGGTGGCCCGTG 1500
QY 1996 GGGGAGGGAAGTCTCCCTGTGTCGCGCTCTCTGGGAGCTGTCAAAGTGGAGGG 2055
Db 1501 GGAGCAGGGAAGTCACTGTTAAGTCCGCTGCTCGGGAATTTGGCCCAAGTCAAGG 1560
QY 2056 TTCGTGAGCATCAGAGGTGTGTGGCTAGTGTGCCAGGAGGCTTGGTGCAGAACACC 2115
Db 1561 CTGGTCAGCTGTCATGGAAGATTGCTATGTCTCAGCAGCCTGGGTGTTCTCGGGA 1620
QY 2116 TCTGTGTAGAGAAATGTGCTTCGGCAGAGCTGGACCCACCCCTGGTGGAGAGATA 2175
Db 1621 ACTCTCAGGAGTAATATTTTATTTGGGAAGAAATACGAAAGAACGATATGAAAAAGTC 1680
QY 2176 CTAGAAGCCTGTCCCTGCAGCCAGATGTGCAGAGCTTCCTCAGGGAATCCACACTTCA 2235
Db 1681 ATAAAGCTTGTCTCTGAAAAGGATTTACAGCTTTGGAGATGTGATCTGACTGTG 1740
QY 2236 ATTGGGAGCAGGGCATGATCTCTCCGGAGCCAGAGCAGCGGTGAGCCTGGCCCGG 2295
Db 1741 ATAGGAGATCGGGGAACCAAGCTGAGTGGAGGCGAGAAACGCGGTAAACCTTTGCAAGA 1800
QY 2296 GCTGTATACAGAAAGCAGCTGTGTACCTCTGTGATGACCCCTGGCGGCTGGATGCC 2355
Db 1801 GCAGTGTATCAAGATGCTGACATCTATCTCTGGAGCATCTCTCAGTGCAGTAGATCGG 1860
QY 2356 CAGTTGGCCAGCATCTCTCAACAGGTTCATTGGGCTGTGGCTGTACTCCAGGGAACA 2415
Db 1861 GAAGTTAGACAGACACTGTTCGAACTGTGTTTGTCAAATTTTGCATGAGAGATCACA 1920
QY 2416 ACAGGATTTCTGTGACGACGACGATCCACATCTCTGCCAGGCTGATTTGGATCATAGT 2475
Db 1921 -----ATTTTAGTACTCATCAGTTGCAGTACCTCAAAGCTGCAAGTCAAGTCTGATA 1974
QY 2476 CTGGCAAAATGGGCCATTCGAGAGATGGGTTCCTACAGAGAGCTTCTGCAGAGAAAGGG 2535
Db 1975 TTGAAAGATGGTAAATGGTGCAGAGGGGACTTACACTGAGTTCTCTAAATCTGTGTATA 2034
QY 2536 GCCCTCGTGTCTCTTGGATCAAGCCAGACAGCCAGGAGATAGAGGAGAGGAACA 2595
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Db 2035 GATTTTGGCTCCCTTTTAAAGAGGATAATGAGAAAGTGAACACCTCCAGTTCACGA 2094
QY 2596 GNACTGGGACAGACCAAGACCCAGAGACCTCTGACAGGAGGAGGCCCCGAGCTT 2655
Db 2095 ACTCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTG-----GTCTCAACAAT 2149
QY 2656 AGACGCGAGAGTCCATCAAGTCAGTCCCTGAGAGGACCGTACCACITCACAAGCCCGAG 2715
Db 2150 CTTCTAGACCTCCCTTGAAGATGCTGCTGGAGAGCAAGATACAGAGAATGTCCCGAG 2209
QY 2716 ACAGAGTTCTCTTGATGACCCCTGACAGGCGAGGATGCCAGAGGAAGACAGCATC 2775
Db 2210 TTACACTATCAGAGAGAACCGTTCTGAAGGAAGTTGGTTTTCAGGCGCTATAGAAT 2269
QY 2776 CAATAGCGAGGGTGAAGGCGACAGTGCACCTGGCCCTACCTGCGTGGCGTGGGACCCCG 2835
Db 2270 ACTTCAGAGCTGGTCTCACTGGATTGCTTCATTTCTCTTATCTCTCTAAACATGCGAG 2329
QY 2836 CTCTGCCCTTACGCACCTCTCTCTCTCTCTCCAGCAAGTGGCCCTCTCTGCGGGGC 2895
Db 2330 CTCAGTTGGCTATGTGCTTCAAGTGTGGTCTTCACTGGGCTTTCACTGGGCAAAACAAGTA 2389
QY 2896 TACTGGCTGACCCCTGTGGGCGGACGACCCCTGCACTGAGTGGGCGACAGACGAGCGACCC 2955
Db 2390 TGCATAATGTCACTGTAAATGGAGGAGGAATGTAACCGAGAAGCTAGATCTTAATG-- 2447
QY 2956 CTGGTGGCGGATCTTCGGGCTCTCGGCTGTCTCCAAAGCCATTTGGGCTGTTCGCCCTCC 3015
Db 2448 GTACTTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTCTCTTTTGGCATAGCAAGATC 2507
QY 3016 ATGGCTGGGTGCTCCTAGTGGGCGCGGCATCCAGTTGCTCTCTCCAGAGGCTCTG 3075
Db 2508 TCTATTGGTATCTACGTCTTGTAACTCTTCAAAACTT--TGCACAAACAAATGTTT 2565
QY 3076 TGGATGTGGTGCATCTCCATCAGCTTCTTTGAGCGGACACCCATTTGGTCACTGCTA 3135
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QY 3136 AACCGCTTCCAAAGGAGACAGACGGTTGACGTGGACATTCACAGACAAATCCGGTCC 3195
Db 2626 AATCGTTTCTCAAAGACATTTGGACACTTGGATGATTTGCTGCGCGCTGACGCTTTTAGAT 2685
QY 3196 CTGCTGATGACGCTTTGGACTCTCGAGGCTCAGCTGCTGGTGGGAGTGGCTACCCCA 3255
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; Sequence 536, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822.827
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 536
; LENGTH: 6140

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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:05:00 ; Search time 89.9185 Seconds
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15378.431 Million cell updates/sec

Title: US-09-647-140A-7

Perfect score: 4509

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1227.6	27.2	5011	1	US-08-463-092B-3
2	1227.6	27.2	5011	2	US-08-462-109A-3
3	1227.6	27.2	5011	2	US-08-460-907B-3
4	1227.6	27.2	5011	3	US-08-463-179A-3
5	1227.6	27.2	5011	3	US-08-461-384B-3
6	1222.8	27.1	5011	1	US-08-141-893-1
7	1222.8	27.1	5011	1	US-08-463-092B-1
8	1222.8	27.1	5011	2	US-08-462-109A-1
9	1222.8	27.1	5011	2	US-08-460-907B-1
10	1222.8	27.1	5011	3	US-08-463-179A-1
11	1222.8	27.1	5011	3	US-08-461-384B-1
12	1222.8	27.1	5011	3	US-08-407-207A-1
13	1189.8	26.4	5889	1	US-08-463-092B-5
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42 271.4 6.0 6140 4 US-09-439-313-536 Sequence 536, App
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44 264.2 5.9 6082 4 US-09-439-313-535 Sequence 535, App
45 264 5.9 5232 4 US-08-972-927-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-463-092B-3
; Sequence 3, Application US/08463092B
; Patent No. 5766880
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,092B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1546
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 3:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..4788
US-08-463-092B-3

Query Match      27.2%; Score 1227.6; DB 1; Length 5011;
Best Local Similarity 55.8%; Pred. No. 4e-281;
Matches 2538; Conservative 0; Mismatches 1934; Indels 80; Gaps 7;

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DB 2097 TGTCAAAGAGCGGGGGCACGAACGATCACCGTGAAGGAATGCCACATTCACCTGGGC 2156
QY 1917 CAGGAAAGCCCTCCTGCTGCTCAGAGATTAACCTCAGGCTGGCCCGGCTGCTGCTGCTGCTGCT 1976
DB 2157 CAGGAGCGAGCTTCCACACTGAATGGCATCACTTCTCCATCCCGGAAGGTGCTTTGGT 2216
QY 1977 GGCTGTTGTCTCAGTGGGGCAGGGAAGTCTCTCCCTGCTGCTCCGCTTCTTCCGGGA 2036

DB 2217 GGCGTGTGGCCAGGTGGGCTGGGAAGTCTGCTCTCTCAGCCCTTTGGCTGA 2276
QY 2037 GCTGTCAAAGTGGAGGGTTCTGTGAGCATCGAGGCTGCTGTGGCTACTAGTGCCTCCAGCA 2096
DB 2277 GATGACAAAGTGGAGGGGACGTGGCTATCAAGGCTCCGTGGCTATGTGCCACAGCA 2336
QY 2097 GGCCTGGGTGACAAACCTCTGTGGTAGAATGTGTGCTTGGGCGAGGAGCTGGACCC 2156
DB 2337 GGCTGGATTGAGAATGATCTCCGAGAAACATCTTTTGGATGTCAGCTGGAGGA 2396
QY 2157 ACCCTGGCTGAGAGAGTACTAGAACCTGTGCCCTGAGCAGATGTGGACAGCTTCCC 2216
DB 2397 ACCATATTACAGTCCGTGATACAGGCTGTGCCCTCTCCAGACCTTGGAAATCCTGCC 2456
QY 2217 TGAGGGAATCCACACTTCAATTGGGGAGCAGGCGATGAATCTCTCCGAGGCGCAAGCA 2276
DB 2457 CAGTGGGATCGGACAGAGATTGGCGAGAGGCGTGAACCTGTCTGGGGACACAGCA 2516
QY 2277 GCGCTGAGCCTGGCCCGGCTGTATACAGAAAGCAGCTGTGTACCTGTGCTGGATGACCC 2336
DB 2517 GCGGTGAGCCTGGCCCGGCTGTACTTCCAAAGCTGACATTTACCTCTTCGATGATCC 2576
QY 2337 CTTGCGGCTGTGATGCCACCTTGGCCAGCATCTTCAACAGGTCATTTGGGCTGG 2396
DB 2577 CTTCTCAGCAGTGGATGCCATGTGGGAAACACATCTTTGAAATGTGATTTGGCCCA 2636
QY 2397 TGGCTACTTCCAGGAAACACACGATTTCTGTGACGACGACCTCCACATCTCTGCCCA 2456
DB 2637 GGGATGCTGAAGAACAGACGCGGATCTTGTACGACAGCATGAGCTACTTCCCGCA 2696
QY 2457 GGCTGATTTGATATAGTGTGGCAATTTGGGCGCATCCGAGAGATGGTTCCTACCAGGA 2516
DB 2697 GGTGAGCTCATCATCTGTCATGAGTGGGCGCAAGATCTCTGAGATGGCTCTTACCAGGA 2756
QY 2517 GCTTCTCAGAGGAGGGGCGCTGCTGTGCTTCTGATCAAGCCACAGACGACAGGA 2576
DB 2757 GCTGCTGCTCAGACGCGGCTTCCG-CTGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2815
QY 2577 TAGAGGAGAGGAGAAACAGAACTTGGGACCAAGGACCCCGAGAGCACCCTCTGCG 2636
DB 2816 AGGAGCAGGATGACAGAGAGAGAGGCTGACGGGCTCAGCGGTCCAGGGAAGGAGCA 2875
QY 2637 AGGAGGAGGCGCGCTTACAGCGGAGAGTCTCATGATCAGTCCCTGAGAG- 2691
DB 2876 AGCAATGGAGATGGCATGCTGTGACGGACAGTGGCAGGGAAGCAACTGACAGAGAC 2935
QY 2692 -----GACCGTACACTTCAAGAGCCAGAA- 2716
DB 2936 TCAGCAGCTCTCTCTCTATAGTGGGACATCAGCAGGACCAACACAGCAGCAGAAC 2995
QY 2717 CAGAGTTCCTCTGATGACCTTACAGGCGGAGGATGGCCAGGAGAAAGGACATCC 2776
DB 2996 TGCAGAAAGCTGAGGCCCAAGAGAGGAGACCTGGAAGCTGATGGAGCTCAGCAGGCGC 3055
QY 2777 AATACGCGAGGTTCAAGCCACAGTGCACCTGGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCT 2836
DB 3056 AGACAGGCGAGTCAAGCTTTTCCGTACTTGGGACTACATGAAGGCCATCGGACTCTTCA 3115
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DB 3116 TCTCTCTCTCAGCATCT 3175
QY 2897 ACTGGCTGAGCCTGTGGCGGACGACCTGCAATAGTGGGACGACGACGACGACGACGACGACGAC 2956
DB 3176 ATTGGCTCAGCCTCTGGACTGATGACCCCTCTGCTCAAGGAGCTCAGGAGCAGCAGAAAG 3235
QY 2957 TGGGTGGCGGATCTTGGGCTCTCGGCTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3016
DB 3236 TCGGCTGAGCGCTATGAGGCGCTTGGGCAATTTCAAGAGGATCGCGCTGCTGCTGCTGCTGCT 3295
QY 3017 TGGCTGCGGTGCTCTCTAGTGGGCGCGGCTCAGGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3076

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Db 3356 ACAGCATCTGGGTGTCACCATAGCTTCTTTGAGCGGACCCCGAGTGGGAACCTGGTGA 3415
Qy 3137 ACCGCTTCTCAAGGAGACACAGCGGTGACGTGGACATTCACAGAAACCTCCGGTCC 3196
Db 3416 ACCGCTTCTCAAGGAGCTGACACAGTGGACTCATCATCCGGAGGTCAATCAAGATG 3475
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Db 3476 TCATGGGCTCCCTGTTCAACGTCATTTGGTGGCTGATCGTTATCTGCTGGCCACGCCCA 3535
Qy 3257 TGGCAGCTGTGGCCATCTGCGACCTGTTTCTCTCTACGCTGGGTTCAGAGCCCTGTATG 3316
Db 3536 TGGCGGCCCATCATCTCCGCGCCCTTGGCCCTCATCTCTCTGTCAGAGGTTCCTAG 3595
Qy 3317 TGGTGTAGCTCATGCGAGCTGAGACGCTTGGAGTCAGCCAGCTACTGCTGTCTGCTCC 3376
Db 3596 TGGCTTCTCCCGGAGCTGAAGCGCTCGAGTCGCTCAGCGCTCCCGGCTCTATTCC 3655
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Db 3656 ATTTCAAGAGACCTTGTGGGGGTGAGCGTCAATTCGAGCCCTTCAGGAGCAGGAGCGCT 3715
Qy 3437 TTGTGGCTCAGAACATCTCGGTGATGAAGCCAGAGATCATGTTTCCCGGACCTGG 3496
Db 3716 TCATCCACAGAGTACCTGAAGGTGGAGAGAACCAAGAGCCCTTATACCCACGATCG 3775
Qy 3497 TGGCTGACAGCTGGCTTGGCGCAATGTGGAGCTCTCTGGGAAATGGCTGTGTTGGAG 3556
Db 3776 TGGCCACAGCTGGCTGCGCTGGCTGGAGTGTGGGCAACTGATCTGTTGTTG 3835
Qy 3557 CGGCCAGCTGTGCTGTGAGCAAGCCACCTCAGTGTGCTGCTGCTGCTGCTGCTGCTG 3616
Db 3836 CTGCGCTGTTGGCGGTGATCTCCAGGCACAGCTCAGTGTGCTGCTGCTGCTGCTGCT 3895
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Qy 3677 TAGAAGACAGCTGCTGTGATGAGCGGATGCGAGCTATGCTGCGGACGCCCAAGAGG 3736
Db 3956 TGGAAACCAACATGTCGCTGCTGAGAGCTCAAGGATATTCAGAGACTGGAAGAGG 4015
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Db 4016 CGCCTTGGCAATCCAGGAGACAGCTCGCCCGCAGCAGCTGCGCCAGCTGGGCCAGTGG 4075
Qy 3797 AGTTCGGGACTTTGGCTAGATGCTGCGACCTGAGCTCCGCTGCTGCTGCTGCTGCTGCT 3856
Db 4076 AATTCGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4135
Qy 3857 CTTTCAAGATCCAGCAGAGAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3916
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Qy 3917 CCTCCTGCGGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3976
Db 4196 CGTCCCTGACCTGGCTTATTTGGATCAACAGTCTGCGGAGGAGAGATCATCATCG 4255
Qy 3977 ACGGGTCCCATTTGCCACCTGGGCTGACACACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4036
Db 4256 ATGGATCAACATCCCAAGATGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 4315
Qy 4037 CCCAGGACCCCATCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4096
Db 4316 CCCAGGACCCCTGTTTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4375
Qy 4097 ACTCGGAGGCTGATCTGGGCGCCCTGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4156
Db 4376 ACTCGGATGAAGAGTCTGGAGCTCCCTGGAGCTGGCCCGCTGAGGACTTCTGCTGCTGCTG 4435

Qy 4157 GCCTGCCCGCCAGCTGCAGTACAGTGTGCTACCGAGCGGAGGACCTGAGCGTGGGCC 4216
Db 4436 CCCTTCTTCCAGAGCTAGACCATGAATGTGCAGAGCGGAGGAGAACCTCAGTGTGGGC 4495
Qy 4217 AGAAGACAGCTCTGCTGCTGGCAGCTGCTTCTCCGGAAGACCCAGATCCTCATCTGG 4276
Db 4496 AGCGCAGCTTGTGCTGCTAGCCGCGGCTGCTGAGGAAGACGAAGATCCTTGTGTTGG 4555
Qy 4277 ACGAGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4336
Db 4556 ATGAGGCCACGCGAGCGCTGGACCTGGAAGGAGGACGCTCATCCAGTCCACCATCGGA 4615
Qy 4337 GCTGCTTGTGACAGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4396
Db 4616 CACAGTGTGAGGACTGCAACCTGCTTCTTCTACAGCATGSCCAAGACGCGCTTGGT 4675
Qy 4397 GTGCCCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4456
Db 4676 ACACAAGGTGATGCTTGTGCAAGAGGAGAAATCCAGAGTACGGCGGCCCATCGGACC 4735
Qy 4457 TCTGCTGCCCAAGAGGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4508
Db 4736 TCTGCTGAGCAGAGTCTTCTTCTACAGCATGSCCAAGACGCGCTTGGT 4787

RESULT 3

US-08-460-907B-3
; Sequence 3, Application US/08460907B
; Patent No. 5891724
; GENERAL INFORMATION:
; APPLICANT: Deeley, Roger G.
; APPLICANT: Cole, Susan P.C.
; TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
; RESISTANCE ON A CELL
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,907B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1551
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5011 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 196..4788
US-08-460-907B-3

Query Match 27.2%; Score 1227.6; DB 2; Length 5011;
Best Local Similarity 55.8%; Pred. No. 4e-281;
Matches 2538; Conservative 0; Mismatches 1934; Indels 80; Gaps 7;

QY 36 GGTCTGGAACACAGACAGAGCTGAACCTGGCCGACACAGCTGCTGAGCCTGTGCTTCCT 95
DB 237 GCTCTGGAGCTGGAATGACGTGGAAATACAGAACCCGACCTTACCAAGTCTTTCA 296

QY 96 GAGAACAGCAGGGGTCTGGGTACCCCATGATCTGCTGGGTCTTGGTCCCATCTACCT 155
DB 297 GAACAGGCTCTCGTGGGTGCTTGTCTTTTACCTCTGGGCTGTTCCCTCTCTACTT 356

QY 156 CTTCTTCATCCACACACATCGCGGGGCTACCTCCCGATGTCGCCATCTTCAAGCCAA 215
DB 357 CCTCTATCTCTCCGACATACCGGAGCTACATTCAGATGACACCTCTCAACAAACCAA 416

QY 216 GATGGTCTTGGATTCGCCCTCATAGTCCCTGTGTACCTCCAGGTGCTGCTGCTTTG 275
DB 417 AACTGCCCTGGGATTTTGTCTGGATGCTGCTGCTGGGACACCTCTTCTACTCTTTCTG 476

QY 276 GAAATCCAAAGAGGACGCTGAGGCCCCAGAAATTCCTCATCTACTGTGTGGCT 335
DB 477 GGAAGAAGTCGGGCATATCTCTGGCCGACAGTGTCTGTGTCAGCCCACTCTTTGGG 536

QY 336 CACACAGATGAGTTTGCAGTGTTCCTGTATACACCGAGAGGAAAGGAGTCCAGTC 395
DB 537 CATCACACGCTCTGCTGCTACCTTTTAAATTCAGCTGGAGAGGAGGAGGAGTTCAGTC 596

QY 396 ATCTGGAGTCTGTTTGGTTTACTGGCTTCTGCTTGTCTTGGCAGCTACCAACGCTGC 455
DB 597 TTCAGGATCATCTCTACTTCTGCTGGCTGTAGCCCTAGTGTGCTCCATGCCATCTCGAG 656

QY 456 CCAGCAG-----GCCCTCGAGAGGGGCTTCCAGAGAGCCCTGTCGCCACCTGTC 506
DB 657 ATCAAAATATGACAGCCTTAAAGAGGATGCCAGGTGGACCTGTTGCTGACATCAC 716

QY 507 CACTACCTATGCTGCTCTGCTGGTGGGCACAGTTTGTCTGCTGCTGCTGGGGATCA 566
DB 717 TTTCTAGCTACTTTTCCCTCTTACTCAATTCAGCTGCTGTTGCTGTTTCTCAGATCG 776

QY 567 ACCCCCTCTTCCCTGAAGACCCGACAGTCTTAACCCCTGTCCAGAGACTGGGGCAGC 626
DB 777 CTCACCCCTGTTCTCGAARACATACACAGACCTATCCCTGCCAGATCCAGCGTTC 836

QY 627 CTTCCCTCCAAAGCCACGCTTCTGGTGGTCTTCTGGCCTGGTCTGGAGGGATACAGAG 686
DB 837 CTTCCCTCGAGGATCACCTTCTGGTGGATCACAGGGTTGATGTCGGGGCTACCGCCA 896

QY 687 GCCACTGAGACCAAAAGACCTCTGCTGGCTTTGGGAGAGAAATCTCTCAAGAACTTGT 746
DB 897 GCCCTCGAGGGGAGTGACCTCTGGTCTTAAACAAAGGAGACACGCTCGGAACAAGTCGT 956

QY 747 TTCCTGGCTTGAAGAGGATGAGGACCGC-----AGTGAGCCCGGAGGCACACAA 802
DB 957 GCCTGTTTGGTAAGAACTGGAAGAGGAATGCGCCACAGCTAGGAAGCGCGGTGAA 1016

QY 803 AGCAATAGCATTTAAAGAGAAAGGGCGAGTGGCATGAAGGCTCA-----849
DB 1017 GGTGTGTACTCTCCAGGATCTGCCAGCCGAAAGAGAGTTCCAAGTGGATGCGAA 1076

QY 850 -----GAGACCGAGCCCTTCTTAGGCAAGAAGGAGCCAGTGGCGCCACTGTCT 899
DB 1077 TGAGGAGGTGGAGGCTTTGATCGTCAAGTCCCAAGAGGAGTGAACCCCTCTCTGTT 1136

QY 900 GAAGGCCATCTGGCAGGTGTTCCATTCTACCTTCTCTCTGGGACCCCTCAGCCTCATCAT 959
DB 1137 TAAGGTGTATACAAGACCTTTTGGGCCCTTCTCTCATGAGCTTCTTCTCAAGGCCAT 1196

QY 960 CAGTGATGCTTTCAGGTTTCACTGTCCCCAAGCTGTCCAGCCTTCTCTCGAGTTATTGG 1019
DB 1197 CCAGACCTGATGATGTTTCCGGGCCGAGATCTTAAAGTTGCTCATCAAGTTCGTGAA 1256

QY 1020 TGATCCCAAGCCTCCAGCCTGGAAGGCTTACCTCTCGCCGCTGCTGATGTTCTCTCAGC 1079
DB 1257 TGACACGAAGGCCCCAGACTGTCAGGGCTTCTTACACCGTGTCTGTTGTTGCTCAGCTGC 1316

QY 1080 CTGCTGCAAAAGCCTGTTTGTAGCAGCAGAACATGTACAGGCTCAAGGTGCCGAGATGAG 1139
DB 1317 CTGCTGCAAGCCCTGCTGCTGTCACCACTTCTCTCATGCTCTGCTCAGTGGCATGAG 1376

QY 1140 GTTGGGCTGGCCATCACTGGCTGTGTGTACAGAAAGGTCTCTGCTGCTGCTCAGCGGCTC 1199
DB 1377 GATCAAGACCGTGTCTATTTGGGCTGTCTATCGGAAGGCCCTGGTGATCACCAATTCAGC 1436

QY 1200 CAGAAAGCCAGTGGGCTGTGTGTCAATCTGTGTCTCGTGGAGCTGCAGCGGCT 1259
DB 1437 CAGAAATCCTCCACGCTGCGGAGATGTCAACCTCATGCTGTGGAGCCTCAGAGGTT 1496

QY 1260 GACGAGAGCTCTCTTACCTCAACGGGCTGTGGTGTGCTCTGCTTGGATCGTGGTCTG 1319
DB 1497 CATGACTTGGCCAGCTATTAACATGATCTGTGTCAGCCCCCTGCAAGTCACTCTTGC 1556

QY 1320 CTTGCTCTATCTCTGGCAGCTCTGGGCCCTCCGCCCTCACTGCTGCTGCTCTTCTCT 1379
DB 1557 TCTCTACCTCTGTGGCTGATCTGGGCCCTTCCGCTGCTGGTGGAGTGGCGGTGATGCT 1616

QY 1380 GAGCCTCTCTCTGTAATTTCTTCAATCCAAAGAAAGAACCACTCAGAGGAGCA 1439
DB 1617 CCTCATGCTGGCCGTCATGCTGTGATGCGATGAAGACCAAGAGCTATCAGTGGCCCA 1676

QY 1440 AATGAGCAGAGGACTCACGGCAGCTCAGCAGCTCTATCTCTCAGAGAACTCAAGAC 1499
DB 1677 CATGAAGCAAGAACTCGATCAAGCTGATGAACGAAATTTCTCAATGGGATCAAACT 1736

QY 1500 CATCAAGTTTCACTGGCTGGGAGGAGCCTTTCTGACAGAGCTCTGGGACCTCCGAGGCA 1559
DB 1737 GCTAAAGCTTTATGCTGGAGCTGGCATTCAGGACAAAGGTGCTGGCCATCAGCAGGA 1796

QY 1560 GGAGCTGGCGCTTGGCGACCTCGCGGCTCTCTTCTCTGCTGCTGCTGCTGCTCTTCCA 1619
DB 1797 GGAGCTGAAGTGTGTAAGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1856

QY 1620 AGTGTCTACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1679
DB 1857 CTGACCGCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1916

QY 1680 TGCTA---TGAATGACAGAAAGCCTTTGTGACTCTACAGTCTTCAACATCTCAACAA 1736
DB 1917 CAACATCTGTGATGCCAGACAGCTTCTGCTGCTTGGCCTTGTTCACATCTCTCCGTT 1976

QY 1737 GGCCAGCCTTCTGCTGCTTCTCCATCCACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1796
DB 1977 TCCCTGAACATTTCTCCCATGCTCAGCAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 2036

QY 1797 CCGTCTGGTCACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1856
DB 2037 ACGCTGAGGATCTTCTCTCCCATGAGGAGCTGGAACCTGACAGCATCGAGCGACGCC 2096

QY 1857 CTCCTGGAAGCCTCGCGGAGGATTTGATCACCATACACAGTGCACCTCTCGCTGCTGCT 1916
DB 2097 TGTCAAGACGCGGGGCGACAGACGATCACCTGAGGAATGCCATTACCTGCTGCTGCT 2156

Db	4316	CCGAGGACCCCTGTTTGTGTTTCCGTTCCCTCCGAATGAACCTGGACCCATTACACCGAGT	4375
QY	4097	ACTCGGAGGAGGCTATCTGGGACGACCCCTGGAGACCGTCCAGCTCAAAGCCCTTGGTGGCCA	4156
Db	4376	ACTCGGATGAAGAAGTCTGGAGCTCCCTGGAGCTGGCCACCTGAAGSACTTCGTGTTCAG	4435
QY	4157	GCTCTGCCGCGCAGCTGCAGTCAAAAGTGTCTGACCGAGGCGAGSACTGAGCGTGGGCC	4216
Db	4436	CCCTTCTTGACAAAGCTAGACCATGAATGTGCAAGAAGCGGGGAGAACTCAGTGTGCGGC	4495
QY	4217	AGAAACAGCTTCTGTCTGTGGCACGCTGCCCTTCTCCGAAACACCCAGCATCTCATCTCGG	4276
Db	4496	AGCGCCAGCTTGTGTGCTTAGCCCGGCGCTCTGTAGAAAGACAGAGATCCTTGTGTGTGG	4555
QY	4277	ACGAGGCTACTGCTGCGCTGGACCCCTGGCACGAGSCTGCAGATCGAGGCCATGCTCGGGA	4336
Db	4556	ATGAGGCCACGCGACGCGTGGACCTTGGAAACGGACGACCTCATCCAGTCCACATCCGGA	4615
QY	4337	GCTGGTTTGCACAGTGCACATGTGCTGCCCATTTGCCACCGGCTCGCTCGGTGATGGACT	4396
Db	4616	CACAGTTTCGAGGACTGCACCGTCTTACCATTGCCCCCGGCTCAACACCATCATGGACT	4675
QY	4397	GTCCCGGGTCTTGTCATGGAACAAGGGCGAGTGGCAGAGAGCGGACGCCCGGCCAGC	4456
Db	4676	ACACAAGGGTGATCGTCTTGGACAAAGGAGAAATCCAGGAGTACGGCGCCCCCATCGGACC	4735
QY	4457	TGCTGCCCCAGAAGGCGCTGTTTTACAGACTTGGCCCCAGGAGTCAGGCCTCGT	4508
Db	4736	TCTTCGACGAGAGAGGTCTTTTCTACAGCATGGGCAAGACCGCGGCTTGGT	4787

RESULT 4

US-08-463-179A-3
Sequence 3, Application US/08463179A
Patent No. 6001563
GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: METHODS FOR IDENTIFYING CHEMOSENSITIZERS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463.179A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-OCT-1992
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-OCT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A. Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: POI-002CP8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:

Db 1077 TGAGGAGGTGGAGGCTTTGATCGTCAAGTCCCCACAGAAAGGAGTGGAAACCCCTCTCTGTT 1136
QY 900 GRAGGCCATCTGGCAGGTGTTCCATCTACCTTCTCTCCCTGGGACCCCTCAGCCCTCATCAT 959
Db 1137 TAAGTGTGTTATACAGACCTTTGGGCCCTTACTTCCCTCATGAGCTTCTCTCAAGGCCAT 1196
QY 960 CAGTGAATCTTTCAGGTTCACGTGTCTCCCAAGCTGTCTCAGCCCTTTTCTCGAGTTCATTTGG 1019
Db 1197 CACAGACCTGATGATGTTTTCGGGCCCGCAGATCTTAAAGTTGCTCATCAAGTTCGTGAA 1256
QY 1020 TGATCCCAAGCCTCCAGCCTGGAAGGGCTACCTCTCTCGCGTGTCTGATGTCTCTCAGC 1079
Db 1257 TGACACGAAGGCCCCAGACAGTGCAGGGCTACTTCTACACCGTGTCTCTGTTGCTACTGC 1316
QY 1080 CTGCGCTGCAAAAGCGCTTTTGACAGCAGAACATGTACAGGCTCAAGGTGCGCGCAGATGAG 1139
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QY 1200 CAGAAAGCGCAGTGGCGGTGATGTGTCTCAATCTGTGTCTCGTGGAGCTGCAGCGGCT 1259
Db 1437 CAGAAAATCTCCACGGTCTGGGGAGATTTCTCAACCTCATGTCTGTGGACGCTCAGAGGTT 1496
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Db 1617 COTCATGGTGGCCGCTCAATGTCTGATGCGATGAAGACCAAGACGATATCAGGTGGCCCA 1676
QY 1440 ANTGAGGCAAGGACTCAGGCGAGGCTCACCAGCTCTNTCTCAGAACTCGAAGAC 1499
Db 1677 CATGAAGACAAAGACAATCGGATCAAGCTGATGAACGAAATTTCTCAATGGGATCAAGT 1736
QY 1500 CATCAAGTTTCAATCTGTGGAGGAGGCTTCTTCTGGACAGAGTCTCTGGGATCCGAGGCCA 1559
Db 1737 GCTAAGCTTTATGCTGGAGCTGGCATTCAGGACAGAGGTGCTGGCCATCAGGCAGGA 1796
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QY 1620 AGTGTCTACATTTCTGGTGGCACTGTGTGTGTTGCTGTCCACACTCTGTGTGGCCGAGAA 1679
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QY 1680 TGCTA---TGAATCAGAGAAAGCTTTGTGACTCTCACAGTTTCTCAACATCTCTCAACAA 1736
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QY 1737 GGCCCAAGGCTTTCCTGCGCTTCTCATCCACTCCTCTGTCAGGCGCGGCTGTCTTTGA 1796
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QY 1797 CGCTGTGTCTACCTTCTCTGTCTGCTGGAAGAGTGTGACCCCTGGTGTGTAGACTCAAGTTC 1856
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Db 2097 TGTCAAGACGCGGGGCAACAGCATCACCGTGAAGATGCCAATTCACCTGGGC 2156
QY 1917 CCAGGAAGCCCTCTCTGCTCTCCACAGATAAACCCTCAGCGTGCCGCCAGGGTGTCTGT 1976
Db 2157 CAGGAGCGACCCCTCCACACTGAATGGCATCACCTTCTCCATCCCGGAAGGTGCTTTGCT 2216

QY 1977 GGCTGTTGTCTCGTCCAGTGGGGGAGGAAAGTCTCCTCTGCTGTCCGCCCTCTCTTTGGGA 2036
Db 2217 GGCCGTGGTGGGCGAGTGGGCTCGGAAAAGTGTCTCCTGCTCTCAGCCCTCTTTGGGTGA 2276
QY 2037 GCTGTCAAAAGGTGAGGGGTTCTGTGAGCATCGAGGTGCTGTGGCCCTACGTGCCCCAGGA 2096
Db 2277 GATGGACAAGTGGAGGGGACGTGGCTATCAAGGGGTCTCGTGGCCCTATGTGTGCCACAGCA 2336
QY 2097 GGCTGGGTGAGAAACACCTCTCTGTGTGAGAAATGTGTCTTGGGGAGGAGCTGGACCC 2156
Db 2337 GGCTGGATTCAGATGATCTCTCCGAGAAACATCTTTTGGATGTACGTGGGAGGA 2396
QY 2157 ACCTGGCTGGAGAGTACTAGAGCCTGTGCCCTGCAGCCAGATGTGGACACTTCTCC 2216
Db 2397 ACCATATTACAGTCTCGATACAGGCTGTGCCCTCTCCAGACCTTGGAAATCTCTGCC 2456
QY 2217 TGAGGGAATCCACACTTCAATTGGGAGCAGGCAATCTCTCCGAGGCCAGAGCA 2276
Db 2457 CAGTGGGATCGACAGAGATTGGCAGAGGGGCTGAACTGTCTGGGGACAGAGCA 2516
QY 2277 GCGGCTGAGCCTGGCCGGGCTGTATACAGAAAGGCAAGCTGTGTACCTGTGGATGACCC 2336
Db 2517 GCGGCTGAGCCTGGCCGGGCTGTACTTCCAGGCTGACATTTACCTCTTCGATGATCC 2576
QY 2337 CCTTGGCGGCTGGATGCCACGTTGGCCAGCATGTCTTCAACCAAGTCTATTGGGCTGG 2396
Db 2577 CCTCTCAGCAGTGGATGCCATTTGGGAAAACACATCTTTGAAAATGTGATTGGCCCAA 2636
QY 2397 TGGGCTACTCCAGGGAACACAGGATTTCTGTGACGACGCACTCCACATCTCTGCCCA 2456
Db 2637 GGGATGTGGAAGAACAGACGCGGATCTTGGTCAACACAGCATGAGCTACTTGGCCGCA 2696
QY 2457 GGCTGATTTGATCATAGTGTGTCGCAATGGGGCCATCGCAGAGATGGTCTTCTTACCAGGA 2516
Db 2697 GGTGAGCTCATCATCTGTCATGAGTGGCGCAAGATCTCTGAGATGGGCTCTTACCAGGA 2756
QY 2517 GCTTCTCAGAGAAAGGGGCGCTCTGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGA 2576
Db 2757 GCTGTCTGGCTCGAGAGCGGCGCTTCG-CTGAGTCTCTGCTGCTATGCTCCAGCAGACAGC 2815
QY 2577 TAGAGAGAGGAGAAACAGAACTGGGACCAAGCCACCAAGGCCCCAGAGGACCTCTGC 2636
Db 2816 AGGACAGAGTGCAGAGGAGACGGGTACGGGCTCAGCGGTCCAGGGAAGAACAA 2875
QY 2637 AGCAGAGGCGCGAGCTTAGACGCGCAGAGGTCCATCAAGTCACTTCTCTTCTGAGAA- 2691
Db 2876 AGCAATGGAGAAATGGCATGCTGTGACGACAGTGCAGGGAAGCAACTGCAGAGACAGC 2935
QY 2692 -----GACCGTACCCTTCAGAAAGCCCA-- 2716
Db 2936 TCAGCAGCTCTCTCTTATAGTGGGGAACATCAGAGGCAACCAACAGACCCGACAGAAC 2995
QY 2717 CAGAGTTCCTCTGAGTGAOCCTTGACAGGCGAGGATGGCCAGAGAAAGACAGCATCC 2776
Db 2996 TGCAGAAAGCTGAGGCCCAAGAGGAGGAGACCTTGAAGCTGATGAGGCTTGACAAGGCGC 3055
QY 2777 AATACGGCAGGTGAAGGCCACAGTGGCCTTACCTTACCTGCGTGGCGTGGGACACCCCC 2836
Db 3056 AGACAGGCGAGGTCAAGCTTTCGCTGTACTGGGACTACATGAAGGCCCATCGGACTCTTCA 3115
QY 2837 TCTGCGCTCTACGCACTTCTCTCTCTCTGCCAGCAAGTGGGCTCTCTTCTGCGGGGCT 2896
Db 3116 TCTCTCTCTCAGCATCTTCTCTTTTCTATGTGTAACTATGTCTCGGCTGGCTTCCAAT 3175
QY 2897 ACTGGCTGAGCCTGTGGGGGAGCAGCCCTGACGTAGTGGGCGAGCAGCAGCAGCAGCC 2956
Db 3176 ATTGGCTCAGCCTCTGAGCTGATGACCCCATCTGTCAAGGGGACTCAGGACACAGAAAG 3235
QY 2957 TGGCTGGCGGATCTTGGGCTCTCTGGCTGTCTTCCAAGCCATTTGGGCTGTCTTTCCTCCA 3016
Db 3236 TCGGCTGAGCGCTTATGAGGCGCTTGGGCATTTTCAAGGGATCGCGCTGCTTTGGCTACT 3295

QY	3017	TGGCTGCGGTGCTCCTTAGTGTGGGGCCCGGCATCCACAGTTTGCTCTTCCAGAGGCTCCTGT	3076
Db	3296	CCATGGCCGTGCTCCATCGGGGGATCTTGCTTCCCGCTGCTGCCAGTGGACCTGCTGC	3355
QY	3077	GGGATGTGGTGGCATCTCCCATCAGCTTCTTTGAGGGACACCCATTTGGTTCACCTGCTAA	3136
Db	3356	ACAGCATCTCTGCGGTCACCCATAGCTTCTTTGAGGGACCCCACTGGCAACTGGTGTA	3415
QY	3137	ACCGCTTCTCCAAAGGAGACACACGCTTGACGTGGACATCTCCAGACAAACTCCGGTCCC	3196
Db	3416	ACCGCTTCTCCAAAGGAGTGGACACAGTGCACATGATCCCGGAGGTGCATCAAGATGT	3475
QY	3197	TGCTGATGTACGCCCTTTGGACTCCTGAGGTACGCTTGGTGTGGAGTGGCTTACAGAGCTGTATG	3256
Db	3476	TCATGGGCTCCCTGTTCACAGCTCATTTGGTGGCTGCATGGTTATCCTGCTGGCCACGCCA	3535
QY	3257	TGSCCACTGTGGCCATCTCTGCCACTGTTTCTCTACCGTGGGTTTCAGAGCTGTATG	3316
Db	3536	TCGCCGCCATCATATCTCCCGCCCTTTGGCTCATCTACTTCTTCGTCAGAGGTTCTACG	3595
QY	3317	TGGTTAGCTCATGCCAGCTGAGACGTTGAGGTGACGCCAGTACTCGTCTGTCTGTGCTGCC	3376
Db	3596	TGGCTTCTCTCCCGCAGCTGAAGCGCTCGAGTCGTGACGCGCTCCCGGCTCATTTCCG	3655
QY	3377	ACATGGCTGAGACGTTTCCAGGGCAGCACAGTGTCTCGGGCATTTCCAAACCAGGCCCT	3436
Db	3656	ATTTCACGAGACCTTGTCTGGGGTCAGCGTCATTTCGAGCCCTTCGAGGAGCAGGACGGT	3715
QY	3437	TTGTGGCTCAGAACATGCTCGGTAGATGAAGCCAGAGGATCAGTTTCCGCGCACTGG	3496
Db	3716	TCATCCACAGAGTGCACCTGAAGGTGGAGAGAACCAAGAAGCCATTATCCCCAGCATCG	3775
QY	3497	TGGCTGACAGGTGGCTTGGCGCAATGTGAGCTCTCTGGGAAATGGCCTGGTGTGTGCAG	3556
Db	3776	TGGCCACAGGTGGCTTGGCCGTGCGGTGGAGGTGTGGGCAACTGCATCTGTCTGTG	3835
QY	3557	CCGCCACGTGCTGTGCTGTAGCAAGCCACTCAGTCTGGCCTCGTGGGCTCTCTCG	3616
Db	3836	CTGCCCTGTTTGGGTGATCTCCAGCACAGCCTCAGTCTGGCTTGGTGGGCTCTCAG	3895
QY	3617	TCCTGCTGCTCCAGTGCACCCAGACACTGCAGTGGTGTTCGCAACTGGACAGACC	3676
Db	3896	TGCTCTACTCATGTGAGGTACACCGTACTTGAACGTGGCTTCCGGATGTCTATCTGAAA	3955
QY	3677	TAGAAACAGCATCTGTCTAGTGGAGCGGATCAGGACTATGCCCTGGAGCCCAAGAGG	3736
Db	3956	TGGAACAACATCTGTGGCGGTGAGAGGCTCAAGAGTATTCAGAGACTGAGAGGAGG	4015
QY	3737	CTCCCTGGAGGTGCCACATGTGCAGTCAAGCCCCCTGGCCTCAGGCGGGCAGATCG	3796
Db	4016	CGCCCTGGCAATCCAGGAGACAGTCTCGCCCCAGCAGCTGGCCCCAGGTGGGCCAGTGG	4075
QY	3797	AGTTCGGGACTTTGGGCTAGATGCCACCTCAGCTCCCGCTGGCTGTGCAGGGCGTGT	3856
Db	4076	AATTCGGAACTACTGCTGCGCTACCGCAGGAGACTGGACTTGTCTCAGGCACATCA	4135
QY	3857	CTTTCAAGATCCAGCAGGAGAGTGGGCATCTGTTGGCAGGACCGGGCAGGGAAGT	3916
Db	4136	ATGTCAGATCAATGGGGAGAAAGTTCGCGATCTGGGGCGGACGGGAGCTGGGAAAT	4195
QY	3917	CCTCCTGGCCAGTGGGTGCTGCGGCTCCAGGAGCAGCTGAGGGTGGGATCTGGATCG	3976
Db	4196	CGTCCCTGACCTGGGCTTATTTCCGATCAACGAGTCTGCCGAAGGAGATCATCATCG	4255
QY	3977	ACGGGTTCCCATTTGCCACGTGGGCTGTCACACTGCGCTCCAGGATCAGATCATCC	4036
Db	4256	ATGGCATCAATCGCAAGATCGGCTGTCAGACCTCCCGCTTCAAGATCACCATCATCC	4315
QY	4037	CCCAGAGCCCCATCTGTCTCCCTGGCTCTCTGCGGATGAACCTCGACCTGCTGCAGGAC	4096
Db	4316	CCCAGGACCTGTTTTGTTTCGGGTTCCCTCCCAATGAACCTGAGCCCATTCAGCCAGT	4375
QY	4097	ACTCGGACGAGGCTATCTGGCAGCCCTGGAGACGGTGCAGCTCAAAGCCTTGTGGTCA	4156

[illegible]

RESULT 5

RESOL 3
US-08-461-384B-3
: Sequence 3, Application US/08461384B
: Patent No. 6025473
: GENERAL INFORMATION:
: APPLICANT: Cole, Susan P.C.
: APPLICANT: Deeley, Roger G.
: TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: PARTO RESEARCH & DEVELOPMENT INNOVATIONS
: STREET: Queen's University at Kingston
: CITY: Kingston
: STATE: Ontario
: COUNTRY: CANADA
: ZIP: K7L 3N6
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII text
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/461,384B
: FILING DATE: 05-JUN-95
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/966,923
: FILING DATE: 27-OCT-1992
: APPLICATION NUMBER: 08/029,340
: FILING DATE: 8-MAR-1993
: APPLICATION NUMBER: 08/141,893
: FILING DATE: 26-OCT-1993
: APPLICATION NUMBER: 08/407,207
: FILING DATE: 20-MAR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Steeg, Carol Miernicki
: REGISTRATION NUMBER: 39,539
: REFERENCE/DOCKET NUMBER: Q1547
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (613) 545-2342
: TELEFAX: (613) 545-6853
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5011 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double

1

QY	1080	CTGCGCTGCAAAAGCGCTGTTTGGACGACGACAACATGTACAGGCTCAAGGTGCGCGCAGATGAG	1139
DB	1317	CTGCGCTGCAGACCCCTCGTCTCGACACGATGACTTCCACATCTGCTTCGTAGTGGCATGAG	1376
QY	1140	GTTGCGGTGGGCATCACTATGGCCCTGGTGACAGAAAGGTCCTTGGCTCTCTCCACAGCGCTC	1199
DB	1377	GATCAAGACCGCTGTCAATGGGGCTGTCTATCGGAAGGCCCTGGTGATCACCAATTCAGC	1436
QY	1200	CAGAAAGGCCAGTGGGTGGGTGATGTGTCATCTGGTGTCCGTGGAGCGTGACAGCGGCT	1259
DB	1437	CAGAAAAATCCCTCCAGCGTGGGGAGATTCAACCTCATGTCTGTGGAGCGCTCAGAGGTT	1496
QY	1260	GACCCAGAGCGTCCTTACTCCAAAGGGCTGTGGCTGCGCTCTGCTGTGGATCGTGTCTG	1319
DB	1497	CATGGACTTGGCCACGTATCAATTAACATGATCTGGTCAGCCCCCTGCAAGTCATCCTTGC	1556
QY	1320	CTTCTGCTATCTCTGGCAGCTCCTCGGGGCCCTCCGGCCCTCAATGCCATCGCTGTCTTCC	1379
DB	1557	TCCTTACCTCTGTGGCTGAATCTGGCGCCTTCCGCTCTCTGGCTGGAGTGGCGGTGATGGT	1616
QY	1380	GAGCCTCCTCCTCTGAATTTCTTATCTCCAAGAAAGAACACCACCATCAGGAGGACGA	1439
DB	1617	OCCTATGTGGCCGTCAATGCTGTGATGGCGATGAAGACCAAGACGTATCAGGTGGCCCA	1676
QY	1440	AATGAGGCAGAGGACTCACGGCAGCGCTCACAGCTCTATCTCTCAGGAATCTCAGGAAC	1499
DB	1677	CATGAAGAGCAAGAACATCGGATCAAGCTGATGAACGAAATTTCAATGGGATCAAGT	1736
QY	1500	CATCAAGTTTCATGCTGGGAGGAGCCCTTCTTGACACAGAGTCCTGGGCATCCGAGGCCA	1559
DB	1737	GCTAAAGCTTTATGCTGGGAGCTGGCATTTCAAGGACAGAGTGCTGGCCATCAGGCAGGA	1796
QY	1560	GGAGTGGGGCCTTGGGACCTCGGCCCTCCTCTTCTGTGTGTCGTGGTGTCTCTTCCA	1619
DB	1797	GGAGCTGAAGTGCTGAAAGATCTGCGCTACCTCTCAGCCGTGGGACCTTCACCTGGGT	1856
QY	1620	AGTGCTACATTTCTGGTCGCACTGGTGGTGTGTCGTGCCACACTCTGGTGGCGCAGAA	1679
DB	1857	CTGCAGCGCCCTTTCTGGTGGCCCTGTGCACATTTGCCGTCTACGTGACCATTTGACAGAA	1916
QY	1680	TGCTA---TGAATCGAGAGAAAGCCCTTTGTGACTCTCAAGTTCACACTCCTCAACAA	1736
DB	1917	CAACATCCTGGATGCCACAGACGCTTCTGTCTTTTGGCCTTGTTCACATCCTCCGGTT	1976
QY	1737	GGCCAGGCTTTCGTGCCCTTCTCCATCCACTCCCTCGTCCAGGCCCGGGTGTCTTTGA	1796
DB	1977	TCCCTTGAACTTCTCCCATCGGTATCAGCAGCATCTGTGACGGGAGTGTCTCCCTCAA	2036
QY	1797	CCGTCTGTGCTACCTTCTCTCGCTGGAAAGAGTTGACCTGTGTCGTAGACTCAAGTTC	1856
DB	2037	ACGCTGAGGATCTTCTCTCCCATGAGGAGCTGGAACCTGACAGCATCGACGAGCGGC	2096
QY	1857	CTCTGGAAGCGTGGCCGGGAAGATTGCATCACCATACAGAGTGCCACTTCGCCCTGTGTC	1916
DB	2097	TGTCAAAGACGGCGGGGCAGCAACAGCATCACCGTGAAGAAATGCCATTCACCTGGGC	2156
QY	1917	CCAGGAAGCCCTCCCTGCCCTCCACAGAAATAACCTCAGGTGCCCCCAGGCGTGTCTGCT	1976
DB	2157	CAGGAGCGACCTCCCACTGAATGGGATCACCTTCTCCATCCCGGAAGTGCTTTGGT	2216
QY	1977	GGCTGTTGTCCGTCCAGTGGGGGAGGAAAGTCCCTCCCTGTGTCGGCCCTCCTTTGGGA	2036
DB	2217	GGCCGTGTGGCCAGGTGGGCTGGGAAGATTGTCCCTGCTCTCAGCCCTCTTGGCTGA	2276
QY	2037	GCTGTCAAGGTGAGGGGTTTCGTGAGCATCGAGGGTGCTGTGGCTTACGTGCCCGGCA	2096
DB	2277	GATGCACAAAGTGGAGGGGCAGTGGCTATCAAGGGCTCCGTGGCCCTATGTGCCACAGCA	2336
QY	2097	GGCCTGGTGCAGAACACTCTGTGGTAGAAGATGTGCTTCCGGGCGAGGAGCTGCACCC	2156
DB	2337	GGCCTGGATTTCAGATGATCTCTCCGAGAAACATCTCTTTTGGATGTACGTCTGGAGGA	2396

QY	2157	ACCTCGCTGGAGAGTACTAGAGCGCTGTGCCCTGCGCCAGCCAGATGTGGACAGCTTCCC	2212
Db	2397	ACCATATTACAGTCTCGTGATACAGCGCTGTGCCCTCCCTCCAGACGTGGAATTCCTGCC	2456
QY	2217	TGAGGGAATCCACACTTCATTTGGGAGCAGGGCCATCAATCTCTCCGGAGGCCAGGAACA	2276
Db	2457	CAGTGGGGATCGGACAGAGATTGGCAGAAAGGCGTGAACCTCTCTGGGGAGCAGGAACA	2516
QY	2277	GGCGCTGAGCCTGGCCCGGGCTGTATACAGAAAGGCAGCTGTCTACTCTGCTGATGACCC	2336
Db	2517	GGCGTGTAGCCTGGCCCGGGCGCTGTACTCCACGCTGACATTTTACTCTTCCATGATCC	2576
QY	2337	CTTGGCGGCCCTGGATGCCACAGFTTGGCAGCATGTCTTTCAACAGGTCAATTTGGGCGCTGG	2396
Db	2577	CCCTCTCAGCAGTGGATGCCCATCTGGGAAACACATCTTTGAAATGTGATTGGCCCA	2636
QY	2397	TGGGCTACTCCAGGGAACACAGGATTTCTGTGACGCGACCACTCCACATCCTGTGCCCA	2456
Db	2637	GGGATGTCTGAAGACAGCGGGATCTTGTGTCAGCACGATGAGCTACTTTGCGCA	2696
QY	2457	GGCTATTGGATCATAGTCTGGCAATGGGGCCATCGCAGAGATGGTTCCTTACCAGGA	2516
Db	2697	GGTGGACGTCACTCATGATGGCGGCAGATCTCTGAGATGGCTCTCTTACCAGGA	2756
QY	2517	GGTTCTGCAGAGAAAGGGGGCCCTCGTGTCTTCTTGGATCAAGCCAGACAGCAGCAGGA	2576
Db	2757	GCTGCTGGCTCAGACGGCGCCTTCG-CTGAGTTCCTCGCTACCTATGCCAGCACAGGC	2815
QY	2577	TAGAGGAAGAGAAACAGACTCTGGGACAGCACCAAGGACCCAGAGGCACCTCTCTGC	2636
Db	2816	AGGACAGGATCGAGAGAAACGGGGTCCAGCGGCTCAGCGGTCCAGGGAAGGAAGCAA	2875
QY	2637	AGGAGAGGCGCCGAGCTTTAGAGCGGAGAGGTCCTCAAGTCAGTCCCTGAGAAG----	2691
Db	2876	ACCAATGGAGAATGGCATCTGTGTACCGACAGTGCAGGGGAAGCAACTGCAGAGACAGC	2935
QY	2692	-----GACCGTACCACCTTCAGAAGCCCAAGA--	2716
Db	2936	TCAGCAGCTCCTCCTCTCTATAGTGGGGACATCAGAGGCCACCACACACCGCAGAAC	2995
QY	2717	CAGAGGTTCTCTGGATGACCTTGACAGGCGAGGATGGCCAGGAGGAAGGACAGCATCC	2776
Db	2996	TCGAGAAAGCTGAGGCCAAGAGGAGGAGACCTTGAAGCTGATGGAGGCTGACAAGGCGC	3055
QY	2777	AATAGCGCAGGCTGAAGGCCACAGTGCACCTGGCCTTACCTGCTGCGTGGCGGCACCCGCC	2836
Db	3056	AGACAGGCGAGTCAAGCTTTCCTGTACTGGGACTACATGAAGGCCATCGGACTCTTCA	3115
QY	2837	TCTGCTCTACGACTCTTCCCTCTTCTCTGCCAGCAAGTGCCCTCTTCTGCGGGGCT	2896
Db	3116	TCTCCTTCTCAGCATCTTCTCTTTTCATGTGTAACCATGTGTCCGCGCTTCCAACT	3175
QY	2897	ACTGGCTGAGCCTGTGGGCGGAGACCCTGTCAGTAGGTGGGCGAGCAGCGCAGGAGCCGC	2956
Db	3176	ATTGCTCAGCCTCTGGATGATGACCCCATCGTCAACGGGACTCAGGAGCACACGAAAG	3235
QY	2957	TGCGTGGGGGATCTCGGGCTCTCGGCTGTCTCCAAGCCCATTTGGCGTGTTCCTTCCA	3016
Db	3236	TCCGGCTGAGCCTCTATGGAGCCCTTGGCATTTTCAAGGGGATCGCCGTGTGTGGCTACT	3295
QY	3017	TGGCTGCGGTGCTCTAGSTGGGGCCCGGCATCCAGGTTGCTCTTCCAGAGGCTCTGT	3076
Db	3296	CCATGGCGTGTCCATCGSGGGGATCTTGGCTTCCCGCTGTCTGCACGTGGACCTGCTGC	3355
QY	3077	GGGATGTGGTGGCATCTCCCATCAGTTCTTTGAGCGGACACCCATTTGGTTCAGTGCTAA	3136
Db	3356	ACAGCATCTTGGCGTCAACCATGAGCTTCTTTGAGCGGACCCCATGAGTGGGAACCTGGTGA	3415
QY	3137	ACCGCTTCTCCAAGCAGACAGCGTTTACGCTGGCATTTCCAGCAAACTCCGCTCCC	3196
Db	3416	ACCGCTTCTCCAAAGAGCTGGACAGTGGATTCATGATCCCGGAGGTCTCAAGATGT	3475
QY	3197	TGCTGATGTACGCCCTTTTGACCTCTGGAGGTCAGCCTGTGTGGCAGTGGCTACCCAC	3256

Db 3476 TCATGGCTCCCTGTTCAACGTCATTTGGTGCCTGCATCGTTATCTCTGCTGCCACGCCCA 3535
QY 3257 TGGCCACTGTGGCCACTCCCTGCTCCTCTACGCTGGGTTTCAGAGCCTGTATG 3316
Db 3536 TGGCCCACTCATCATCCCGCCCTTGGCTCTATCTACTTCTTCGTCACAGAGTTCTACG 3595
QY 3317 TGGTTAGCTCATCCAGCTTGAGACGCTTGGAGTACGCCAGCTACTCGTCTGTCTGCTCC 3376
Db 3596 TGGCTTCCTCCCGGACGCTGAAGCGCTCGAGTCGCTCAAGCCGCTCCCGGCTATTTCC 3655
QY 3377 ACATGCTCAGACGTTCCAGCGCAGCACAGTGTGCTCGGGCATTCCGAAACCCAGGCCCT 3436
Db 3656 ATTTCACAGACCTTGTCTGGGGTCAGGTCATTCAGAGCTTCGAGGACGAGGCGCT 3715
QY 3437 TTGTGCTCAGAACATGCTCGCGTAGATGAAGCCAGAGGATFAGTTTCCCGCAGCTGG 3496
Db 3716 TCATCCACAGAGTACCTGAAGGTGCAGCAGAGAACAGAGGCTATTACCCAGCATCG 3775
QY 3497 TGGCTCAGAGTGGCTTGGGCCAATGTGGAGCTCTCTGGGAATGGCTGGTGTTCGAG 3556
Db 3776 TGGCCACAGGTGGCTGGCGCTGCGGCTGGAGTGTGTGGGCACTGCATCGTTCTGTTG 3835
QY 3557 CGCCACGCTGTCTGTGCTGAGCAAGCCACCTCAGTGTGCTGCTGCTGCTGCTGCTGCTG 3616
Db 3836 CTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3895
QY 3617 TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3676
Db 3896 TGTCTTACTCATTTGCAAGTTCACACGCTACTTGAACCTGGCTGCTGCTGCTGCTGCTG 3955
QY 3677 TAGAGACAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3736
Db 3956 TGGAAACCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4015
QY 3737 CTCCCTGGAGGCTGCCACATGCTGAGCTCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 3796
Db 4016 CGCCCTGGCAATCCAGGAGACACGCTCCGCCACGAGCTGGCCCGAGTGGCCGAGTGG 4075
QY 3797 AGTTCGGGACTTTGGGCTTAAGATCCGACCTGAGCTCCCGTGGCTGCTGCTGCTGCTGCTG 3856
Db 4076 AATTCGGAACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4135
QY 3857 CTTCAAGATCCACGAGAGAGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3916
Db 4136 ATGTCAGCATCAATGGGGAGAAAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4195
QY 3917 CTTCCCTGGCAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3976
Db 4196 CGTCCCTGACCTGGGCTTATTTCCGATCAACAGTCTCCGAGAGAGATCATCATCG 4255
QY 3977 AGGGGTCCCAATGTCACAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4036
Db 4256 ATGGGATCAACATCCCAAGATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4315
QY 4037 CCCAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4096
Db 4316 CCAGAGCCCTGTTGTTTTCGGGTTCCTCCGAATGAACCTGGACCCATCAGCCAGT 4375
QY 4097 ACTCGGAGGAGCTATCTGGGAGCCCTCGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4156
Db 4376 ACTCGGATGAAGATCTGGAGCTCCCTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4435
QY 4157 GCTTCGGGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4216
Db 4436 CCGTCTCTGACAAGTAGACCATGAATGATGTCAGAGGCGGGGAGAACCTCAGTGTGCGGC 4495
QY 4217 AGAAGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4276
Db 4496 AGCGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4555
QY 4277 ACGAGGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4336

Db 4556 ATGAGCCACCGCAGCGCTGGACCTGGAACGAGGAGACCTCATCTCAGTCCACCATCCGGA 4615
QY 4337 GCTGGTTTGACAGTGCACCTGTGCTGCCCATTTGCTGCCACCGCTGCTGCTGCTGCTGCTG 4396
Db 4616 CACAGTTTCGAGGAGTGCACCGTCTCTCACCATCGCCACCGCTCAACACCATCATGACT 4675
QY 4397 GTGCCCGGTTCTGGTCTATGACAGAGGCGGAGGTGGGAGAGGCGGAGCGGCCCGCCAGC 4456
Db 4676 ACAAGAGGTGATGCTCTTGGCAAGAGAGAAATCCAGGAGTAGGGGCGCCCATCGGACC 4735
QY 4457 TGTGTCGCCACAGAGGCGCTGTTTACAGACTGGCCCGAGGAGTCAAGGCTGCTGCTGCT 4508
Db 4736 TCTGTCAGCAGAGGCTCTTTTCTACAGCTGGCCCAAGAGCGCGGCTTGGT 4787

RESULT 7

US-08-463-092B-1
; Sequence 1, Application US/08463092B
; Patent No. 576880
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deesley, Roger G.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 435
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; CLASSIFICATION: 435
; APPLICATION DATA:
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; APPLICATION DATA:
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1546
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS

QY 2097 GGCCTGGGTGAGAACACCTCTGTGGTAGAAGATGTGTGCTTGGGCGAGGAGCTGGACCC 2156
DB 2337 GGCCTGGGATCAGATGATCTCTCCGAGAAACATCTTTTGGATGTACAGAGA 2396
QY 2157 ACCCTGGGTGAGAGAGTACTAGAACCTGTGGCCCTGACCGACAGATGTGGACAGCTTCC 2216
DB 2397 ACCATATTACAGGTCGATGATAGAGCGCTGTGCCCTCTCCAGACCTTGAATACTTGCC 2456
QY 2217 TGAGGGAATCACACTTCAATTGGGGAGAGGCAATGATCTCTCCGGAGGCCAAGAGA 2276
DB 2457 CAGTGGGATCGGACAGAGATTTGGCGAAGGGCTGAACCTGTCTGGGGGACAGAAACA 2516
QY 2277 GCGCTGAGCTGGCCCGGCTGTATACAGAAAGCAGCTGTGTACCTGCTGGATGACCC 2336
DB 2517 GCGCTGAGCTGGCCCGGCGGTGTATCTCAACGCTGACATTTACCTTCTCGATGATCC 2576
QY 2337 COTGGCCCTGGATGCCACCTGTGGCAGCATCTTTCAACAGGTCATTTGGGCTGG 2396
DB 2577 COTCTCAGCAGTGGATGCCATGTGGGAAACACATCTTTGAATAATGTGATTGGCCCAA 2636
QY 2397 TGGGCTACTCCAGGGAACACACAGGATCTCTGTGAGCAGCAGCTCCACATCTCTGCCCA 2456
DB 2637 GGGGATGTGAAGAACAAAGACCGGATCTTGTCTACGCACACAGCATGAGCTACTTCCGCA 2696
QY 2457 GGCTGATTGGATCATAGTGTCTGGCAAAATGGGGCCATCCAGAGATGGGTTCCTACCAAGA 2516
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[illegible]

RESULT 8

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US-08-462-109A-1
; Sequence 1, Application US/08462109A
; Patent No. 5882875
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deceley, Roger G.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,109A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PQI-002CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..4788
; IS-08-462-109A-1

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RESULT 9
US-08-460-907B-1
; Sequence 1, Application US/08460907B
; Patent No. 5891724
; GENERAL INFORMATION:
; APPLICANT: Deeley, Roger G.
; APPLICANT: Cole, Susan P.C.
; TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
; TITLE OF INVENTION: RESISTANCE ON A CELL
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,907B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

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QY 4217 AGAAGAGCTCTGTCTCTGGACGTCGCTTCTCCGGAGACCCAGATCTCTATCTGG 4276
Db 4496 AGCGCCAGCTTGTGTGCTAGCCCGGGCCCTGCTGAGGAGAGCAAGATCTTGTGTGG 4555
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QY 4457 TGTGCCCCAGAAAGGCTGTGTTTACAGACTGGCCCGAGGAGTCAGGCTGGT 4508
Db 4736 TCTGCAGCAGAGGCTCTTTTCTACAGCATGSCCAAGACGCGGCTGGT 4787

RESULT 10

US-08-463-179A-1
; Sequence 1, Application US/08463179A
; Patent No. 6001563
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING CHEMOSENSITIZERS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSES: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,179A
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PQI-002CP8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS

LOCATION: 196..4788
US-08-463-179A-1
Query Match 27.1%; Score 1222.8; DB 3; Length 5011;
Best Local Similarity 55.7%; Pred. No. 5.5e-280;
Matches 2535; Conservative 0; Mismatches 1937; Indels 80; Gaps 7;
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QY 396 ATCTGAGTGTCTGTTGGTGTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 455
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Qy	1200	CAGAAAGCCAGTCCGGTGGGTGATGTGCTCAATCTGTGTCTCCGTGGACGTGCAGACGGCT	1259
Db	1437	CAGAAATCTCCACGCTGGGGAGATTCTCAACCTCATGTCTGTGGACGCTCAGAGGTT	1496
Qy	1260	GACCGAGAGCGTCTCTTACCTCAACGGGCTGTGGCTGTGCTCTGTGATGTGGTGTG	1319
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Db	2217	GGCGGTGGGCGAGTGGCTGCGGAAGTGTGCTCTCTCAGCCCTCTTGGCTGA	2276
Qy	2037	GCTGTCAAGAGTGGAGGGTTCGTGAGCATCAGGAGGTGCTGTGGCCTACGTGCCCCAGGA	2096
Db	2277	GATGGACAAAGTTGGAGGGCAGTGGCTATCAAGGGTTCGGTGGCCATATGTGCCACAGCA	2336

QY	2097	GGCCTGGGTGCAGACACACCTCTGTGTGTAGAGAAATGTGTCTCGGCGAGAGCTGGACCC	2155
DB	2337	GGCCTGGATTCAGAAATGATTCCTCCGAGAAACAATCCCTTTTGGATGTACGTGGAGGA	2396
QY	2157	ACCCTGGCTGGAGAGAGTACTAGAAGCCCTGTGCCCTGCCAGCCAGATGTGTGACAGCTTC	2216
DB	2397	ACCATATTTACAGGTCCGTGATACAGGCCCTGTGCCCTCCCTCCCAAGACTCTGGAAATCCTGC	2456
QY	2217	TGAGGGAAATCCACACTTCAATTTGGGAGCAGGGCATGAATCTCTCCGGAGGCCAGAA	2276
DB	2457	CAGTGGGATCGACACAGANTTTGGCGAAGAGCGCTGAACCTGTCTGTGGGGACAGAA	2516
QY	2277	CGCGGTAGCCTTGGCCCCGGCTGTATACAGAAAGGACGTGTGTACTCTGTGTGATGACCC	2336
DB	2517	CGCGCTGAGCCTGGCCGGCCGTGTACTCCAACGCTGACATTTTACCTCTTCGATGATCC	2576
QY	2337	CCTGGGGCCTTGGATGGCCACCGTTGGCCACGATGTCTTCAACCAGGTCAATTTGGGCTTG	2396
DB	2577	CCTCTCAGCAGTGGATGGCCATGTGGGAAACAACATCTTTGAAATGTGATTTGGCCCCAA	2636
QY	2397	TGGGCTACTTCCAGGGAAACAACACGGATTCCTCGTGCAGCAGCACTCCACATCTCTGCCCA	2456
DB	2637	GGGGATCTGAAGACACACGCGGATCTTTGFTACGACAGCATGAGCTACTTGGCGCA	2696
QY	2457	GGCTGATTGGATCATAGTCTGGCAATGGGCCATCGCAGAGATGGTTCCTTACCAGGA	2516
DB	2697	GGTGACGTCATCATCGTCTAGTGGCGCAAGATCTCTGAGATGGCTCTTACCAGGA	2756
QY	2517	GCTTCTGCAGAGAGGGGGCCCTGTGTCTTCTTGGATCAAGCCACAGACCGACGAGA	2576
DB	2757	GCTGTGGCTCGAGACGGCGCCTTGG-CGTGAGTTCTTGGCTACTATGCCAGCACAGAC	2815
QY	2577	TAGAGGAGAGGAGAAACAAGCACTTGGGACACAGCAACCAAGGACCCACAGGCACTCTGC	2636
DB	2816	AGGACAGGATCGAGGAGAACGGGTACGGGCGCTCAGGGTCCAGGGAAGGAAGCAA	2875
QY	2637	AGGCAGGAGGCCGAGCTTTAGACGGGAGAGGTCCATCAAGTCAGTCCCTTGAGAAG----	2691
DB	2876	AGCAAAATGGAGAAATGSCATGCTGGTGACGGACAGTGCAGGGAAGCAACTGACAGACAGC	2935
QY	2692	-----GACCGTACCACCTTCAGAAGCCCAAG--	2716
DB	2936	TCAGCAGCTCTCTCTATAGTGGGACATCAGCAGGACCAACACACACCGCAGAAC	2995
QY	2717	CAGAGTCTCTCGATGACCTGACAGGCGAGGATGGCCAGCAGGAAAGCAGCATCC	2776
DB	2996	TCCAAAGCTCAGGCCAAGAGGAGGACCTTGGAACTGATGAGGCTGACAAAGGCGC	3055
QY	2777	AATACGGCAGGTTGAAGGCCACAGTGCACCTGGCTTACCTGGTGCCTGGGCACCCCCC	2836
DB	3056	AGACAGGCGAGTCAAGCTTTCCGTGTACTGGGACTACATGAAGCCATCGGACTCTTCA	3115
QY	2837	TCTGCCTTACCATCTTCTCTCTCTGCTGCCAGCAAGTGGCTCTCTTCTGCCCCGGGT	2896
DB	3116	TCTCTCTCTCAGCATCTTCTTTTTCATGTGTAACCATGTGCTCCGGCTTCCAACT	3175
QY	2897	ACTGGCTGAGCCTGTGGGCGGACCCCTGACGTAGTGGGCGACAGACGCGAGGACGCC	2956
DB	3176	ATTGGCTCAGCCTGTGGACTGATGACCCCATCGTCAACGGGACTCAGGAGACACAAAG	3235
QY	2957	TGCGTGGGGGATCTTCGGGCTCTCGGCTGTCTCCAAGCCATTTGGGCTTTTGCCTCCA	3016
DB	3236	TCCGGCTGAGCGTCTATGGAGCCCTTGGGCATTTTCAAGAGGATCGCGTGTTTGGCTACT	3295
QY	3017	TGGCTGCGGTGCTCTAGTGGGGCCCCGGGCATCCAGTTGCTTCTTCCAGAGGCTCTGT	3076
DB	3296	CCATGGCCGTGCCATCGGGGGGATCTTGGCTTCCCGCTGCTGCACGTTGGACCTTCTG	3355
QY	3077	GGGATGTGGTGGATCTCCCATCAGTCTTTTGGGGGACACCCATTTGCTACCTGCTAA	3136
DB	3356	ACAGCATCTCTGGGTACCCATGAGCTTCTTTTGGCGGACCCCGAGTGGGAACCTGTGA	3415

Best Local Similarity 55.7%; Pred. No. 5.5e-280;
Matches 2535; Conservative 0; Mismatches 1937; Indels 80; Gaps 7;

QY	36	GGTCTGGAAACACAGACAGCTGAACCTGCGCCGACAGCTGCTGAGCGCTGCTTCTCT	95	1257	TGACAGAAAGCCCGACAGCTGCGAGGGCTACTTCTACACCGTCTCTGTTTGTCTACTGC	1316
Db	237	GCTCTGGAGCTGGAAATGTCAGCTGGAAATACAGCAACCCGACCTTACCAAGTGTCTTCA	296	1080	CTGCTCTGCAAAACGCTGTTTGTAGCAGCAAGAACATGTACAGGCTCAAGGTGCCGAGATGAG	1139
QY	96	GAGAACAGCAGGGTCTGGGTACCCCATCTACTCTCTGGTCTCTGGTCTCTGCTCCATCTACT	155	1317	CTGCTCTGCAAGCCCTGCTGCTGACAGTACTTCCACATCTCTGCTTGTGAGTGCATGAG	1376
Db	297	GAACACGGTCTCTGTGGGTGCTTGTGTTTACTCTGGGCCCTGTTTCCCTCTCTACTT	356	1140	GTTCGGGTGGCCATCAGTGGCTTGGTGTACAGAAAGTCTCTGGCTCTCTGTCAGCGGCTC	1199
QY	156	CCTCTTATCCACACCATGCGCGGGCTACTCTCCGGATGTCGCCACCTCTTCAAGCCAA	215	1377	GATCAAGACCGCTGTCATTTGGGGCTGTCTATCGAAGGCCCTGGTGATCACCAATTCAGC	1436
Db	357	CCTCTATCTCTCCGACATGACCGAGGCTACATTCAGATGACACTCTCAACAAACAA	416	1200	CAGAAAGGCCAGTGGGTGATGTGCTCAATCTGGTGTCTCGTGGAGCTGCGAGCGGCT	1259
QY	216	GATGGTCTGGATTCGGCTTACGTCTGTGTACCTTCCAGCTGAGGCTGTCTGCTCTTTG	275	1437	CAGAAATCTCTCCAGGTGGGAGATGTCAACCTCATGTCTGTGGAGCTCTCAGAGGT	1496
Db	417	AACTGCCCTTGGGATTTTGTCTGGATCGTCTGCTGGGACACCTTCTTACTCTTTCTG	476	1260	GACCGAGAGCTCTCTACTCAACGGGCTGTGGCTGCTCTCTGTGTGATCTGTGCTGTG	1319
QY	276	GAAATCCACAGGAAGCGCTGAGGCCCGCAGAAATCTCTATTCTACTGTGTGCT	335	1497	CATGGACTTGGCCAGCTACATTAACATGATCTGGTCAAGCCCTCTGCAAGTCTATCTTGC	1556
Db	477	GGAAGAGTGGGGCATATCTCTGGCCCCAGTGTCTGTGTCAGCCCACTCTCTTGGG	536	1320	CTTCTCTATCTCTGGCAGCTCTGGGGCCCTCCGGCCCTCACTGCTGCTGTCTTCTCT	1379
QY	336	CACACAGTACGCTTCGACAGTGTCTCTGATTACACCGAGAGAAAGGAGTCCAGTC	395	1557	TCCTACCTCTCTGTGGCTGAATCTGGGCCCTTCCCTGCTGGTGGAGTGGCGTGTATG	1616
Db	537	CATCACCGCTGCTGCTACTCTTTTAAATTCAGCTGGAGGAGGAGGAGTTCAGTC	596	1380	GAGCCTCTCTCTCTGAATTTCTTCTATCTCCAAAGAAAGAACCACTCAGSAGGCA	1439
QY	396	ATCTGGAGTGTCTGTTGTTACTGCTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT	455	1617	CCTCATGTGCTCCATGCTGTGATGGGATGAAGACCAAGACGTATCAGGTGGCCCA	1676
Db	597	TTACGGGATCATGCTCACTTCTGCTGGTAGCCCTAGTGTGTGCTGCTGCTGCTGCT	656	1440	AATGAGGAGAGGACTCACGGGACGGCTCACAGCTCTATCTCTCAGGAACCTCGAAGAC	1499
QY	456	CCACGAG-----GCCCTGGAGCGGCTTCCAGAGGACCCCTGTCCGCCACTGTCT	506	1677	CATGAAGAGCAAGAACATCGGATCAAGCTGATGAACGAAATCTCAATGGGATCAAGT	1736
Db	657	ATCCAAATATGACAGCTTAAAGAGGATGCCCCAGGTGGACCTGTTCTGTGACATCAC	716	1500	CATCAAGTTCATGCTGGGAGGAGCCCTTCTGACAGAGTCTCTGGGCAATCCGAGGCCA	1559
QY	507	CACCTACTATGCTCTCTGTGTGTGGACACATTTGTGCTGCTCTGCTGCTGGGATCA	566	1737	GCTAAAGCTTTTATGCTGGAGCTGGCATTTCAAGGACAAAGTGTCTGGCCATCAGGCAG	1796
Db	717	TTTCTACGTACTTTTCCCTCTTACTCATTCAGCTGCTGTGCTGCTTCTCAGATCG	776	1560	GGAGCTGGCGCTTTCGCGACCTCCGCGCTCTCTCTCTCTGCTGCTGCTGCTGCTTCCA	1619
QY	567	ACCCCTCTTCCCTGAAGACCCCGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	626	1797	GGAGCTGAAGTGTCTGAAGAGTCTGCTTACCTGTACGCCGTGGGACCTTCCACCTGGGT	1856
Db	777	CTCACCCCTGTTCTCGGAAACATCCACAGACCCCTTAATCCCTGCGCCAGCTCCAGCG	836	1620	AGTGTCTACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1679
QY	627	CTTCCCTCTCAAGCCAGCTCTGCTGGTCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTG	686	1857	CTGCACGCTTCTGCTGGCTTGTGCACATTTTCCGCTGCTGCTGCTGCTGCTGCTGCTG	1916
Db	837	CTTCTCTGAGGATACCTTCTGCTGGATCAGAGGCTGATGCTGCTGCTGCTGCTGCTG	896	1680	TGCTA---TGAATCGAGAGAAAGCCCTTGTGACTCTCAGAGTCTCAACATCTCAACAA	1736
QY	687	GCCACTGAGACCAAGACCTCTGCTGCTTGGGAGAGAAACTCTCTCAGAAAGACTTGT	746	1917	CAACATCTGTGATGCCAGACAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1976
Db	897	GCCCTGGAGGCGAGTCACTCTGCTTAAACAGAGGACAGCTCGGAACAGTCTGT	956	1737	GGCCAGGCTTTTCTGCTGCTTCTCCATCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTG	1796
QY	747	TTCCCGCTTGAAGAGTGGATGAGAACCGC-----ATGACGCCCGGAGGACACAA	802	1977	TCCCTGAACTTCTCCCATGGTCTCAGCAGCATCTGAGGAGTGTCTCCTCTCA	2036
Db	957	GCCTGTTTGGTAAAGAACTGGAGAGGAATGCGCAAGACTAGGAAGCGCGGTGA	1016	1797	CCGCTGTCTACCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1856
QY	803	AGCAATAGATTTAAAGAGAAAGGCGGAGTGCATGAAGGCTCA-----	849	2037	ACGCTGAGGATCTTCTCTCCATGAGGAGCTGGAACCTGACAGCATCGAGCGAGGCC	2096
Db	1017	GTTTGTACTCTCCAGGATCTGCCCCAGGAAAGAGAGTTCAGAGTGGATGGCGAA	1076	1857	CTCTGGAAGCGCTCCCGGGAAGGATTCATCACCATACAGTGCACCTTCCGCTGCTG	1916
QY	850	-----GAGACCGAGCCCTCTCTACCGCAAGAGGAGGAGGAGTGGGCCCTGCT	899	2097	TGTCAAAGAGCGCGGGGACGAAACAGCATCACCCTGAGGAATGCCATTTACCTGGGC	2156
Db	1077	TGAGGAGTGGAGCTTTGTATGCTCAAGTCCCGACAGAGAGTGGAAACCTCTCTGTT	1136	1917	CCAGAAAGCCCTCTCTGCTCCACAGAAATAAATCTACGGTGGCCCGGAGGCTGTCT	1976
QY	900	GAAGGCCATCTGGAGGTGTTCATTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	959	2157	CAGAGCGACCTCTCCACACTGAATGGCTACCTTCTCATCTCCCGAAGTGTCTTGGT	2216
Db	1137	TAAGGTATTAACAAGACCTTTGGGCCCTACTTCTCTCATGAGCTTCTTCTTCAAGG	1196	1977	GGCTGTTGTCAGTGGGGGAGGAAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2036
QY	960	CAGTATGCTTCAAGTTCACTTCCCAAGCTGCTCAGCCTTTTCTGAGTATTATGG	1019	2217	GGCGTGTGGCCAGCTGGGCTGCGGAAAGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCT	2276
Db	1197	CCAGGACCTGATGTTTTCGGGGCGGAGATCTTAAAGTGTCTCATCAAGTTCGTGAA	1256	2037	GCTGTCAAGGTGGAGGGTTCGTGAGCATCAGGGTCTCTGGCTTACGTGCTGCTGCTG	2096
QY	1020	TGATCCCAAGCTTCCAGCCTTGAAGGCTACCTCTCTGCTGCTGCTGCTGCTGCTG	1079	2277	GATGGACAAAGTGGAGGGGACGTGGCTTATCAAGGGCTTCCGCTGCTGCTGCTGCTG	2336
				2097	GGCCTGGTGCAGAACACCTCTCTGTTGATGAAGATGTGCTTCCGGCAGGAGCTGACCC	2156
				2337	GGCCTGGATTCAGAATGATCTCTCCGAGAAACATCCTTTTGGATGCTCAGCTGGAGGA	2396

Db 4556 ATGAGGCCAGCGCGTGGACCTGGAAGAGGAGGACCTCATCCAGTCCACCATCCGGA 4615
QY 4337 GCTGGTTTGCACAGTGCAGTGTGCTGCCCATGTCGCCACCGCGCTCGCTGATGAGACT 4396
Db 4616 CACAGTTCGAGGAGTGCACGCTGCTCACCATCGCCACCGGCTCAACACCATCATGAGCT 4675
QY 4397 GTCCCGGGTTCGTGTCATGACGAAGGGCAGGTGGCAGAGCGGCGAGCCCGCCAGC 4456
Db 4676 ACACAGGGTGATGCTTGGACAAGAGGAGAAATCAGAGGATACGGCGGCCCATCGGACC 4735
QY 4457 TGCTGCCCCACAGAGGCGCTGTTTTACAGACTGGCCAGGAGTACAGGCGCTGGT 4508
Db 4736 TCCTGCAGCAGAGAGTCTTTCTACAGCATGCCCCAAGAGCGCGGCTTGGT 4787

RESULT 12
US-08-407-207A-1
; Sequence 1, Application US/08407207A
; Patent No. 6063621
; GENERAL INFORMATION:
; APPLICANT: Deeley, Roger G.
; APPLICANT: Cole, Susan P.C.
; TITLE OF INVENTION: ANTIBODIES TO A MULTIDRUG RESISTANCE PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/407,207A
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1512
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..4788
US-08-407-207A-1

Query Match 27.1%; Score 1222.8; DB 3; Length 5011;
Best Local Similarity 55.7%; Pred. No. 5.5e-280;
Matches 2535; Conservative 0; Mismatches 1937; Indels 80; Gaps 7;
QY 36 GGTCTGGAAACACAGACAGAGCTGGAACCTGGCGCCACAGGCTGCTGAGCTGTGCTTCT 95

Db 237 GCTCTGGGACTGGAATGTACGTGGAATACACAGAACCCCGACTTACCAAGTGTCTTCA 296
QY 96 GAGAACAGCAGGGGTCTGGGTACCCCGCATGTACCTCTGGTCTCTTGGTCCCATCTACCT 155
Db 297 GAACACGGTCTCTGCTGGTGGTCCCTTTTACCTCTGGGCTCTTCCCTCTCTACTT 356
QY 156 CCTCTTCAATCCACACATGCGCGGGGTACCTCCGGATGTCCCACTCTTCAAGCCAA 215
Db 357 CCTCTATCTCTCCGACATGACCGAGGCTACATTCAGATGACACCTCTCAACAAACCAA 416
QY 216 GATGCTGCTTGGATTCGCGCTCATAGTCTGTACCTCCAGCTGGTGTGCTCTTTG 275
Db 417 AACTGCTTGGGATTTTGTCTGTGATCGTCTGTGGCAGACCTTCTTACTCTTTCTG 476
QY 276 GAAATCCACAGGGAAGCGCTGAGGCGCCCAAGATTCCTCATCTTCTACTGTGTGCT 335
Db 477 GAAAGAAAGTGGGCGCATATTCTTGGCCCGAGTGTCTGTGTCAGCCCACTCTCTTGG 536
QY 336 CACCACGATGAGCTTCGAGTGTTCCTGATTCACACGAGAGGAGGAGTCCAGTC 395
Db 537 CATCACACGCTGCTGTGCTTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 596
QY 396 ATCTGGAGTGTGTTGTTACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 455
Db 597 TTCAGGATCATGCTCACTTCTGCTGGTGTAGCCCTAGTGTGCTCTCTCTCTCTCTCT 656
QY 456 CCAGCAG-----GCCTCCGGAGGGGCTTCCAGAGCGACCTGTCCGCGACCTCTC 506
Db 657 ATCCAAAATATGACAGCCTTAAAGAGGATGCCAGGTGGACCTGTTCTGTGACATCAC 716
QY 507 CACTACTATGCTCTCTGCTGGTGGCAGATTTGTGCTGCTCTCTCTCTCTCTCTCTCTCT 566
Db 717 TTTCTAGCTACTTTTCT 776
QY 567 ACCCGCTTCTTCCCTGAAGACCGCCAGCAGTCTTAACCTCTCCAGAGACTGGGGAGC 626
Db 777 CTCACCCCTGTTCTCGGAACCATCCAGACCTTAATCCCTGCGCAGAGTCCAGCGCTTC 836
QY 627 CTTCCCTCCAAAGCCAGTCTCTGCTGGTGTCTGCTGCTGCTGAGGGGATACAGAG 686
Db 837 CTTCTCTGTCGAGGATCACCTTCTGCTGATCACAGGCTTGTATCTCGGGGCTACCGCCA 896
QY 687 GCCACTGAGACCAAGACCTCTGCTGCTGGGAGAGAAACTCTCAGAAAGTCTGT 746
Db 897 GCCCTGGAGGAGTACCTCTGCTCTTAAACAAAGGAGGACAGTCGGAACAAAGCTG 956
QY 747 TTCGGGCTTGAAGAGGAGTGTGAGGAACCGG-----AGTGCAGCGCGGAGGACACA 802
Db 957 GCCTGTTTGTAAAGACTGGAAAGAGGAAATGCGCCCAAGACTAGGAAGCAGCGGTGA 1016
QY 803 AGCAATAGCATTAAAGAGGAGGCGGAGTGGCATGAAGGCTTCCA----- 849
Db 1017 GGTGTGTACTCTCCAAAGATCTGCGCCAGCGGAAAGAGAGTTCCAAGGTGGATGCGAA 1076
QY 850 -----GAGACCGAGCCCTTCTTACGGCAAGAGGAGGAGGAGGCGCCGCTGCT 899
Db 1077 TGAGGAGGTGGAGGCTTTGATCTCAAGTCCCGACAGAGGAGTGAACCCCTCTCTGTT 1136
QY 900 GAAGGCGCATCTGGCAGGTGTTCATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 959
Db 1137 TAAGTGTATACAGACCTTTTGGGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1196
QY 960 CACTGATGTCTCAGGTTCACTGTCCCAAGCTGCTCAGCTCTTCTCTGAGGTTTATTTG 1019
Db 1197 CCACGACCTGATGATGTTTTCCGGCGCGCAGATCTTAAAGTTGCTCATCAAGTTCGTGA 1256
QY 1020 TGATCCCAAGCCTCCAGCCTGGAGGCTACCTCTCTGCGCGTGTGCTGATTTCTCTCAGC 1079
Db 1257 TGACAGAAAGGCGCCAGAGCTGGCAGGCTACTTCTACACCGTGTGCTGTTTGTCTGTC 1316
QY 1080 CTGCTGCAAAACCTGTTTGGAGCAGAGACATGTACAGGCTCAAGGTGCGCGCAGATGAG 1139
Db 1317 CTGCTGACAGACCTCTGCTGCTGCACCACTACTTCCACATCTCTCTCTCTCTCTCTCT 1376

QY 1140 GTTGGCGTGGCCATCACTGGCTGGTGTACAGAAAGTCTGGCTGTCTGTCCAGCGGCTC 1199
DB 1377 GATCAAGACCGGTGTCTATTTGGGCTGTCTATCGGAGGCCCTGGTGATCACCAATTCAGC 1436
QY 1200 CAGAAAGCCAGTGGGTGGTGTATGTGTTCAATCTGGTGTCCGAGCGTGCAGCGGT 1259
DB 1437 CAGAAATCCCTCCAGGTCGGGGAGATTGTCAACCTCATGTCTGTGGAGCGCTCAGAGGTT 1496
QY 1260 GACGAGAGCGTCTCTACCTCAACGGGCTGTGGCTGTGGCTCTCTGTCTGTGATCGTGGTCTG 1319
DB 1497 CATGGACTTGGCCACGTATCAATTAACATGATGTGTCAGCCGCCCTTGCAGAGTCATCTTGC 1556
QY 1320 CTTGGTCTATCTCTGGAGCTCTCTGGGCGCTTCCGCCCTCACTGTCATCGCTGTCTTCT 1379
DB 1557 TCTCTACCTCTGTGGTGAATCTGGGCGCTTCCGCTCTGGCTGGAGTGGCGGTATGGT 1616
QY 1380 GAGCCTCTCTCTGTGAATTTCTATCTCAAGAAAGAAAGAACCAACCATCAGGAGGACA 1439
DB 1617 CCTCATGGTGGCGCTCAATGCTGTGATGGCGATGAAGACCAAGACGTATCAGGTGGCCCA 1676
QY 1440 AATGAGCAGAGGACTCACGGGCACGGCTCACAGCTCTATCTCAGAACTCAAGAC 1499
DB 1677 CATGAAGAGCAAGACATCGGATCAAGCTGATGAACGAAATTTCAATGGGATCAAGT 1736
QY 1500 CATCAAGTTCCATGCTGGGAGGAGCCTTTCTGGACAGAGTCTCTGGGCATCCGAGGCCA 1559
DB 1737 GCTAAGCTTTATGCTGGGAGCTGGCAATCAAGGACAAAGTGTGGCCATCAGGACGA 1796
QY 1560 GGAGCTGGGCGCTTGGGAGCTCCGGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 1619
DB 1797 GGAGCTGAAGTGTGAAGAAGTCTGCCCTACCTGTGACCGCTGGGCACCTTCACTGGGT 1856
QY 1620 AGTGTCTACATTTCTGTGTCGACATGGTGTGTGCTGTCTCACACTCTGTGGCGGAGAA 1679
DB 1857 CTGACGCGCTTTCTGGTGGCTTTGTGCACATTTGCGCTCTACGTGACCATTTGACGAGAA 1916
QY 1680 TGCTA---TGAATCAGAGAAAGCTTTGTGACTCTCACAGTTCTCAACATCTCTCAACAA 1736
DB 1917 CAACATCTGTGATGCCAGACAGCTCTGTCTTTGGCTTTGTCAACATCTCTCGGTT 1976
QY 1737 GGCCAGAGCTTTCTGGCCTTCTCCATCCACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCA 1796
DB 1977 TCCCTGAACATCTCCCATAGTTCATCAGCAGCATCTGACGGCGAGTGTCTCTCTCA 2036
QY 1797 CCCTCTGTACCT 1856
DB 2037 ACGCTGTAGGATCTTCTCTCCATGAGGAGTGGAACTGACAGCATCTGACGCGACGGCC 2096
QY 1857 CTCTGGAAGCGCTGCGGGAGGATTTGCATCACCATACACAGTGCACCTCTCGCTGTGTC 1916
DB 2097 TGTCAAGACGCGGGGCACGACAGATCACCTGTAGGAATGCCATTCACCTGGGC 2156
QY 1917 CCAGAAAGCCCT 1976
DB 2157 CAGGAGGACCCCTCCACATGAAATGGCATCACCTTCTCCATCTCCCGAAGTGTCTTGT 2216
QY 1977 GCTGTGTCTGCTCAGTGGGGGAGGAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2036
DB 2217 GGCCGTGTGGGCGAGGTGGGCTGCGGAAGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2276
QY 2037 GCTGTCAAAAGTGGAGGGTTCGTGAGCATCGAGGGCTGTCTGGCCTACGTGGCCCGCAGCA 2096
DB 2277 GATGGACAAAGTGGAGGGACGTGGCTATCAAGGGCTCTCTGGCTATGTGGCACAGCA 2336
QY 2097 GGCCGTGGTGCAGAACCTCTGTGGTAGAAGATGTGTCTTTCGGGAGGAGCTGGAGCC 2156
DB 2337 GGCCGTGGATTCAGATGATCTCTCCGAGAAACATCTCTTTTGGATGTCAGCTGGAGGA 2396
QY 2157 ACCCTGGCTGGAGAGTACTAGAGGCTGTGCCCTGACGCGCATGTGGAGAGCTTCCC 2216
DB 2397 ACCATATTACAGGTCGTGATAGGCGTGTGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2456

QY 2217 TGAGGGAATCCACACTTCAATTGGGAGCAGGCGATGAATCTCTCCGAGGCCAGAGCA 2276
DB 2457 CAGTGGGATCGGACAGAGATTGGCGAAGGCGGTGAACCTCTCTGGGGACAGAGCA 2516
QY 2277 GCGGTGAGCTTGGCCCGGCTGTATACAGAAAGGAGCTGTGTACTCTGTGTGATGACC 2336
DB 2517 GCGCTGAGCCTTGGCCCGGCGGTGTACTTCCAACTGTACATTTACTCTCTGTATGATCC 2576
QY 2337 CCGTGGGCGCTTGGATGCCACGTTGGCCAGCATGTCTTCAACAGGTCTATTGGGCTGG 2396
DB 2577 CTTCTCAGCAGTGGATGGCCATGTGGGAAACACATTTTGAATAATGTGATGGCCCAA 2636
QY 2397 TGGGTACTTCCAGGGAACACACAGGATTTCTGTGAGCAGCGACTCCACATCTGTGCCCA 2456
DB 2637 GGGATGCTGAAGAACAGACGGGATCTTGTTCAGCAGCATGATGACTTGTGCGCA 2696
QY 2457 GGCTGATTGGATCATAGTCTGGCAATGGGCCATTCGACAGATGGTTCCTACAGGA 2516
DB 2697 GGTGACGCTCATCATGCTGAGTGGCGCAAGATCTCTGAGATGGCTCTTACCAGGA 2756
QY 2517 GCTTCTGACAGAGGCGGCTCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2576
DB 2757 GCTGCTGGCTCAGACGGCGCTTCG-CTGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2815
QY 2577 TAGAGGAAGGAGAAACAGAACTCTGGGACACAGCACCAAGACCCCGAGGACCTCTGTC 2636
DB 2816 AGGACAGGATCGAGGAGACGGGTCTACGGCGCTCAGCGGTCCAGGGAAGAGCA 2875
QY 2637 AGGACAGGCGCGGCTTTAGACGGGAGGTTCATCAAGTCACTCTCTCTCTCTCTCTCTCTCT 2691
DB 2876 AGCAATGAGAAATGGCATGCTGTGACGACAGTGCAGGGAAGCACTCGACGACAGC 2935
QY 2692 -----GACCTTACCCTTCAGAAAGCCAGCA-- 2716
DB 2936 TCAGCAGTCT 2995
QY 2717 CAGAGTCTCTCTGATGACCTCTGACGGCAGGATGGCCAGGAGGAGGAGGAGGAGGAGGAGG 2776
DB 2996 TGCAGAAAGCTCAGGCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3055
QY 2777 AATACGGCAGGTGAAGGCCACAGTGCACCTGGCCTACCTGTCTCTCTCTCTCTCTCTCTCTCT 2836
DB 3056 AGACAGGCGAGTCAAGCTTTCCGCTACTTGGGACTTACATGAAGGCACTCGGACTCTTCA 3115
QY 2837 TCTGCTCTCTACGACT 2896
DB 3116 TCT 3175
QY 2897 ACTGCTGAGCTGTGGGCGGACGACCTCTGCTAGTGGGAGCAGAGGAGGAGGAGGAGGAGGAG 2956
DB 3176 ATTGCTCAGCTCTGAGTGTGATGACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3235
QY 2957 TCGTGGGCGGATCTTGGGCT 3016
DB 3236 TCGGCTGAGCTCTATGAGGCGCTGGGATTTTCAAGGAGTTCGCGCTGTCTCTCTCTCTCTCT 3295
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DB 3296 CCATGGCGTGTCT 3355
QY 3077 GGGATGTGGTGGATCT 3136
DB 3356 ACAGCATCTCTGGGTCACCCATGAGCTTCTTGGAGCGGAGGAGGAGGAGGAGGAGGAGGAG 3415
QY 3137 ACCGCTTCTCAAGGAGACAGACGAGTGTGAGTGTGAGATTCAGACAAACTCTCGGTCCC 3196
DB 3416 ACCGCTTCTCAAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 3475
QY 3197 TGCTGATGTACGCTTGTGAGTCT 3256
DB 3476 TCATGGGCT 3535
QY 3257 TGGCCACTGTGGCCATCT 3316

Db 3536 TCGCCGCATCATATCCCGCCCTTGGCTCATCTTCTTCGCCAGAGGTTCTACG 3595
QY 3317 TGGTTAGCTCATCGCAGCTGAGACGGTTGGAGTACAGCAGCTACTGCTGTGCTGCTGCC 3376
Db 3596 TGGCTTCTCCCGCAGCTGAGCGCTCGAGTGGTTCGAGCGCTCCCGGCTTATTCGCC 3655
QY 3377 ACATGGCTGAGAGTTCACAGGCGAGCAGCAGTGTCCGGGCAATCCGAACACAGCGCCCT 3436
Db 3656 ATTTCAACAGACTTGTCTGGGGTTCAGCTCATTTGAGCTTCGAGGAGCAGGAGCGCT 3715
QY 3437 TTGTGGCTCAGAACAAATGCTCGCTAGATGAAGAGCAGAGATCAGTTTCCCGCACTGG 3496
Db 3716 TCATCCACAGAGTACCTGAAGTGGAGCAGAGAACAGAGGCTTATACCCAGCAGTCG 3775
QY 3497 TGCGCTCAGAGTGGCTTGGGCGCAATGTGGAGCTCTCTGGGAATGGCTGTGTTGTCAG 3556
Db 3776 TGGCCAAACAGTGGCTGGCGCTGGAGTGTCTGGGCAACTGCATCGTTCTGTTG 3835
QY 3557 CGGCCAGTGTGCTGCTGAGCAAGCCACCTCAGTGTGCTGCTGCTGCTGCTGCTGCTG 3616
Db 3836 CTGCTGTTGGGCTGATCTCAGGACAGCCTCAGTGTGCTGCTGCTGCTGCTGCTGCTG 3895
QY 3617 TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3676
Db 3896 TGTCTTACTTATTCAGAGTCAACACCTGACTTGAATGCTGCTGCTGCTGCTGCTGCTG 3955
QY 3677 TAGAAGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3736
Db 3956 TGGAAACCAACATCGTGGCGCTGGAGAGCTCAAGAGTATTCAGAGACTGAGAGGAGG 4015
QY 3737 CTCCCTGAGGCTGCCACATGTGACGCTCAGCCCTGCTGCTGCTGCTGCTGCTGCTG 3796
Db 4016 CGCCCTGGCAATCCAGGAGACACGTCGCGCCAGCAGCTGCGCCAGGTTGGCGGAGTGG 4075
QY 3797 AGTTCGGGACTTGGGCTGAAGTGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3856
Db 4076 AATTCGGGAACTACTGCTCGGCTACCGAGAGACCTGACTTCTGCTCAGGACATCA 4135
QY 3857 CCTTCAAGATCCAGCAGAGAGAGAGTGGGCTATCTTGGCAGGACCGGGGAGGAAAT 3916
Db 4136 ATGTACAGATCAATGGGAGAGAAAGTGGCATCTGCTGGGCGGCGGAGCTGGGAAT 4195
QY 3917 CTCTCTGCGCAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3976
Db 4196 CGTCTGAGCTGGGCTTATTCGATCAACGAGTCTGCGGAGGAGAGATCATCTG 4255
QY 3977 ACGGGTCCCATTTGCCACGTGGGCTGCACACATCGGCTCCAGGATCAGCATCATCC 4036
Db 4256 ATGGCATCAACATCGCAAGATCGGCTGCAGGACCTCCGCTTCAAGATCACCATATCC 4315
QY 4037 CCGAGAACCCATCTGTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4096
Db 4316 CCGAGGACCTGTTTGTGTTTTCGGGTTCCCTCGAATGAACCTGGACCCCATTCAGCCAGT 4375
QY 4097 ACTCGAGCAGGCTATCTGGGAGCCCTGAGACGCTGAGCTCAAGCTTGTGGGCCA 4156
Db 4376 ACTCGGATGAAGAAGTCTGGAGCTGCTGAGCTGCTGAGCTGCTGAGGACTTCTGTGTCAG 4435
QY 4157 GCTGTCGCCGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4216
Db 4436 CCTTCTCAGAGCTAGACCATGATGTGCAAGAGCGGGGAGACCTCAGTGTGCGGC 4495
QY 4217 AGAAGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4276
Db 4496 AGCGCCAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4555
QY 4277 ACGAGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4336
Db 4556 ATGAGGCCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4615
QY 4337 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4396

Db 4616 CACAGTTCCAGAGTGCACCGTCTCACCATCGCCACCGGCTCAACACCATCATGGACT 4675
QY 4397 GTGCCCGGTTCTGGTATGACAAAGGCGGAGGTCGAGAGCGGCGGCGGCGGCGGCGG 4456
Db 4676 ACACAAAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4735
QY 4457 TGCTGGCCCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4508
Db 4736 TCCTGACGACAGAGTCTTTTCTACAGCATGGCCAAAGACCGCGGCTTGGT 4787

RESULT 13

US-08-463-092B-5
Sequence 5, Application US/08463092B
Patent No. 5768880
GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen's University at Kingston
CITY: Kingston
STATE: Ontario
COUNTRY: CANADA
ZIP: K7L 3N6
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,092B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-OCT-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,340
FILING DATE: 8-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Miernicki
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: Q1546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5889 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 6 4589
US-08-463-092B-5

Query Match

26.4%; Score 1189.8; DB 1; Length 5889;

Best Local Similarity 55.4%; Pred. No. 3.8e-272;
Matches 2516; Conservative 0; Mismatches 1952; Indels 75; Gaps 8;

Qy 38 TCTGGAACACAGAGAGCTGAACTCGCGCCACAGAGCTGTGTGAGCCGTGTCTCTCTGA 97
Db 49 TCTGGAGCTGGAATGTACATGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 108
Qy 98 GAACAGCAGGGGTCTGGGTGACCCCATGTACCTCTGGGTCTTGGTCCCATCTACCTCC 157
Db 109 ACACGGTCCCTACATGGGTGCTTGTCTACCTCTGGTCTTGTCTTCCCTCTCTCTCTCT 168
Qy 158 TCTTCATCCACACACAGCGCGGGCTACCTCCGATGTCCCACTCTTCAAGCAAGA 217
Db 169 TCTATCTCTCTCGCATGACCGGGCTACATCCAGATGACACACCTCAACAACCAAAA 228
Qy 218 TGGTCTTGGATTGCCCTCATAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 277
Db 229 CTGGCTTAGGATTCTTCTGTGGATCATCTGTGGCAGACCTCTTCTACTCTTCTCTGGG 288
Qy 278 AAATCCACAGGAGAGCTGAGGCCCCAGAAATTCCTCATTCATCTACTGTGTGGCTCA 337
Db 289 AAAGAAGTCAGGGAGTGTCCGAGCCCGGGTGTACTGTGTGACGCCCAACACTGTGGGCA 348
Qy 338 CCAGATGAGCTTCCGAGTGTCTGTGATTTCACACGAGAGGAAAGGAGTCCAGTCAAT 397
Db 349 TCACCATCTCTCGCCACCTTTTGTATACAGCTTGAACGGAGGAGGAGTCCCAATCT 408
Qy 398 CTGAGTGTCTGTTGGTGTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 457
Db 409 CGGGAATATGCTTACTTCTGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 468
Qy 458 AGCAG-----GCCCTCGGAGGGGCTTCCAGAGAGCCCTTCGCGCCACTGTGTCA 508
Db 469 CTAAGATCATCTCTGCTTTAAAGAGATGCTCATGTGTGACGTGTTCGAGATTCACAGT 528
Qy 509 CTAAGTATGCTGTCTGT 568
Db 529 TCTATCTGTACTTCAACCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 588
Qy 569 CCCCTTCTCCCTGAAGACCCCAAGAGTGTAAACCCCTGTCCAGAGACTGGGGAGCCT 628
Db 589 CACCCCTGTCTCTGAAACTGTCTATGACCGGAATCCATGCCCCCAAGTCCAGTCTCTT 648
Qy 629 TCCCTCCAAAGCCACGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 688
Db 649 TCCCTTCCAGGATTAATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 708
Qy 689 CACTGTAGACCAAAAGACCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 748
Db 709 CCCTGTGAGAGCAGTACCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 768
Qy 749 CCCGGCTTGAAGAGT 797
Db 769 CTGT 828
Qy 798 -----CAACAAGCAATAGCATTTAAAGCAAGGCGGAGTGTGTGTGTGTGTGTGT 841
Db 829 TTGTGTATGCCCTCCCAAGATCCCAAGATCCCAAGATCCCAAGATCCCAAGATCCCAAG 888
Qy 842 ---AGGCTCCAGAGACCGCCCTTCTTACGCGCAAGAGGAGGAGGAGGAGGAGGAGGAGG 898
Db 889 ATGAGGAGTGTGAGGCACTGATTGTCAAGTCAACCCCAAGAGTCCGGAGCCCTCTCTGT 948
Qy 899 TGAAGGCCATCTGGAGGTGTCAATTCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 958
Db 949 TCAAGGTGTATACAAGACTTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1008
Qy 959 TCAGTGTGTCTTCAAGTGTCT 1018
Db 1009 TTCATGACCTGATGTGTTCGGCGGCCCAAGATCTTGGAAATGTATATCACTTTCGTGA 1068
Qy 1019 GTGATCCCAAGCTTCCAGCTTGAAGGGCTACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1078
Db 1109 GTGATCCCAAGCTTCCAGCTTGAAGGGCTACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1168

Db 1069 ATCACAGGAGGAGCTCCCGACTGCGAGGGCTACTTTTACACAGCACGTCTGTTGTACGG 1128
Qy 1079 CTTGCTGCTGAAAGCTGTGTTTGTAGCAGCAGAACTGTACAGGCTCAAGGTGCCGAGATGA 1138
Db 1129 CTTGCTGACACACTGGCACTCCACAGTACTTTCATATCTGCTGCTCAGTGGCATGC 1188
Qy 1139 GGTGGGTGCGGCATCACTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1198
Db 1189 GCATCAAGACTGCTGTGTGGGGCTGTCTATCGTAAGGCTCTTTTGATCACCATACTGAG 1248
Qy 1199 CCAGAAAGCCAGTGGGTGGGT 1258
Db 1249 CTAGAAAATCTTCCAGGCTCGAGAGATGTCAACCTCATGTCCGTGGATGCTCAGCGCT 1308
Qy 1259 TGACCGAGAGCTGCTTACCTCAACGGGTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1318
Db 1309 TCATGACATTTGCCACGTATTAACATGATCTGGTCAGCCCTCTGCAAGTCTATCTCTAG 1368
Qy 1319 GCTTGTCTATCTGTGGCAGCTCTGGGGCTTCCGCCCTCTGCTGTGTGTGTGTGTGTGT 1378
Db 1369 CCTCTACTTCTGTGGCTGAGCCTGGGGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1428
Qy 1379 TGAGCTCTCTCTCTGAATTTCTTCATCTCCAAAGAAAGAAACCAACCATCAGAGGAGC 1438
Db 1429 TTTCTATGCTACCTTAATGT 1488
Qy 1439 AAATGAGCAGAAAGACTCACGGGCACGCTCACAGCTCTATCTCTCAGGAACCTCAAGA 1498
Db 1489 ACATGAAGAGCAAGAACCAACCAATCAAGTGTATGAACGAGATCTCAATGGGATCAAG 1548
Qy 1499 CCATCAAGTTCATGCTGGGAGGAGCCTTCTGTGACAGAGTCTCTGGGATCCGAGGCC 1558
Db 1549 TCTCAAGCTGTACGCTGGGAGCTGGCCTTCCAGGACAAAGTATGAGCATCAGCAGG 1608
Qy 1559 AGGAGTGGGCGCTTGGCGAGCTCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1618
Db 1609 AGGAGCTCAAGTGTGTGAAGAAATCTGCCTACCTGCGCAGCTGTAGCACATTCACGTGG 1668
Qy 1619 AAGTGTACATTTCTGTGTGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1675
Db 1669 TGTGACACACTTCTGTGTGGCCTGTCAACCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1728
Qy 1676 AGAATGTATGAATGCAGAAAGCCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1735
Db 1729 GAAATATCTAGATGAAAGAAAGCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1788
Qy 1736 AGGCGGAGGCTTCTGTGCTTCTCCATCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1795
Db 1789 TCCCACTCAACATCTCGCCATGGTTATCAGCAGCATTTGTGACAGGCGAGCTGTCCCTCA 1848
Qy 1796 ACCGTGTGTACCTTCT 1855
Db 1849 AGCGTCTCAGGATTTTCT 1908
Qy 1856 CCTCTGGAAGCGCTCGCGGAAGATTGATCACCATACACAGTGCACCTTCGCTCTGTGT 1915
Db 1909 CGATCAAGAGTGTGAAGGGA---ATAGCATCTCTGTGAAGATGCAACCTTCACCTTGG 1965
Qy 1916 CCCGAAAGCCCTCCCTGCTTCCACAGAAATAACCTCAAGTGTGCGCCAGGCGTGTCTGC 1975
Db 1966 CCAGGGGTGAACCTCCCACTGAATGGCATCACCTTCTCCATTCCTGAAGAGGCCCTTG 2025
Qy 1976 TGGCTGT 2035
Db 2026 TGGCGGT 2085
Qy 2036 AGCTGTCAAAAGTGTGAGGGT 2095
Db 2086 AGATGGAAGGTGTGAGGGAGCATGTGACTCTCAAGGGCTCGGTGCGCTACGTGCCCCAGC 2145
Qy 2096 AGGCTGT 2155
Db 2146 AGGCTGT 2205

QY	2156	CACCTCTGGCTGGAGACAGTACTAGAACCTCTGTCCTCGAGCCAGATGTGGACAGCTTCC	2215
DB	2206	AAATTACTACAGGCAGTTATGGAAGCCTGTGCCCTCTTCCAGATTTGGAAATCCTGC	2265
QY	2216	CTGAGGGAATCCACACTCTCAATTGGGAGCAGGGCATGAATCTCTCGGAGGCCAGAAGC	2275
DB	2266	CCAGTGGGACCCACACAGAGATCGGTGAGAAGGGTGAACCTGTCAAGGGGCCAGAGC	2325
QY	2276	ACGGCTGAGCTGGCCCGGGCTGTATACAGAAGACGCTGTGTACCTGTCTGGATGAAC	2335
DB	2326	AGCGTGTGAGCTGGCCCGGGCTGTGTACTCTAACTCTGACATCTACCTCTTTGTATGACC	2385
QY	2336	CCCTGGGSCCTGGATGCCACGTTGGCCAGCATGCTTCAACACAGGTCAATTTGGGCCCTG	2395
DB	2386	CCCTCTGGCTGTGATGCACATGTTGGGAAGCACATCTTTGAGAAGGTGGTTGGTCCCA	2445
QY	2396	GTGGCTACTCCAGGGAACAACACGGATTCTCGTGACGCACGCACCTCCACATCCTGCCCC	2455
DB	2446	TGGGCTACTGAAGAACAAGACACGGATCCTGTCACCATGGTATCAGTACCTACCTGCC	2505
QY	2456	AGCGTGAATTGGATCATGTGCTGGCAATTTGGGCCCATPCGCAGATGGGTTCCTACACAGG	2515
DB	2506	AAGTGGATGTCAATATGTCATGAGTGGGGCAAGATCTCAGAGATGGGTCTTATCAGG	2565
QY	2516	AGCTTCTGCAGAGGAAGGGGCCCTCGTGTGCTTCTG-----GATC	2557
DB	2566	AGCTGCTAGACCGGATGGGGCCTTCGCTGAGTTCCTGCGACCTATGCCAAGCTTGAGC	2625
QY	2558	AAGCCAGACAGCCAGGAGATGAGGAGAGGAGAAACAGAACTGGGACAGCACCAAGG	2617
DB	2626	AGGACCTGGCCTCGGAGGATGACAGTGTCAAGTGGTTCAGGGAAGGAGTCAAGACCGGTG	2685
QY	2618	ACCCAGAGGCACCTCTCGAGCAGGAGGCCCGCAGCTTAGACGCGAGAGGTTCATCAAGT	2677
DB	2686	AAATTTGGATGCTGTGTGACAGACACCGCTAGSAAAGCACCTGCAAGAGCATCTCAGCAACT	2745
QY	2678	CAGTCCCTTGAGAAGGACCGTACCCTTTCAGAAGCCAGACAGAGGTTCTCTGTGATGACC	2737
DB	2746	CGTCTTCCACAGTGGGATACCAGCCAGCACACAGCAGCATAGCCGAACCTGCAGAGG	2805
QY	2738	CT-----GACAGGCGAGGATGCCAGCAGGAAGACAGCATCCAATACGGCAGGG	2788
DB	2806	CTGAGCTAAGGAGGAGAGCTGGAAGCTAATGGAAGCAGACAAGGCCACAGACAGGCGAG	2865
QY	2789	TGAAGCCACAGTGCACCTGGCCTACTGCTGCGTGGGACACCCCTCTGCTCCTACG	2848
DB	2866	TGCAGCTGTCACTGTACTGGAACTACATGAAGGCCATTGGCCCTCTTCATCAGCTTCTGA	2925
QY	2849	CACCTTCTCTCTCTGCCAGCAAGTGGCCTCTCTTCGCGGGCTACTTGGCTGAGCC	2908
DB	2926	GTATCTCTCTTCTGTGCACACCATGTATCTGCACTGGCCTCTTAACTATTGGCTGAGCC	2985
QY	2909	TGTGGCGGACGACCTTCAGTAGG-----TGGSCAGCAGCAGCGACGCCCTGCGTGGCG	2965
DB	2986	TCTGCAGATGACCCCCCTGTGTCAATGGGACTCAGSCGAACAGGAATTTTCGGCTGA	3045
QY	2966	GGATCTTGGGCTCTCTCGGCTGTCTCCAAAGCATTTGGGCTGTTTGGCTCCATGGCTGCGG	3025
DB	3046	GTGTCTATGGGGCCCTTGGGCATCTTGAAGGTGACGAATAATTTTGGCTACTCCATGGCTG	3105
QY	3026	TGCTCTAGGTGGGCGCCGGGCATCCAGGTTGCTCTTCACAGAGGTCTCTGTGGGATGTGG	3085
DB	3106	TGTCCATCGGGGCATCTTGGCTCCCGTCCGCTTGCACCTGGACCTGTATACATGTTTC	3165
QY	3086	TGCGATCTCCCATCAGCTTCTTTTGGCGGACACCCATTTGGTCACCTGCTAAACCGCTTC	3145
DB	3166	TTCGATCCCATGATTTCTTCGAGCGTACACCCAGTGGGAACCTAGTGAACCGATTCT	3225
QY	3146	CAAGGACACACAGCGTTGACGTGGACATTCACAGACAACTCCGGTCCCTGCTGATGT	3205
DB	3226	CCAAGAGCTGGACACAGTGGACTCCATGATCCGCGAGTCAATCAAGATGTTTCATGGGTT	3285

QY	3206	ACGCCCTTTGACATCTCTGGAGGTCAGCCTGGTGGTGGCAGTGGCTTACCCCACTGGCCACTG	3265
Db	3286	CACCTCTTCACTGATTCATGGAGCTGTCTATCATCATCTCTACTTGGCCACGCCCATTTGCCG	3345
QY	3266	TGCCACTCTGCCACTGTTTCTCCTCTACGCTGGGTTCAGAGCCTGTATGTGTTAGCT	3325
Db	3346	TCATCATCCACCCTTTGGGTCTGGTTTACTTCTTTGTCAGAGAGTTCATATGTGCTTTCCT	3405
QY	3326	CATGCCAGCTGAGACGCTTGGAGTTCAGCCACTACTGCTGTCTGTCTTCCCTCCACATGGCTG	3385
Db	3406	CAAGACAACGTGAAGCGCTGAGTCTGTCTAGCCGCTTCCCTGTGTACTCACACTTCAATG	3465
QY	3386	AGACGTTCCAGGCGACAGACAGTGGTCCGGCATTCCGAACCCAGGCCCCCTTTGTGGCTC	3445
Db	3466	AGACCTTGTGGGAGTCAGTGTCTATCCGTCTTTTGAAGGACAGGAGCGCTTCATTCAACC	3525
QY	3446	AGAAACAATGCTCCGCTAGATGAAGCAGAGGATCAGTTTCCGCGGACTGGTGGCTGACA	3505
Db	3526	AGAGTGACCTGAAGTAGATGAGAACCAAGAGCCCTACTACCCACGATTTGTGGCCAAACA	3585
QY	3506	GGTGGCTTGGCGCAATGTGGAGCTCCTTGGGGAATGCGCTGTGTGTTCAGCGCCGACGCT	3565
Db	3586	GATGGCTTGTCTGTGCGCCTTGAGTGTGTGGCAACTCATTTGTCTGTGTGCTGCCCCCT	3645
QY	3566	GTGCTGTGTGACAAAGCCCACTCAGTGTCTGGCCTCGTGGGCTTCTCTGTCTCTGCTG	3625
Db	3646	TTGCAGTCTATCTCCCGGCACAGCTCAGTGTCTGGCTTGGTGGGCCCTCTCTGTCTTACT	3705
QY	3626	CCCTCCAGGTGACCCAGACACATGCAGTGGGTCTTTCGCAACTGGACAGACCTAGAGACA	3685
Db	3706	CAGTCAGATAACTGCATCTTGAATGGCTGTGTTCGAATGTCTCTCGGAGATGGAGACCA	3765
QY	3686	GCATCTGTCTAGTGGAGCGGATGCAGGACTATCGCTGGAGCCCAAGAGGCTCCCTCGGA	3745
Db	3766	ACATTTGCGAGTGGAGAGACTGAAGGAGTATTTCTGAACAGAGAGGAGGCTCTTGGC	3825
QY	3746	GGTGGCCACATGTGCAGCTCAGCCCCCTTGGCCTCAGGGCGGGCAGATCGAGTTCGGG	3805
Db	3826	AAATCCAGGAAACAGCTCCACCCAGCACCTTGGCCCCCATTTCAAGCCGCTGAGAGTTCGGG	3885
QY	3806	ACTTTGGGCTAAGATCCGACCTGAGCTCCCGCTGCTGTGCAGAGGCGTGTCTCTCAAGA	3865
Db	3886	ATTACTGCTTGAGTATCAGAAGACTTGGACTTGGTTCTCAAGACACATAAATGTCACCA	3945
QY	3866	TCCACGAGGAGAGAAGTGGGCATCGTTGGCAGGACCGGGCGGAGAAAGTCTCCCTCGG	3925
Db	3946	TTGAGGCTGAGAAAGTGGGTATTGTAGTCTGACGGGAGCTGGGAAATCATCTCTCA	4005
QY	3926	CCAGTGGCTGTCTGCGGCTCCAGGAGGCACTGAGGTTGGGATCTGGATCGACGGGCTCC	3985
Db	4006	CCCTGGGTTTGTTCGCGATCAATGAGTCTGCAGAGGGGAGATCATATTGATGGGGTCA	4065
QY	3986	CCATTGCCACGCTGGGCTGCACACACTGGCTCCAGGATCAGCATCATCCCCAGGACC	4045
Db	4066	ACATGCCAAGATCGGCCCTGCACAGCTCGGCTTCAAGATCACCATTCTCCACAGGATC	4125
QY	4046	CCATCTGTTCCTTGCTCTCTGCGGATCAACTCGACCTGTCTGCAGGAGCACTCGGACG	4105
Db	4126	CTGTTTGTCTCGGTTCCCTCCGATCACTTGTGACCCCTTTCAGTCAGTATTCATGATG	4185
QY	4106	AGGCTATCTGGGAGCCCTGGAGAGGTGCAGCTCAAGCCCTTGGTGGCCAGCTGCCCG	4165
Db	4186	AAGAAGTCTGGATGGCCCTGGAGCTTGTCTCACTAAAGGGCTTTTGTGTGTCAGCCTG	4245
QY	4166	GCCAGCTGACGTACAAGTGTGCTGACCGAGGCGAGGACCTGAGCTGGCGCAGAAACAGC	4225
Db	4246	ACAAGCTGAACCATGAGTGTGCAGAAGGTGGAGAGAACCTGAGTGTGGGCGACGACAGC	4305
QY	4226	TCTCTGTCTGCGACGTGCCCTTCTCCGAAGACCCAGATCCTCATCTCTGGAGAGGCTTA	4285
Db	4306	TTGTGTGCTTGGCCCGGCTCTGTCTGAGGAAGACAAAGATTCTAGTGTGGACAGGCTTA	4365
QY	4286	CTGCTGCGCTGGACCCCTGGCAGGAGCTCAGATGCAGGCCATGTCTGGGAGAGCTGTTTG	4345

Db 4366 CCCACCTGTGACCTAGACAGATAACCTTATCCAGTCCACCATCCGGACCGAGTTG 4425
QY 4346 CACAGTGCACTGTGTCGCCATGCCCCACCGCTGCGCTCCGCTGATGGAGTGTGCCCGG 4405
Db 4426 AAGACTGTACTGTGCTACGATGCTCATCGGGCTTAACACCAATAATGGACTACACACGGG 4485
QY 4406 TTCTGGTCATGACAGGGGCGAGTGGCAGAGAGCGGACCGCCCGCCAGCTGCTGCC 4465
Db 4486 TTATTGCTGTGACAAAGAGAGAGTTTCGGGAGTGTGGTGACCCCTGTGAGCTCCTGCAGC 4545
QY 4466 AGAAGGGCCCTGTTTACAGACTGGCCAGGAGTCAAGGCTGGT 4508
Db 4546 AAAGAGGCATCTTACACATGCGCAAGGATGCTGGCTGGT 4588

RESULT 14

US-08-462-109A-5
; Sequence 5, Application US/08462109A
; Patent No. 5882875
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; TITLE OF INVENTION: MULTIDRUG RESISTANT TUMOR CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,109A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: POI-002CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5889 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 6 4589

US-08-462-109A-5

Query Match 26.4%; Score 1189.8; DB 2; Length 5889;
Best Local Similarity 55.4%; Pred. No. 3.8e-272;
Matches 2516; Conservative 0; Mismatches 1952; Indels 75; Gaps 8;

QY 38 TCCTGGAACACAGACAGACGCTGAACCTGCCGCCACACGCTCTGAGCGTGTGCTTCCTG 97
Db 49 TCTGGGATGGAATGTACATGTCACACACACACACACACACACACACACACACACACAC 108
QY 98 GAACAGCAGGGGTCTGGGTACCCCATGTACCTCTGGGTCTGGGTCTGGGTCTGGGTCTGG 157
Db 109 ACAGGTCTTCACATGGTGGCTGTGTTTACCTCTGCTGCTGCTGCTGCTGCTGCTGCT 168
QY 158 TCTTCATCCAC 217
Db 169 TCTATCTCTCTCGCATGACCGGGCTTACATCCAGATGACACACCTCAACACACACACAA 228
QY 218 TGGTGTGATGATGCGGCTCATAGTCTGTGTACTCCAGGTGGCTGTCTGCTCTTTGGA 277
Db 229 CTGCTTAGGATTTCTTCTGTGGATCATCTGCTGGGAGACCTCTCTTACTCTTTCTGG 288
QY 278 AAATCCAAACAGGAACGCTTGGGCCCGGAGGCTTCCATTCATTCCTTACTCTGTGGCTCA 337
Db 289 AAAGAGTCAGGAGTGTCTCGAGCCCGGTTTACTGGTCAGCCCAACACACTGCTGGGCA 348
QY 338 CCAGATGAGCTTCGCAAGTGTTCCTGATTCACACCGAGAGGAGGAGGAGTCCAGTCA 397
Db 349 TCACCATGCTGCTCGCACCTTTTGTATACAGCTTGAACGAGGAGGAGTCCCAATCT 408
QY 398 CTGAGTGTGTTTGGTGTACTGCTTCTGCTGTTGCTTCCAGCTACCAACGCTGCC 457
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QY 458 AGCAG-----GCCTCGGAGGGGCTTCCAGAGGAGCCCTGTCGCCACCTGTCCA 508
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Db 529 TCTATCTGATCTACCTTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 588
QY 569 CCGCTTCTTCCCTGAAGACCCCGAGAGTCTAACCCCTGTCCAGAGACTGGGCGAGCT 628
Db 589 CACCCCTGTTCTCTGAAACTGTCCATGCCGGAATCCATGCCAGAAATCCAGTGCCTCT 648
QY 629 TCCCTCCAAAGCCACGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 688
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QY 749 CCGGCTTGAAGAGGAGTGTGATGAGGAAACCGCAGTGTGAGCCCGGAGGCA----- 797
Db 769 CTGTGCTGTTGAATACTGGAAGAAAGAAATGTGATAAGTCAAGGAAGCAGCTGTACGGA 828
QY 798 -----CAACAAGGCAATAGCATTTAAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAG 841
Db 829 TTGTGTATGCCCTCCCAAAGATCCAGCAAGCTAAGGGAAGTCCAGTGTGATGTGA 888
QY 842 ---AGGCTCCAGAGACCGACCTTCTTCCAGGCAAGGAGGAGGAGGAGGAGGAGGAGGAG 898
Db 889 ATGAGGAGGTGGAGGCACTGATGCTCAAGTCAACCCCAAGGATCGGAGGAGGAGGAGGAG 948
QY 899 TGAAGGCCATCTGGCAGGTGTTCATTCCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 958
Db 949 TCAAGGTGTTATACAGACTTTTGGTCCCTACTTCCCTCATGAGCTTCTGCTGCTGCTGCT 1008
QY 959 TCAGTGTATGTTTCAGGTTTCACTGCTCCCAAGGCTGCTGAGCTTTTCTGAGTTTATTG 1018
Db 1009 TTTATGACCTGATGATGTTTGGCGGCCCCAAGATCTTGGAAATGATTATCACTTCTGTA 1068
QY 1019 GTGATCCCAAGGCTCCAGCTTGAAGGCTACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1078
Db 1069 ATGACAGGAGGCTCCCGAGTGGCAGGCTACTTTTACACAGCACTGCTGTTTGTGACGG 1128

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QY	1139	GGTGGCGGTGCGCCATCACTGSCCTGCTGTACAGAAAGGTCCTGGCTCTGTCTCAGCGGCT	1198
DB	1189	GCATCAAGACTGCTGTGTGGCGCTGTCTATCGTAAGGCTCTTTTGATCACCAATGCAG	1248
QY	1199	CCAGAAAGGCCAGTGCGGTGGGTGTGATGTGCTCAATCTGGTGCCTGGAGCGTGCAGCGGC	1258
DB	1249	CTAGAAATCTTCCACGGTCGGAGAGATTGTCAACCTCATGTCCTGGTGGATGTCTACGGCT	1308
QY	1259	TGACCGAGAGCGTCTCTACCTCAAGGGCGTGTGGCTGCTCTGTCTGTGATCGTGGTCT	1318
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QY	1319	GCTTGGTCTATTCTGTGGAGCTTCTGGGGCCTCCGCCCTCACTGCCATCGCTGTCTTCC	1378
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QY	1439	AAATGAGGAGAAAGCACTACCGGCAACGGCTCACCAAGCTCTATPCTTCAGAACTCGAAGA	1498
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QY	1736	AGGCCAGGCCTTCTGTGCCCTTCTCCATCTCCTCGTGCAGGCCGGGTGTCTCTTGG	1795
DB	1789	TCCCACCTCAACATCTGTGCCATGGTTATCAGCAGCATTTGTGCAGGCCAGCGTGCCTCA	1848
QY	1796	ACCGTCTGGTCACTTCTGTGCTGGGAAGTTGACCCCTGGTGTGCTGTAGACTCAAGTT	1855
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QY	1856	CCTCTGGAAGCGCTGCCGGGAGGATTGCATCACCATACACAGTGGCACCTTGCCTGGT	1915
DB	1909	CGATCAAGAGTGGGAAGGGA---ATAGCATCACTGTGAAGAATGCAACCTTCACTTGGG	1965
QY	1916	CCCAGGAAGCCCTCCTGTCCCTCCACAGAAATAAACCTCAGGTGCCCGCCAGGCGTGTCTGC	1975
DB	1966	CCAGGGTGAACCTCCCACTGAATGSCATCACTTCTCCATTTCTGAGGAGGCCCTTGG	2025
QY	1976	TGGCTGTGTGCTGCTCAGTGGGGGAGGGAAGTCTCTCCTGTGTCCGCCCTCTCTTGGGG	2035
DB	2026	TGGCCGTGGTGGGCGAGGTAGGCTGCGGGAAGTCACTCTGTGTGTCAGCCCTGTGGCTG	2085
QY	2036	AGCTGTCAAAGTGGAGGGGTTCTGTGACATCGAGGGTGTGTGGCTTACGTGCCCGGAG	2095
DB	2086	AGATGGACAAGGTGGAGGGACATGTGACTCTCAAGGGCTCCGTGGCTTACGTGCCCGAGC	2145
QY	2096	AGGCCTGGGTGCAGAAACACCTCTCTGTGTGTAGAGAATGTGTGCTTCTGGGAGGAGCTGGACC	2155
DB	2146	AGGCCTGGATTCAGAACTACTCTCTCCAGAGAGACATACTGTTTGGGACACCCCTGTGAGG	2205
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QY	3026	TGCTCTTAGTTGGGCGCGGCATCCAGTTGCTCTTCAGAGGCTCCTGTGGGATGTGG	3085
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; Sequence 5, Application US/08460907B
; Patent No. 5891724
; GENERAL INFORMATION:
; APPLICANT: Deeley, Roger G.
; APPLICANT: Cole, Susan P.C.
; TITLE OF INVENTION: METHODS FOR CONFERRING MULTIDRUG
; TITLE OF INVENTION: RESISTANCE ON A CELL
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,907B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: 01551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5889 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 6 4589

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Search completed: December 18, 2002, 21:36:12
Job time : 146.919 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:00:25 ; Search time 563.826 Seconds
(without alignments)
18009.573 Million cell updates/sec

Title: US-09-647-140A-7

Perfect score: 4509

Sequence: 1 atggcgcgcctgctagcc.....ccaggagtcaggcctggc 4509

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24:	/SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	4497.8	99.8	4512	AAZ30081	Human ATP-binding
4	4497.8	99.8	4512	AAZ30081	Human ATP-binding
5	4497.8	99.8	4512	AAZ30081	Human ATP-binding
6	4497.8	99.8	4512	AAZ30081	Human ATP-binding
7	4497.8	99.8	4512	AAZ30081	Human ATP-binding
8	4497.8	99.8	4512	AAZ30081	Human ATP-binding
9	4497.8	99.8	4512	AAZ30081	Human ATP-binding

10	4497.8	99.8	4512	AAZ30081	Human ATP-binding
11	4487.4	99.5	4511	AAZ30081	Human ATP-binding
12	3030	67.2	4980	AAZ30081	Rat sequence diffe
13	3007.2	66.7	4980	AAZ30081	Mouse ATP-binding
14	1229.2	27.3	5011	AAZ30081	Human ATP-binding
15	1229.2	27.3	5011	AAZ30081	Human ATP-binding
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27	1222.8	27.1	5011	AAZ30081	Human MRP variant
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34	1106	24.5	4885	AAZ30081	Human MRP variant
35	1076.8	23.9	1612	AAZ30081	Human MRP variant
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38	1052.8	23.3	5193	AAZ30081	Human MRP variant
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40	1039	23.0	4762	AAZ30081	Human MRP variant
41	977.2	21.7	4423	AAZ30081	Human MRP variant
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43	760.8	16.9	4669	AAZ30081	Human MRP variant
44	721	16.0	4864	AAZ30081	Human MRP variant
45	713	15.8	5300	AAZ30081	Human MRP variant

ALIGNMENTS

RESULT 1

ID AAZ30081 standard; CDNA; 4509 BP.

XX AAZ30081;

AC AAZ30081;

XX AAZ30081;

DT 26-JAN-2000 (first entry)

DE CDNA encoding a human MPR-related ABC transporter designated MOAT-E.

XX Human; MPR-related ABC transporter; MOAT protein; MOAT-E;

KW MOAT mediated transport; anticancer drug sensitivity;

KW transporter mediated cellular efflux; anticancer; ss.

XX Homo sapiens.

OS Homo sapiens.

XX Key

XX CDS

FT Location/Qualifiers

FT 1..4509

FT /*tag= a

FT /*product= "MOAT-E"

FT /*transl_except= (pos: 3645..3647, aa: Ala)

FT /*transl_except= (pos: 3820..3822, aa: Tyr)

FT /*transl_except= (pos: 3859..3861, aa: Leu)

FT /*transl_except= (pos: 4363..4365, aa: Leu)

FT /*note= "MPR-related ABC transporter; no stop codon given"

XX WO9949735-A1.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-US06644.

QY	1681	GCTATGAATGCAGAAAGCCCTTTGTGACTCTCAACAGTTCTCAACATCTCTCAACAAGGCC	1740
Db	1681	GCTATGAATGCAGAAAGCCCTTTGTGACTCTCAACAGTTCTCAACATCTCTCAACAAGGCC	1740
QY	1741	CAGGCTTTCCTCCCTTCTCCCATCCACTCCCTCGTCCAGGCCCGGGTGCTCTTTGACCGT	1800
Db	1741	CAGGCTTTCCTCCCTTCTCCCATCCACTCCCTCGTCCAGGCCCGGGTGCTCTTTGACCGT	1800
QY	1801	CTGGTCACTTCTCTGCTGGCTGAAGAAGTTGACCTTGGTGTAGACTCAAGTTCCTCTCT	1860
Db	1801	CTGGTCACTTCTCTGCTGGCTGAAGAAGTTGACCTTGGTGTAGACTCAAGTTCCTCTCT	1860
QY	1861	GGAAAGCGTGGCGGAAGATTGCAATACACATACAGTGCACCTTCGCTGGTCCCAG	1920
Db	1861	GGAAAGCGTGGCGGAAGATTGCAATACACATACAGTGCACCTTCGCTGGTCCCAG	1920
QY	1921	GAAGCCCTCCTCGCTCCACAGAATAAACCTCACGGTGCCTCCAGGGCTGTCTGCTGGCT	1980
Db	1921	GAAGCCCTCCTCGCTCCACAGAATAAACCTCACGGTGCCTCCAGGGCTGTCTGCTGGCT	1980
QY	1981	GTGTGCTGGTCCAGTGGGGGACGGAAGTCTCCCTGCTCTCGGCCCTCCTTGGGGAGCTG	2040
Db	1981	GTGTGCTGGTCCAGTGGGGGACGGAAGTCTCCCTGCTCTCGGCCCTCCTTGGGGAGCTG	2040
QY	2041	TCAAAGTGGAGGGGTTCGTGAGCATCAGAGGTGTGTGGCTACGTGCCCCAGGAGGCC	2100
Db	2041	TCAAAGTGGAGGGGTTCGTGAGCATCAGAGGTGTGTGGCTACGTGCCCCAGGAGGCC	2100
QY	2101	TGGGTGCAGAACCTCTGTGTGACAGAAATGTGCTTCGGGCAGAGCTGGACCCACCC	2160
Db	2101	TGGGTGCAGAACCTCTGTGTGACAGAAATGTGCTTCGGGCAGAGCTGGACCCACCC	2160
QY	2161	TGGTGGAGAGTAGTACTAGAAGCTTGCCTCGACCCAGATGTGGACAGCTTCCCTTGAG	2220
Db	2161	TGGTGGAGAGTAGTACTAGAAGCTTGCCTCGACCCAGATGTGGACAGCTTCCCTTGAG	2220
QY	2221	GGATCCACACTTCAATTTGGGAGCAGGGCATGAATCTCTCGGAGGCCAGAACAGCGG	2280
Db	2221	GGATCCACACTTCAATTTGGGAGCAGGGCATGAATCTCTCGGAGGCCAGAACAGCGG	2280
QY	2281	CTGAGCTGGCCCGGGCTGTATACAGAAGGCAGCTGTCTACTCTGTGGATGACCCCTCG	2340
Db	2281	CTGAGCTGGCCCGGGCTGTATACAGAAGGCAGCTGTCTACTCTGTGGATGACCCCTCG	2340
QY	2341	CGGGCTTGGATGCCACGTTTGGCCAGCATGTCTTCAACAGGTCATTTGGGCTGTGTGGG	2400
Db	2341	CGGGCTTGGATGCCACGTTTGGCCAGCATGTCTTCAACAGGTCATTTGGGCTGTGTGGG	2400
QY	2401	CTACTCAGGGAACAAACAGGATTCGTGAGCAGCAGCACTCCACATCTGCCCCCAGGCT	2460
Db	2401	CTACTCAGGGAACAAACAGGATTCGTGAGCAGCAGCACTCCACATCTGCCCCCAGGCT	2460
QY	2461	GATTGGATCATAGTCTCGGAAATGGGGCCATCGCAGAGATGGTTCCTACAGGAGCTT	2520
Db	2461	GATTGGATCATAGTCTCGGAAATGGGGCCATCGCAGAGATGGTTCCTACAGGAGCTT	2520
QY	2521	CTCAGAGGAAGGGGGCCCTCGTGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGATAGA	2580
Db	2521	CTCAGAGGAAGGGGGCCCTCGTGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGATAGA	2580
QY	2581	GGAGAGGAGAAACAGAACCTGGGACACAGCAACAGGACCCAGAGGCACCTCTCGAGGC	2640
Db	2581	GGAGAGGAGAAACAGAACCTGGGACACAGCAACAGGACCCAGAGGCACCTCTCGAGGC	2640
QY	2641	AGGAGGCCGAGCTTAGACGCGAGAGTCCATCAGTCACTCCCTGAGNAGNAGCCGTACC	2700
Db	2641	AGGAGGCCGAGCTTAGACGCGAGAGTCCATCAGTCACTCCCTGAGNAGNAGCCGTACC	2700
QY	2701	ACTTCAGAAAGCCACAGAGAGTTCTCTGATGATACCCTGACAGGCGAGGATGGCCAGCA	2760
Db	2701	ACTTCAGAAAGCCACAGAGAGTTCTCTGATGATACCCTGACAGGCGAGGATGGCCAGCA	2760
QY	2761	GGAAAGGACAGCATCCAATAGCGAGGTTGAAGGCCACAGTGCACCTTGCCTACCTTGCCT	2820

[illegible]

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Db 3901 ACCGGGGAGGAAGTCTCTCCCTGGCCAGTGGCTGCTGCGCTCCAGAGCAGCTGAG 3960
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Db 3961 GGTGGGATCTGATCGAGGGGTCCCATTTGCCACGTGGGGCTGCACACACTGGGCTCC 4020
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Db 4081 GACCTGCTGCAGGAGACTCGGACGAGGCTATCTGGGAGCCCTGGAGACGCTGAGCTC 4140
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Db 4201 GACCTGAGCGTGGGCCAGAAACAGCTCTCTGTCTGCGACGTGCGCTTCTCCGGAGACC 4260
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Db 4441 GGCAGCCGGCCAGCTGCTGCCAGAGAGGCGCTGTTTACAGACTGGCCCGAGAGTCA 4500
Qy 4501 GGCCTGGTC 4509
Db 4501 GGCCTGGTC 4509

RESULT 2
AADI6231
ID AADI6231 standard; cDNA; 4512 BP.
XX XX
AC AADI6231;
XX XX
DT 19-NOV-2001 (first entry)
XX XX
DE Human ATP-binding cassette transporter ABCB6 (MRP6) cDNA coding sequence.
XX XX
KW Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
KW Multidrug Resistance-associated protein 6; macular degeneration; ABCB6;
KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
KW ss.
XX XX
OS Homo sapiens.
XX XX
FH Key Location/Qualifiers
CDS 1..4512
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FT variation
FT /*tag= b
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FT variation
FT /*tag= v
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FT which results in amino acid change from Arg to Gln"
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FT which results in amino acid change from Phe to Ser"
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FT which results in amino acid change from Leu to Pro"
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FT replace (3341, C)
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FT which results in amino acid change from Ser to Trp"
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FT replace (3904, A)
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FT which results in amino acid change from Gly to Arg"
FT replace (3907, C)
FT /*tag= t
FT /note= "This variation occurs during gene polymorphism
FT which results in amino acid change from Ala to Pro"
FT replace (3940, T)
FT /*tag= u
FT /note= "This variation occurs during gene polymorphism
FT which results in amino acid change from Arg to Trp"
FT replace (3941, A)
FT /*tag= v
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1021 GATCCAAAGCTCCAGCCTGGAAGGCTACCTCTCGCGTGTCTGATGTTCTCTCAGCC 1080
1081 TGCCTGCAAAAGCTGTTTGAAGCAGAGAACATGTACAGGCTCAAGGTGCCGAGATGAGG 1140
1081 TGCCTGCAAAAGCTGTTTGAAGCAGAGAACATGTACAGGCTCAAGGTGTCGACAGATGAGG 1140
1141 TTGGCGTGGCCATCACATGGCTGTGTGTACAGAAAGTTCCTGGCTCTCTCAGCGGCTCC 1200
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1261 ACCGAGAGCTCTTACTCTCAACGGGCTGTGGCTGTCTCTGGATCTGGTCTGCTG 1320
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QY 4261 CAGATCCTCATCTGTCAGCAGGCTACTGCTGCGGTGGACCCCTGGCAGCGAGTGCAGATG 4320
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QY 4321 CAGGCCATGCTCGGAGCTGTTTGCACAGTGCACACTGTGTCGCCATTTGCCACCGCCTG 4380
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QY 4441 GGCAGCCCGGCCAGCTGCTGCGCCAGAAAGGCCCTGTTTTACAGACTGGCCAGAGTCA 4500
Db 4441 GGCAGCCCGGCCAGCTGCTGCGCCAGAAAGGCCCTGTTTTACAGACTGGCCAGAGTCA 4500
QY 4501 GGCCTGGTC 4509
Db 4501 GGCCTGGTC 4509

RESULT 3

AAD16256

ID AAD16256 standard; cDNA; 4512 BP.

XX AAD16256;

XX AC AC (first entry)

DT 19-NOV-2001 (first entry)

XX Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #1.

XX Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
XX Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;
XX ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
XX Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
XX mutant; mutens; ss.

OS Homo sapiens.
OS Synthetic.

FH Key Location/Qualifiers

CDS 1..4512

FT /*tag= a

FT /product= "Human ABCC6 (MRP6) mutant protein"

FT mutation replace (3341, G)

FT /*tag= b

FT PN W0200162977-A2.

PD 30-AUG-2001.

XX 23-FEB-2001; 2001WO-US05741.

XX 23-FEB-2000; 2000US-0184269.

XX (PXEI-) PXE INT INC.

XX (UYHA-) UNIV HAWAII.

XX Boyd CD, Csiszar K, Lesaux O, Urban Z, Terry S;

XX WPI; 2001-536645/59.

XX P-PSDB; AAE09363.

DR Screening presence of Pseudoxanthoma elasticum mutation useful for
DR identifying homozygotes, compound heterozygotes or carriers involves
DR determining presence of mutation in MRP6 (ABCC6) nucleic acid

XX Example 2; Page -, 163pp; English.

XX The invention relates to methods and compositions for diagnosing and
XX treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological
XX dysfunctions. The invention is useful for screening for the presence of
XX a PXE mutation. Mutations associated with PXE maps to the ATP-binding
XX cassette transporter ABCC6 (MRP6-Multidrug Resistance associated
XX protein-6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165
XX kDa protein located in the plasma membrane containing 17 membrane-

|||||
Db 1801 CTGCTACCTTCTCTGCTGGAAGTTGACCTGGTGTGCTAGACTCAAGTCTCT 1860
QY 1861 GGAAGCGCTCCGGGAAGATTGCATACACATACAGTGCACCTTTCCTGGTCCAG 1920
Db 1861 GGAAGCGCTCCGGGAAGATTGCATACACATACAGTGCACCTTTCCTGGTCCAG 1920
QY 1921 GAAAGCCCTCCCTGCTCCACAGATAAACCCTCACGGTGCACAGGCTCTCTGCTG 1980
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QY 1981 GTTGTCCGTTCCAGTGGGGGAGGAAAGTCTCTCCCTGCTGCTCCCTGCTGCTG 2040
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Db 2041 TCAAGGTTGGAGGGTTCGTGACATCGAGGGTCTGCTGCTGCTGCTGCTGCTG 2100
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Db 2161 TGGTGCAGAGACTACTAGAGCTGTGCTGCTGAGCAGATGTGACAGCTTCCCTG 2220
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Db 2221 GGAATCCACACTTCAATTTGGGGAGAGGATGAATCTCTCCGGAGCCAGAGCAG 2280
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Db 2281 CTGAGCTGGCCCGGCTGTATACAGAAAGGAGCTGTGCTGCTGCTGCTGCTGCT 2340
QY 2341 GCGGCCCTTGGATGCCACGTTGGCCAGCATGTCTTCAACAGAGTCAATTTGGGCT 2400
Db 2341 GCGGCCCTTGGATGCCACGTTGGCCAGCATGTCTTCAACAGAGTCAATTTGGGCT 2400
QY 2401 CTACTCAGGGAACACAGGATTTCTGTCGACGACGCTCAACATCTCTGCCCCAGG 2460
Db 2401 CTACTCAGGGAACACAGGATTTCTGTCGACGACGCTCAACATCTCTGCCCCAGG 2460
QY 2461 GATTGGATCATAGTGTGGCAATGGGGCCATCGCAGAGATGGTTCTTACAGGAGCT 2520
Db 2461 GATTGGATCATAGTGTGGCAATGGGGCCATCGCAGAGATGGTTCTTACAGGAGCT 2520
QY 2521 CTGACAGGAAGGGGCCCTCTGCTGCTTCTGGATCAAGCCAGACAGCCAGGATAGA 2580
Db 2521 CTGACAGGAAGGGGCCCTCTGCTGCTTCTGGATCAAGCCAGACAGCCAGGATAGA 2580
QY 2581 GGAGAGGGAACACAGACTGGGACAGCACCAGGACCCAGAGCCCTCTGAGGC 2640
Db 2581 GGAGAGGGAACACAGACTGGGACAGCACCAGGACCCAGAGCCCTCTGAGGC 2640
QY 2641 AGGAGCCCGAGCTTAGACGCGAGAGTCCATCAAGTCAAGTCCCTGAGAGGAGCTACC 2700
Db 2641 AGGAGCCCGAGCTTAGACGCGAGAGTCCATCAAGTCAAGTCCCTGAGAGGAGCTACC 2700
QY 2701 ACTTCAGAGCCCGAGAGGTTCTCTGGATGACCCCTGACAGGCGAGGATGGCCAGCA 2760
Db 2701 ACTTCAGAGCCCGAGAGGTTCTCTGGATGACCCCTGACAGGCGAGGATGGCCAGCA 2760
QY 2761 GGAAGGACAGCATCAATACGCGAGGGTGAAGGCCACAGTGCACCTTACCTGCGT 2820
Db 2761 GGAAGGACAGCATCAATACGCGAGGGTGAAGGCCACAGTGCACCTTACCTGCGT 2820
QY 2821 GCGGTGGGACCCCTCTGCTCTACGACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2880
Db 2821 GCGGTGGGACCCCTCTGCTCTACGACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2880
QY 2881 TCCTTCTGCGGGGCTACTGCTGAGCCCTGTGGCGGAGACCCCTGCTGCTGCTGCTG 2940
|||||

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Db 2941 CAGACGAGGAGCCCTGCTGCGGGGATCTTCGGGCTCCTCGGCTGTCTCAAGCCATT 3000
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Db 3001 GGGCTGTTGCTCTCATGGCTGCGGTGCTCTAGTGGGGCCCGGCATCCAGTTGCTC 3060
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QY 3361 TCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3420
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Db 3721 TGGACGCCCAAGAGGCTTCCCTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3780
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Db 3781 CAGGGCGGCGAGATCGAGTTCGGGACTTTCGGGCTAAGATACCGACCTGAGCTCC 3840
QY 3841 GCTGTGAGGCGCTGCTTCAAGATCCACGAGAGAGAGTGGGATCGTTGGGACG 3900
Db 3841 GCTGTGAGGCGCTGCTTCAAGATCCACGAGAGAGAGTGGGATCGTTGGGACG 3900
QY 3901 ACCGGCGAGGAGTCTCTCCCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3960
Db 3901 ACCGGCGAGGAGTCTCTCCCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3960
QY 3961 GGTGGGATCTGGATCGACGGGCTCCCATTTGCCACGCTGGGGCTGCACACACTGCG 4020
Db 3961 GGTGGGATCTGGATCGACGGGCTCCCATTTGCCACGCTGGGGCTGCACACACTGCG 4020

Db 2581 GGAGAGGAGAAACAGAACCTGGACAGCACCAGGACCCAGAGGCACCTCTGCGAGC 2640
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QY 3181 GACAACTCCGCTCCTGTGATGATGACGCTTTGGATCCTTGAGGTACAGCTGGTGGTG 3240
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Db 3421 CGAACCAGGCCCCCTTTGTGCTCAGAAATGCTCGGTAGATGAAAGCCAGAGGATC 3480
QY 3481 AGTTTCCCGGACTGGTGGCTCACAGTGGCTTGGGCCAATGTGAGCTCTCTGGGAAAT 3540
Db 3481 AGTTTCCCGGACTGGTGGCTCACAGTGGCTTGGGCCAATGTGAGCTCTCTGGGAAAT 3540
QY 3541 GGCCTGGTGTTCAGCCCGCCAGCTGTGTGCTGCTGAGCAAGACCCACCTCAGTGTGTC 3600
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QY 3601 CTCGTGGGCTTCTCTCTCTCTCTGCTGCCCTCCAGGTGACCCAGACACTGCAGTGGTGT 3660
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QY 3661 CGCAACTGGACAGACCTAGAGAACAGCTGCTGCTAGTGGAGCGGATGAGGACTATGCC 3720
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QY 3721 TGCACGCCCAAGAGGCTCCTCTGGAGGCTGCCACATGTGCAGCTCAGCCCCCTGCGCT 3780
Db 3721 TGCACGCCCAAGAGGCTCCTCTGGAGGCTGCCACATGTGCAGCTCAGCCCCCTGCGCT 3780
QY 3781 CAGGCGGGCAGATCGAGTTCCGGGACTTTGGGCTAAGATGCCGACCTGAGTCCCGCTG 3840
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QY 3841 GCTGTGCAGGGCGTCTCTTCAAGATCCACGAGGAGAGGTGGCATCTGTTGGCAGG 3900
Db 3841 GCTGTGCAGGGCGTCTCTTCAAGATCCACGAGGAGAGGTGGCATCTGTTGGCAGG 3900
QY 3901 ACCGGGGCAGGGAAGTCTCCCTGGCCAGTGGGCTGCTGGGCTCCAGGAGGAGCTGAG 3960
Db 3901 ACCGGGGCAGGGAAGTCTCCCTGGCCAGTGGGCTGCTGGGCTCCAGGAGGAGCTGAG 3960
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Db 4021 AGGATCAGCATCATCCCCAGGACCCCATCTGTTCCCTGGCTCTCTGCGGATGAACCTC 4080
QY 4081 GACCTGCTGCAGGAGCACTCGGAGGAGCTATCTGGGACGCCCTGGAGAGCGGTGCACTC 4140
Db 4081 GACCTGCTGCAGGAGCACTCGGAGGAGCTATCTGGGACGCCCTGGAGAGCGGTGCACTC 4140
QY 4141 AAAGCCTTGGTGCCAGCCTGCGCGGCGAGCTGCAGTACAAAGTGTGCTGACCCGAGCGAG 4200
Db 4141 AAAGCCTTGGTGCCAGCCTGCGCGGCGAGCTGCAGTACAAAGTGTGCTGACCCGAGCGAG 4200
QY 4201 GACCTGAGCGTGGGCGAGAAACAGCTCCTGTGTGTCGACAGTGCCTTCTCCGGAAGACC 4260
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QY 4261 CAGATCTCATCTCTGGACGAGGCTACTGTGCGGTGACCTTGGCAGGAGCTGCAGATG 4320
Db 4261 CAGATCTCATCTCTGGACGAGGCTACTGTGCGGTGACCTTGGCAGGAGCTGCAGATG 4320
QY 4321 CAGGCCATGCTCGGGAGCTGTTTGACAGTGCAGTGTGCTGCCCATTTGCCACCGCTG 4380
Db 4321 CAGGCCATGCTCGGGAGCTGTTTGACAGTGCAGTGTGCTGCCCATTTGCCACCGCTG 4380
QY 4381 CGTCCGTGATGACTGTGCCCGGTTCTGTGTCATGACAAAGGGGAGGTGGCAGAGC 4440
Db 4381 CGTCCGTGATGACTGTGCCCGGTTCTGTGTCATGACAAAGGGGAGGTGGCAGAGC 4440
QY 4441 GGCAGCCCGGCCAGCTGTGCGCCAGAGGGCTGTTTACAGACTGGCCAGGAGTCA 4500
Db 4441 GGCAGCCCGGCCAGCTGTGCGCCAGAGGGCTGTTTACAGACTGGCCAGGAGTCA 4500
QY 4501 GGCCTGGTC 4509
Db 4501 GGCCTGGTC 4509

RESULT 5

AAD16258

ID AAD16258 standard; cdna; 4512 BP.

XX AAD16258;

XX 19-NOV-2001 (first entry)

XX Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cdna #3.

Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;
ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
mutant; mutein; ss.

CC useful in the area of genetic testing, carrier detection and prenatal
CC diagnosis. The present sequence is human ATP-binding cassette (ABC)
CC transporter, ABC6 (MRP6) mutant cDNA. This mutant cDNA results in an
CC amino acid change from Val to Phe at position 1298 of MRP6 protein.
CC Note: The present sequence is not shown in the specification but is
CC derived from human ATP-binding cassette transporter ABC6 (MRP6) cDNA
CC (SEQ ID NO: 2) shown in page 130-137 of the specification (AAD16231).
XX
SQ Sequence 4512 BP; 835 A; 1380 C; 1353 G; 944 T; 0 other;

Query Match 99.8%; Score 4497.8; DB 22; Length 4512;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4502; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGGCGCGCCCTGCTGAGCCCTGCGGGGAGGGGCTGGAACACAGACAGCCGTGAA 60
DB 1 ATGGCGCGCGCCCTGCTGAGCCCTGCGGGGAGGGGCTGGAACACAGACAGCCGTGAA 60
QY 61 CCTGCGCGCACAGCCTGCTGAGCCTGTGCTTCCTGAGAACAGCAGGGGTCTGGGTACCC 120
DB 61 CCTGCGCGCACAGCCTGCTGAGCCTGTGCTTCCTGAGAACAGCAGGGGTCTGGGTACCC 120
QY 121 CCCATGTACCTCTGGGTCTTGGTCCCATCTACCTCCCTTTCATCCACACCATGSCCGG 180
DB 121 CCCATGTACCTCTGGGTCTTGGTCCCATCTACCTCCCTTTCATCCACACCATGSCCGG 180
QY 181 GGTACCTCCGGATGTCCTCCACTCTTCAAGCCAGATGGTCTTGGATTCGCCCTCAT 240
DB 181 GGTACCTCCGGATGTCCTCCACTCTTCAAGCCAGATGGTCTTGGATTCGCCCTCAT 240
QY 241 GTCTCTGTGTACCTCCAGCGTGTGCTGTCTTGGTCTTTCGAAATCAACAGGAACGCTGAG 300
DB 241 GTCTCTGTGTACCTCCAGCGTGTGCTGTCTTGGTCTTTCGAAATCAACAGGAACGCTGAG 300
QY 301 GCCCAGAAATTCCTCATTCATCTACTGTGTGGCTTCAACACGATGAGTTCGCAGTGTTC 360
DB 301 GCCCAGAAATTCCTCATTCATCTACTGTGTGGCTTCAACACGATGAGTTCGCAGTGTTC 360
QY 361 CTGATTCACCGAGAGAAAGGAGTCCAGTATCTGGAGTCTGTGGTGTACTGG 420
DB 361 CTGATTCACCGAGAGAAAGGAGTCCAGTATCTGGAGTCTGTGGTGTACTGG 420
QY 421 CTTCTCTCTGTGTCTGCCAGCTACCAACGCTGCCAGCAGCGCTCCGGAGCGGCTTC 480
DB 421 CTTCTCTCTGTGTCTGCCAGCTACCAACGCTGCCAGCAGCGCTCCGGAGCGGCTTC 480
QY 481 CAGAGCGACCTGTCCGCCACTGTCCACCTACCTATGCCTGTCTCTGTGTGGTGCACAG 540
DB 481 CAGAGCGACCTGTCCGCCACTGTCCACCTACCTATGCCTGTCTCTGTGTGGTGCACAG 540
QY 541 TTTGTGCTGCTGCTGCTGGCGGATCAACCCCGCTTCTTCCCTGGAAGACCCCGAGCTCT 600
DB 541 TTTGTGCTGCTGCTGCTGGCGGATCAACCCCGCTTCTTCCCTGGAAGACCCCGAGCTCT 600
QY 601 AACCCCTGTCCAGAGACTGGGCGAGCCTTCCCTCCAAAGCCACCTTCTGTGGTGTCT 660
DB 601 AACCCCTGTCCAGAGACTGGGCGAGCCTTCCCTCCAAAGCCACCTTCTGTGGTGTCT 660
QY 661 GGCCTGTGCTGGAGGGGATACAGAGGCGCACTGAGACCAAGAGCCTCTGTGTCTGGG 720
DB 661 GGCCTGTGCTGGAGGGGATACAGAGGCGCACTGAGACCAAGAGCCTCTGTGTCTGGG 720
QY 721 AGAGAAACTCCTCAGAGAACTGTGTTCCCGGCTTGAAGAGGATGGATGAGGAACCGC 780
DB 721 AGAGAAACTCCTCAGAGAACTGTGTTCCCGGCTTGAAGAGGATGGATGAGGAACCGC 780
QY 781 AGTCAGCCCGGAGGCAACAAGCAATAGCATTTAAAGGAAAGGCGGAGTGGCATG 840
DB 781 AGTCAGCCCGGAGGCAACAAGCAATAGCATTTAAAGGAAAGGCGGAGTGGCATG 840
QY 841 AAGGCTCCAGAGACCGCCCTTCTACGGCAAGAGGAGCGAGTGGCGCCACTGTGT 900
DB 841 AAGGCTCCAGAGACCGCCCTTCTACGGCAAGAGGAGCGAGTGGCGCCACTGTGT 900

QY 901 AAGGCCATCTGGCAGTGTTCCATTCTACCTTCTCTGGGGACCCTCAGCCTCATCATC 960
DB 901 AAGGCCATCTGGCAGTGTTCCATTCTACCTTCTCTGGGGACCCTCAGCCTCATCATC 960
QY 961 AGTGATGCTTTCAGGTTCAGTCTGCCCAAGCTGCTCAGCCCTTTTCTGGAGTTTATGGT 1020
DB 961 AGTGATGCTTTCAGGTTCAGTCTGCCCAAGCTGCTCAGCCCTTTTCTGGAGTTTATGGT 1020
QY 1021 GATCCCAAGCCTCCAGCCTGGAAGGCTTACCTCTCGCCGTGCTGATGTTCTCTCAGCC 1080
DB 1021 GATCCCAAGCCTCCAGCCTGGAAGGCTTACCTCTCGCCGTGCTGATGTTCTCTCAGCC 1080
QY 1081 TGCCTGCAAAACGCTGTTTGAGCAGCAGAACATGTACAGGCTCAAGGTGCGCAGATGAGG 1140
DB 1081 TGCCTGCAAAACGCTGTTTGAGCAGCAGAACATGTACAGGCTCAAGGTGCGCAGATGAGG 1140
QY 1141 TTGCGGTGCGCCATCACTGCGCTGGTGTACAGAAAGTCTGCTCTGTCCAGCGGCTCC 1200
DB 1141 TTGCGGTGCGCCATCACTGCGCTGGTGTGTACAGAAAGTCTGCTCTGTCCAGCGGCTCC 1200
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DB 1321 TTGCTCTATCTCTGGCAGTCTCTGGGCGCTCCGCGCTCACTGCCATCGCTGTTCTCTG 1380
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DB 1381 AGCCTCTCCCTCTGAATTTCTTCTATCTCCAGAAAGAACCCATCAGGAGGAGCAA 1440
QY 1441 ATGAGGCAAGAGACTCAGGGCAGCGCTCACCAGCTCTATCTCAGGACTCAGAGACC 1500
DB 1441 ATGAGGCAAGAGACTCAGGGCAGCGCTCACCAGCTCTATCTCAGGAACTCAGAGACC 1500
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DB 1621 GTGTCTACATTTCTGGTCCGACTGGTGGTGTGCTGTCCACACTCTGGTGGCGGAGAT 1680
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DB 1681 GCTATGAATGACAGAAAGCCTTTGTGACTCTCACAGTTCTCAACATCTCTCAACAGGCC 1740
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DB 1741 CAGGCTTTCTGCCCTTCTCCACTCCCTCGTCCAGCGCGGCTGCTTTGACCGT 1800
QY 1801 CTGGTTCACCTTCTGCTGCTGGAAGATTGACCTTGTGCTGTAGCTCAAGTCTCT 1860
DB 1801 CTGGTTCACCTTCTGCTGCTGGAAGATTGACCTTGTGCTGTAGCTCAAGTCTCT 1860
QY 1861 GGAAGCGCTGCGGGAAGATTGACATCACAGTGCACACTTCCGCTGTGCTGCCAG 1920
DB 1861 GGAAGCGCTGCGGGAAGATTGACATCACAGTGCACACTTCCGCTGTGCTGCCAG 1920
QY 1921 GAAAGCCCTTCTGCTGCTCCACAGAAATAACCTCACGCTGCCAGGGCTGTCTGTGGT 1980
DB 1921 GAAAGCCCTTCTGCTGCTCCACAGAAATAACCTCACGCTGCCAGGGCTGTCTGTGGT 1980

Qy 1981 GTTGTGCTCCAGTGGGGGAGGAAAGTCCCTCCCTGCTGTCGCGCCCTCTTTGGGAGCTG 2040
Db 1981 GTTGTGCTCCAGTGGGGGAGGAAAGTCCCTCCCTGCTGTCGCGCCCTCTTTGGGAGCTG 2040
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Db 2041 TCAAAGTGGAGGGGTTGCTGAGCATCGAGGCTGCTGGGCTACGTGCCCCAGAGGCC 2100
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Qy 2821 GCGTGGGACCCCGCTCTGCTAGCCTCTAGCCTCTTCTCTCTCTCTGCTGCTGCTGCTGCT 2880
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Qy 2881 TCCTTCTGCGGGGCTACTGGCTGAGCCTGTGGCGGAGCAGACCCCTGCAGTAGGTGGGAG 2940
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Qy 2941 CAGACGAGCAGCCCTGCTGCTGGGAGTCTCGGGCTCTCTGCTGCTCTCTGCTGCTGCTGCT 3000
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Db 3481 AGTTTCCCGGACTGTGGCTGACAGTGGCTTGGGGCCAAATGTGGAGCTCTCTGGGGAAT 3540
Qy 3541 GGCCTGGTGTTCAGCGCCGACAGTGTGTGTGAGCAAAAGCCACCTCAGTGTCTGTC 3600
Db 3541 GGCCTGGTGTTCAGCGCCGACAGTGTGTGTGAGCAAAAGCCACCTCAGTGTCTGTC 3600
Qy 3601 CTGCTGGCTTCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
Db 3601 CTGCTGGCTTCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
Qy 3661 CGCAACTGGACAGACTTAGAAGACATCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
Db 3661 CGCAACTGGACAGACTTAGAAGACATCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
Qy 3721 TGGAGCCCAAGAGGCTTCCCTGAGGCTGCCACATGTGAGCTCAGCCCCCTTGGCT 3780
Db 3721 TGGAGCCCAAGAGGCTTCCCTGAGGCTGCCACATGTGAGCTCAGCCCCCTTGGCT 3780
Qy 3781 CAGGCGGGCAGATCGAGTTCGGGACTTGGGCTTAAGATGCCAGCTCAGCTCCCGCTG 3840
Db 3781 CAGGCGGGCAGATCGAGTTCGGGACTTGGGCTTAAGATGCCAGCTCAGCTCCCGCTG 3840
Qy 3841 GCTGTGAGGCGGTGTCTTCAAGATCCACGAGAGAGAGGTGGGCTCCAGAGGACCTGAG 3900
Db 3841 GCTGTGAGGCGGTGTCTTCAAGATCCACGAGAGAGAGGTGGGCTCCAGAGGACCTGAG 3900
Qy 3901 ACCGGGCGAGGAGTCTCTCCCTGGCAGTGGGCTGCTGGGCTCCAGAGGACCTGAG 3960
Db 3901 ACCGGGCGAGGAGTCTCTCCCTGGCAGTGGGCTGCTGGGCTCCAGAGGACCTGAG 3960
Qy 3961 GGTGGGATCTGGATCGAGGGGTCCCATTTGCCAGCTGGGCTGCTGCTGCTGCTGCTGCT 4020
Db 3961 GGTGGGATCTGGATCGAGGGGTCCCATTTGCCAGCTGGGCTGCTGCTGCTGCTGCTGCT 4020
Qy 4021 AGGATCAGCATCATCCCCAGAGCCCATCTCTGTTCCCTGCTGCTGCTGCTGCTGCTGCT 4080
Db 4021 AGGATCAGCATCATCCCCAGAGCCCATCTCTGTTCCCTGCTGCTGCTGCTGCTGCTGCT 4080
Qy 4081 GACCTGCTGAGGAGACTCGGAGAGGCTATCTGGGCGAGCCCTGGAGACGGTGCAGCTC 4140
Db 4081 GACCTGCTGAGGAGACTCGGAGAGGCTATCTGGGCGAGCCCTGGAGACGGTGCAGCTC 4140
Qy 4141 AAAGCCTTGGTGGCAGCTGCGCGGCGAGCTGCGAGTACAGTGTGCTGACCGGCGGAG 4200

Qy	601	AACCCCTGTCAGAGACTGGGCAGCGCTTCCCTCCAAAGACCACCTTCTGTTGGTGTCT	660
Db	601		660
Qy	661	GSCCTGTCTGGAGGGGATACAGGAGGCCACTGAGACCAAAAGACCTCTGTCGCTTGGG	720
Db	661		720
Qy	721	AGAGAAAACCTCCTCAGAAGAACCTTGTTTTCCC GGCTTGTAAGAGGAGTGGATCAGGAACCGC	780
Db	721		780
Qy	781	AGTCAGCCCGAGGAGCACAAAGCAATAGCATTTAAAGAAAGCGGCAGTGGCATG	840
Db	781		840
Qy	841	AAGSCTCCAGAGACCGAGGCCCTTCTACGGCAAGAGGAGGCCAGTGGCGCCCACTGCTG	900
Db	841		900
Qy	901	AAGGCCAATCTGGCAGGTGTTCCATCTACCTTCTCCTTGGGGACCCCTCAGCCTCATCATC	960
Db	901		960
Qy	961	AGTGATGCTTTCAGGTTCACTGCCCAAGCTGCTCAGSCCTTTTCCCTGGAGTTATTGGT	1020
Db	961		1020
Qy	1021	GATCCC AAGCTCCAGSCCTGG AAGGGCTACCTTCTCGCGCGCTGCTGATGTTCTCTCAGCC	1080
Db	1021		1080
Qy	1081	TGCCTGCAAAACGCTGTTTGAGCAGCAGACAATGTACAGGCTCAAGTGCCTCTCTCAGCC	1140
Db	1081		1140
Qy	1141	TTGCGGTGCGCCATCACTGGCCTGGGTACAGAAAGTCTCGGCTCTGTCCAGGGCGTCC	1200
Db	1141		1200
Qy	1201	AGAAAGCCAGTGC GGTGGGTGATGTGTCAATCTPGTGTCCGTGGACGTGCAGCGGCTG	1260
Db	1201		1260
Qy	1261	ACGAGAGCGTCTCTACCTCAACGGCTGTGGCTGCTCTGCTCGATCGTGGTCTGC	1320
Db	1261		1320
Qy	1321	TTGCTCTATCTTGGCAGCTCCTGGGGGCCCTCGGCCCTCACTGCCATCGTGTCTTCCG	1380
Db	1321		1380
Qy	1381	AGCCTCTCTGCTGAAATTTCTTCAATCTCAAAGAAAGGAACCAACATCAGGAGGAGCAA	1440
Db	1381		1440
Qy	1441	ATGAGCGAAGAGACTCACGGGACGGCTCACAGCTCTATCTCTCAGSAATCGAAGACC	1500
Db	1441		1500
Qy	1501	ATCAAGTTCATGGCTGGGAGGAGCCCTTTCTGGACAGAGTCTCTGGGCATCCGAGGCCAG	1560
Db	1501		1560
Qy	1561	GAGCTGGGGCCCTTGGCGACCTTCGCGCCCTCTCTTCTGTGTGCTGTGTCTTCTTCCAA	1620
Db	1561		1620
Qy	1621	GTGCTACATTTCTGCTCGCACTGCTGTGTGTTTCTGTCTCACACTCTGTGTGGCGGAGAAT	1680
Db	1621		1680

Qy	1681	GCTATGAATGCAGAGAAAGCCTTTGTGACTCTCACAAGTTCTCAACATCTCTCAACAGGCC	1740
Db	1681	GCTATGAATGCAGAGAAAGCCTTTGTGACTCTCACAAGTTCTCAACATCTCTCAACAGGCC	1740
Qy	1741	CAGGCTTTCCCTGCCCTTCTCCACTCCCTCGTCCAGGCCGGGTGTCCTTTGACCGT	1800
Db	1741	CAGGCTTTCCCTGCCCTTCTCCACTCCCTCGTCCAGGCCGGGTGTCCTTTGACCGT	1800
Qy	1801	CTGGTCACCTTCTCTGCTGGGAAGAAGTTGACCTTGGTGTCTGTAGACTCAAGTTCTCTCT	1860
Db	1801	CTGGTCACCTTCTCTGCTGGGAAGAAGTTGACCTTGGTGTCTGTAGACTCAAGTTCTCTCT	1860
Qy	1861	GGAAAGCGTCCGGGAAGGATTGCATACATACAGATGCCACTTCGCTGGTCCCAG	1920
Db	1861	GGAAAGCGTCCGGGAAGGATTGCATACATACAGATGCCACTTCGCTGGTCCCAG	1920
Qy	1921	GAAGCCCTCCCTGCTCCACAGATAAACCTCACGGTGCCACAGGGCTGTCTGCTGGCT	1980
Db	1921	GAAGCCCTCCCTGCTCCACAGATAAACCTCACGGTGCCACAGGGCTGTCTGCTGGCT	1980
Qy	1981	GTTGTGCGTCCAGTGGGGCAGGGAAGTCTCTCCCTGCTCTCGCCCTCTCTTGGGGAGCTG	2040
Db	1981	GTTGTGCGTCCAGTGGGGCAGGGAAGTCTCTCCCTGCTCTCGCCCTCTCTTGGGGAGCTG	2040
Qy	2041	TCAAAGTGGAGGGGTTCGTGAGCATCGAGGTTGTTGGCCCTACGTGCCACAGGAGGCC	2100
Db	2041	TCAAAGTGGAGGGGTTCGTGAGCATCGAGGTTGTTGGCCCTACGTGCCACAGGAGGCC	2100
Qy	2101	TGGGTGCAGAACACCTCTGTGTGTAGAGATGTGTGCTTCGGGCAGAGCTGNACCCACCC	2160
Db	2101	TGGGTGCAGAACACCTCTGTGTGTAGAGATGTGTGCTTCGGGCAGAGCTGGACCCACCC	2160
Qy	2161	TGGCTGGAGAGAGTACTAGAAGCCTGTGCCCTCGACGCAGATGTGGACAGCTTCCCTGAG	2220
Db	2161	TGGCTGGAGAGAGTACTAGAAGCCTGTGCCCTCGACGCAGATGTGGACAGCTTCCCTGAG	2220
Qy	2221	GGAAATCCACACTTCAATTTGGGAGCAGGGCATGAATCTCTCGGAGGCCAGAAGCAGCG	2280
Db	2221	GGAAATCCACACTTCAATTTGGGAGCAGGGCATGAATCTCTCGGAGGCCAGAAGCAGCG	2280
Qy	2281	CTGAGCCTGGCCCGGCTGTATACAGAAGGCAGCTGTGTACCTCTGTGATGACCCCTTG	2340
Db	2281	CTGAGCCTGGCCCGGCTGTATACAGAAGGCAGCTGTGTACCTCTGTGATGACCCCTTG	2340
Qy	2341	GGGGCCCTGGATGCCACAGTTTGGCCAGCATGTCTTCAACAGAGTCATTTGGGCTGTGTGG	2400
Db	2341	GGGGCCCTGGATGCCACAGTTTGGCCAGCATGTCTTCAACAGAGTCATTTGGGCTGTGTGG	2400
Qy	2401	CTACTCAGGGAACAAACAGGATTCCTGTGACGACAGCATCCACATCTCTGCCACAGGT	2460
Db	2401	CTACTCAGGGAACAAACAGGATTCCTGTGACGACAGCATCCACATCTCTGCCACAGGT	2460
Qy	2461	GATTGGATCATAGTCTGCAANTGGGGCCATCGCAGAGATGGGTTCCTACAGGAGCTT	2520
Db	2461	GATTGGATCATAGTCTGCAANTGGGGCCATCGCAGAGATGGGTTCCTACAGGAGCTT	2520
Qy	2521	CTGCAGAGGAAGGGGGCCCTCGTGTGTCTCTGGATCAAGCCAGACAGCCAGGAGATAGA	2580
Db	2521	CTGCAGAGGAAGGGGGCCCTCGTGTGTCTCTGGATCAAGCCAGACAGCCAGGAGATAGA	2580
Qy	2581	GGAGAGGAGAAACAGAACCTTGGGACCAAGCACCCAGAGGACCTCTCTCAGGC	2640
Db	2581	GGAGAGGAGAAACAGAACCTTGGGACCAAGCACCCAGAGGACCTCTCTCAGGC	2640
Qy	2641	AGGAGGCCGAGCTTAGACGGCAGAGGTCCATCAAGTCAGTGCCTTGAGAAGGACCGTACC	2700
Db	2641	AGGAGGCCGAGCTTAGACGGCAGAGGTCCATCAAGTCAGTGCCTTGAGAAGGACCGTACC	2700
Qy	2701	ACTTCAGAGCCCGACAGAGAGTTCCCTCTGGATGATACCCTGCACAGGGCAGGATGGCCAGA	2760
Db	2701	ACTTCAGAGCCCGACAGAGAGTTCCCTCTGGATGATACCCTGCACAGGGCAGGATGGCCAGA	2760
Qy	2761	GGAAAGGACGATCCCAATAGGCAGGGTGAAGGCCACAGTGCACCTTGGCCTTACCTGCTGT	2820

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Db 2761 GGAAGGACAGCATCCAAATACGGCAGGGTGAAGCCACAGTGCACCTGGCCCTACCTGGCT 2820
QY 2821 GCCGTGGGACACCCCTCTGCTCTACGCACTCTTCCTCTTCCTCTGCGCAAGTGGCC 2880
Db 2821 GCCGTGGGACACCCCTCTGCTCTACGCACTCTTCCTCTTCCTCTGCGCAAGTGGCC 2880
QY 2881 TCCTTCTGCCGGGCTACTGGCTAGCCTGTGGCGGACGACCCCTGCAGTAGTGGGCGAG 2940
Db 2881 TCCTTCTGCCGGGCTACTGGCTAGCCTGTGGCGGACGACCCCTGCAGTAGTGGGCGAG 2940
QY 2941 CAGACGAGCAGCCGCTGCGGTGGGGATCTTCGGGGTCCCTGCGCTGCTCAAGCCATT 3000
Db 2941 CAGACGAGCAGCCGCTGCGGTGGGGATCTTCGGGGTCCCTGCGCTGCTCCAGCCATT 3000
QY 3001 GGGCTGTTGGCTCCATGGCTGCGGTGCTCCTAGTGGGGCGGGCATCCAGTTGCTC 3060
Db 3001 GGGCTGTTGGCTCCATGGCTGCGGTGCTCCTAGTGGGGCGGGCATCCAGTTGCTC 3060
QY 3061 TTCAGAGGCTCCTGTGGGATGTGGTGGATCTCCCATCAGCTTCTTTGAGCGGACACC 3120
Db 3061 TTCAGAGGCTCCTGTGGGATGTGGTGGATCTCCCATCAGCTTCTTTGAGCGGACACC 3120
QY 3121 ATTGGTCACCTGCTAAACCGCTTCTCAAGGAGACAGACGCTTGAGCTGGACATTCGA 3180
Db 3121 ATTGGTCACCTGCTAAACCGCTTCTCAAGGAGACAGACGCTTGAGCTGGACATTCGA 3180
QY 3181 GACAACTCCGGTCCCTGCTGATGATGAGCTTTCAGCTGAGGAGTCCCTGAGGAGTGC 3240
Db 3181 GACAACTCCGGTCCCTGCTGATGATGAGCTTTCAGCTGAGGAGTCCCTGAGGAGTGC 3240
QY 3241 GCAGTGCTACCCACAGTGGCAGCTGCGCCATCTGCGCATCTGCTTCTACGCTGGG 3300
Db 3241 GCAGTGCTACCCACAGTGGCAGCTGCGCCATCTGCGCATCTGCTTCTACGCTGGG 3300
QY 3301 TTTTCAGAGCCTGTATGTGGTGTAGCTCATGCCAGCTGAGACGCTTGGAGTCAAGCCAGCTAC 3360
Db 3301 TTTTCAGAGCCTGTATGTGGTGTAGCTCATGCCAGCTGAGACGCTTGGAGTCAAGCCAGCTAC 3360
QY 3361 TCGTCTGTCTCCACATGCTGAGACGTTCCAGGCGACAGTGTGCTCGGCGCATTC 3420
Db 3361 TCGTCTGTCTCCACATGCTGAGACGTTCCAGGCGACAGTGTGCTCGGCGCATTC 3420
QY 3421 CGAACCCAGGCCCCCTTTGTGGCTCAGAACAAATGCTGCGTAGATGAAGCCAGAGGATC 3480
Db 3421 CGAACCCAGGCCCCCTTTGTGGCTCAGAACAAATGCTGCGTAGATGAAGCCAGAGGATC 3480
QY 3481 AGTTTCCCGGAGCTGTGGCTGACAGGTGGCTTGGGCGCAATGTGGAGCTCCTGGGGAAT 3540
Db 3481 AGTTTCCCGGAGCTGTGGCTGACAGGTGGCTTGGGCGCAATGTGGAGCTCCTGGGGAAT 3540
QY 3541 GGCCTGTGTTTGAGCGCGGACAGCTGTGCTGTGAGCAAGCCACCTCAGTGTGCTGGC 3600
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QY 3601 CTCGTGGGCTTCTGCTGCTGCTGCTCCAGGTGACCCAGACATGCTCAGTGGGTTCTT 3660
Db 3601 CTCGTGGGCTTCTGCTGCTGCTGCTCCAGGTGACCCAGACATGCTCAGTGGGTTCTT 3660
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Db 3661 CGCAACTGGACAGACCTTAGAAGACAGATCGTGTGAGTGGAGCGGATGACGACTATGCC 3720
QY 3721 TGGACGCCAAGGAGGCTCCTTGAGGCTGCCACATGTGAGCTCAGCCCTCCCTGGCCT 3780
Db 3721 TGGACGCCAAGGAGGCTCCTTGAGGCTGCCACATGTGAGCTCAGCCCTCCCTGGCCT 3780
QY 3781 CAGGGCGGCGAGATCGAGTTCCGGGACTTTGGGCTAGATGCCGACCTGAGCTCCCGCTG 3840
Db 3781 CAGGGCGGCGAGATCGAGTTCCGGGACTTTGGGCTAGATGCCGACCTGAGCTCCCGCTG 3840
QY 3841 GCTGTGAGGGCGTGTCTCTCAAGATCCACGAGGAGAGGTTGGGCTGCTGTTGGCAGG 3900
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Db 3841 GCTGTGCAGGGCGTGTCTTCAAGATCCACGAGGAGAGAGGTGGGCATCGTTGGCAGG 3900
QY 3901 ACCGGGGGAGGAAGTCTCTCCCTGGCCAGTGGGCTGCTCGGGCTCAGGAGGAGCTGAG 3960
Db 3901 ACCGGGGGAGGAAGTCTCTCCCTGGCCAGTGGGCTGCTCGGGCTCAGGAGGAGCTGAG 3960
QY 3961 GGTGGGATCTGATCGAGGAGGCTCCCATTTGCCAGTGGGCTGCACACACTGGCCTCC 4020
Db 3961 GGTGGGATCTGATCGAGGAGGCTCCCATTTGCCAGTGGGCTGCACACACTGGCCTCC 4020
QY 4021 AGGATCAGCATCATCCCCCAGGACCCCATCTCTTCCCTGGGCTCTCTGGGATGAACCTC 4080
Db 4021 AGGATCAGCATCATCCCCCAGGACCCCATCTCTTCCCTGGGCTCTCTGGGATGAACCTC 4080
QY 4081 GACCTGCTGCAGGAGCACTCGGACGAGGCTATCTGGGCGAGCCCTGGAGACGGTGCAGCTC 4140
Db 4081 GACCTGCTGCAGGAGCACTCGGACGAGGCTATCTGGGCGAGCCCTGGAGACGGTGCAGCTC 4140
QY 4141 AAAGCCTTTGGTGGCGCAGCTGCGCGCCAGCTGCAGTACAAGTGTGCTCACCGAGCGGAG 4200
Db 4141 AAAGCCTTTGGTGGCGCAGCTGCGCGCCAGCTGCAGTACAAGTGTGCTCACCGAGCGGAG 4200
QY 4201 GACCTGAGCGTGGGCGCAGAAACAGCTCTCTGTGTGGCAGCTGCCCTTCTCGGGAAGACC 4260
Db 4201 GACCTGAGCGTGGGCGCAGAAACAGCTCTCTGTGTGGCAGCTGCCCTTCTCGGGAAGACC 4260
QY 4261 CAGATCCTCATCTCTGGAGAGGCTACTGTGCTGGCGAGCCCTGGCAGGAGTGCAGATG 4320
Db 4261 CAGATCCTCATCTCTGGAGAGGCTACTGTGCTGGCGAGCCCTGGCAGGAGTGCAGATG 4320
QY 4321 CAGGCGCATGCTCGGAGCTGTTTGCACAGTGCACACTGTGCTGCCCATTTGCCACCGCCTG 4380
Db 4321 CAGGCGCATGCTCGGAGCTGTTTGCACAGTGCACACTGTGCTGCCCATTTGCCACCGCCTG 4380
QY 4381 CGCTCCGTGATGGACTGTGCCGGGTTCTGTCATGACAAAGGGCAGGTGGCAGAGAGC 4440
Db 4381 CGCTCCGTGATGGACTGTGCCGGGTTCTGTCATGACAAAGGGCAGGTGGCAGAGAGC 4440
QY 4441 GGCAGCCCGGCCAGCTGCTGCCCCAGAGAGGCGCTTTTACAGACTGCCCCAGGAGTCA 4500
Db 4441 GGCAGCCCGGCCAGCTGCTGCCCCAGAGAGGCGCTTTTACAGACTGCCCCAGGAGTCA 4500
QY 4501 GGCCTGGTC 4509
Db 4501 GGCCTGGTC 4509

RESULT 8
AADI6262
ID AADI6262 standard; cDNA; 4512 BP.
XX
AC AADI6262;
XX
DT 19-NOV-2001 (first entry)
XX
DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #7.
XX
KW Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;
ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
mutant; mutein; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key
FT CDS
FT Location/Qualifiers
FT 1. 4512
FT /*tag= a
FT /product= "Human ABCC6 (MRP6) mutant protein"
FT replace (3907, G)
FT mutation
FT /*tag= b
XX
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PN WO200162977-A2.
XX 30-AUG-2001.
XX 23-FEB-2001; 2001WO-US05741.
XX 23-FEB-2000; 2000US-0184269.
XX (PXEI-) PXE INT INC.
XX (UYHA-) UNIV HAWAII.
PI Boyd CD, Csiszar K, Lesaux O, Urban Z, Terry S;
XX WPI: 2001-536645/59.
DR P-PSDB; AAE09369.
XX
PT Screening presence of Pseudoxanthoma elasticum mutation useful for
PT identifying homozygotes, compound heterozygotes or carriers involves
PT determining presence of mutation in MRP6 (ABCC6) nucleic acid -
XX
XX Example 2; Page -: 163pp; English.
XX
CC The invention relates to methods and compositions for diagnosing and
CC treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological
CC dysfunctions. The invention is useful for screening for the presence of
CC a PXE mutation. Mutations associated with PXE maps to the ATP-binding
CC cassette transporter ABCC6 (MRP6-Multidrug Resistance associated
CC protein-6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165
CC kDa protein located in the plasma membrane containing 17 membrane-
CC spanning helices grouped into three transmembrane domains. PXE is
CC inherited as an autosomal recessive phenotype or appears as a sporadic
CC phenotype. PXE is a heritable disorder characterised by mineralisation of
CC elastic fibers in skin, arteries and the retina, that result in dermal
CC lesions with associated laxity and loss of elasticity, arterial
CC insufficiency, cardiovascular disease and retinal haemorrhages leading to
CC macular degeneration. The method is useful for screening a population of
CC individuals in order to identify individuals with one or more PXE
CC associated MRP6 alleles who are then provided with appropriate genetic
CC counselling in view of the PXE status. The methods are useful for
CC identifying homozygotes, compound heterozygotes or carriers and thus are
CC useful in the area of genetic testing, carrier detection and prenatal
CC diagnosis. The present sequence is human ATP-binding cassette (ABC)
CC transporter, ABCC6 (MRP6) mutant cDNA. This mutant cDNA results in an
CC amino acid change from Ala to Pro at position 1303 of MRP6 protein.
CC Note: The present sequence is not shown in the specification but is
CC derived from human ATP-binding cassette transporter ABCC6 (MRP6) cDNA
CC [SEQ ID NO: 2] shown in page 130-137 of the specification (A4D16231).
XX
XX Sequence 4512 BP; 835 A; 1381 C; 1353 G; 943 T; 0 other;
Query Match 99.8%; Score 4497.8; DB 22; Length 4512;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4502; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 ATGGCGCGCCCTGCTGAGCCCTGCGGGGCGAGGGGGTCTGGAACACAGACAGCCCTGAA 60
DB 1 ATGGCGCGCCCTGCTGAGCCCTGCGGGGCGAGGGGGTCTGGAACACAGACAGCCCTGAA 60
QY 61 CTTGCGCGCCACCAAGCCTGCTGAGCCCTGCTTCTTCTGAGAACAGCAGGGGTCTGGGTACCC 120
DB 61 CTTGCGCGCCACCAAGCCTGCTGAGCCCTGCTTCTTCTGAGAACAGCAGGGGTCTGGGTACCC 120
QY 121 CCCATGTACCTCTGGGTCTCTGGTTCGCATCTACCTCCTTCTATCCACCAACCATGCGCGG 180
DB 121 CCCATGTACCTCTGGGTCTCTGGTTCGCATCTACCTCCTTCTATCCACCAACCATGCGCGG 180
QY 181 GCGTACTCTCGGATGTCCTTCTTCAAGCAACAGATGGTCTTGGATTTCGCCCTCATTA 240
DB 181 GCGTACTCTGGATGTCCCATCTCTTCAAGCAACAGATGGTCTTGGATTTCGCCCTCATTA 240
QY 241 GTCTGTGTACCTCCAGCGTGGCTGTCTCTTTTGAAAAATCAACAGGGAACGCTGTAG 300
DB 241 GTCTGTGTACCTCCAGCGTGGCTGTCTCTTTTGAAAAATCAACAGGGAACGCTGTAG 300

QY 301 GCCCCAGAAATTCCTCATTCATCTCTGTTGGGTCAACACAGATGAGTTCCGAGTGTTC 360
DB 301 GCCCCAGAAATTCCTCATTCATCTCTGTTGGGTCAACACAGATGAGTTCCGAGTGTTC 360
QY 361 CTGATTCACACCGAGAGAGAAAAGGAGTCCAGTCACTCTGGAGTCTGTTGGTTACTGG 420
DB 361 CTGATTCACACCGAGAGAGAAAAGGAGTCCAGTCACTCTGGAGTCTGTTGGTTACTGG 420
QY 421 CTTCTCTGCTTGTCTTCCAGCTACCAACGCTGCCAGCAGGCTCCGGAGCGGCTTC 480
DB 421 CTTCTCTGCTTGTCTTCCAGCTACCAACGCTGCCAGCAGGCTCCGGAGCGGCTTC 480
QY 481 CAGAGCAACCTGTCTGCCACCTGTCCACCTACCTATGCTCTCTCTGGTGGTGCACAG 540
DB 481 CAGAGCAACCTGTCTGCCACCTGTCCACCTACCTATGCTCTCTCTGGTGGTGCACAG 540
QY 541 TTTGTGCTGCTCTGCTGGCGGATCAACCCCTCTTCCCTCTGAGACCCCTCAGTCT 600
DB 541 TTTGTGCTGCTCTGCTGGCGGATCAACCCCTCTTCTTCCCTGAGACCCCTCAGTCT 600
QY 601 AACCCCTGTCTCAGAGACTGGGGCAGCCCTTCCCTCTCAAGGCCACGTTCTGTGGTGTTC 660
DB 601 AACCCCTGTCTCAGAGACTGGGGCAGCCCTTCCCTCTCAAGGCCACGTTCTGTGGTGTTC 660
QY 661 GGCTGTCTGGAGGGGATCAGAGGCGCACTGAGACCAAAAGACCTCTGTGCTGTGG 720
DB 661 GGCTGTCTGGAGGGGATCAGAGGCGCACTGAGACCAAAAGACCTCTGTGCTGTGG 720
QY 721 AGAAATCTCTCAGAGAACTTGTTCCTGGCTTGAAGAGGAGTGGATGAGGAACCGC 780
DB 721 AGAAATCTCTCAGAGAACTTGTTCCTGGCTTGAAGAGGAGTGGATGAGGAACCGC 780
QY 781 AGTCAGCCCGGAGGCAACAAGGCAATACATTTAAAGGAAAGGCGGAGTGGCATG 840
DB 781 AGTCAGCCCGGAGGCAACAAGGCAATACATTTAAAGGAAAGGCGGAGTGGCATG 840
QY 841 AAGCTCCAGAGACCGAGCCCTTCTTACGGCAAGAGGAGGAGGAGGAGGAGGAGGAGG 900
DB 841 AAGCTCCAGAGACCGAGCCCTTCTTACGGCAAGAGGAGGAGGAGGAGGAGGAGGAGG 900
QY 901 AAGCCATCTGGCAGGTCTTCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
DB 901 AAGCCATCTGGCAGGTCTTCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
QY 961 AGTGATCTCTTCTAGTCT 1020
DB 961 AGTGATCTCTTCTAGTCT 1020
QY 1021 GATCCCAAGCCTCCAGCCTGGAAGGGGTACCTCTCTGCGCGTGTGATGTTCTCTCAACC 1080
DB 1021 GATCCCAAGCCTCCAGCCTGGAAGGGGTACCTCTCTGCGCGTGTGATGTTCTCTCAACC 1080
QY 1081 TGCTGCAAAAGCCTGTTTGGACAGCAGACATGTACAGGCTCAAGGCTCTCAGATGAGG 1140
DB 1081 TGCTGCAAAAGCCTGTTTGGACAGCAGACATGTACAGGCTCAAGGCTCTCAGATGAGG 1140
QY 1141 TTGCGGTGCGCCCATCACTGGCCTGGTGTACAAAAGGTCTCTGGCTCTCTCCAGCGGCTCC 1200
DB 1141 TTGCGGTGCGCCCATCACTGGCCTGGTGTACAAAAGGTCTCTGGCTCTCTCCAGCGGCTCC 1200
QY 1201 AGAAAGCCAGTGGGTGGTGTGTTCAATGTGTGTCCTGAGGAGTGTGAGCGGCTG 1260
DB 1201 AGAAAGCCAGTGGGTGGTGTGTTCAATGTGTGTCCTGAGGAGTGTGAGCGGCTG 1260
QY 1261 ACCGAGAGCCTCTCTACCTCAACGGGCTGTGGCTGCTCTCTCTCTCTCTCTCTCTCTCT 1320
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QY 1321 TTGCTCTATCTCTGGCAGCTCTCTGGGCGCCCTCCGCGCTCACTGCGCATCGCTGTCTTCCTG 1380
DB 1321 TTGCTCTATCTCTGGCAGCTCTCTGGGCGCCCTCCGCGCTCACTGCGCATCGCTGTCTTCCTG 1380


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Db 3541 GGCCTGGTGTGTTGTCAGCTGGCCACGTGCTGCTGCTGAGAAAGCCACCTCAGTGGCTGGC 3600
QY 3601 CTCGTGGGCTTCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3660
Db 3601 CTCGTGGGCTTCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3660
QY 3661 CGCAACTGGACAGACCTAGAGAACAGCATGCTGTCAGTGGAGCGGATGCGAGACTATGCGC 3720
Db 3661 CGCAACTGGACAGACCTAGAGAACAGCATGCTGTCAGTGGAGCGGATGCGAGACTATGCGC 3720
QY 3721 TGGACGCCCAAGGAGGCTCCCTGGAGGCTGCCACATGTCAGCTCAGCCGCCCTGGCGCT 3780
Db 3721 TGGACGCCCAAGGAGGCTCCCTGGAGGCTGCCACATGTCAGCTCAGCCGCCCTGGCGCT 3780
QY 3781 CAGGGCGGGCAGATCGAGTTCCGGGACTTTGGGCTAAGATGCGGACCTGAGCTCCCGCTG 3840
Db 3781 CAGGGCGGGCAGATCGAGTTCCGGGACTTTGGGCTAAGATGCGGACCTGAGCTCCCGCTG 3840
QY 3841 GCTGTGCAGGCGGTGCTCTTCAAGATCCAGCAGGAGAGAGTGGGCTGCTGTTGGCAGG 3900
Db 3841 GCTGTGCAGGCGGTGCTCTTCAAGATCCAGCAGGAGAGAGTGGGCTGCTGTTGGCAGG 3900
QY 3901 ACCGGGCGAGGAGTCTCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGGAGGAGCTGAG 3960
Db 3901 ACCGGGCGAGGAGTCTCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGGAGGAGCTGAG 3960
QY 3961 GGTGGGATCTGGATTCGACGGGGTCCCATTTGCCACCTGCGGCTGTCACACACTGCGCTCC 4020
Db 3961 GGTGGGATCTGGATTCGACGGGGTCCCATTTGCCACCTGCGGCTGTCACACACTGCGCTCC 4020
QY 4021 AGGATCAGCATCATCCCGCAGGAGCCCATCTGTTCCCTGGCTCTGCGGATGAACTC 4080
Db 4021 AGGATCAGCATCATCCCGCAGGAGCCCATCTGTTCCCTGGCTCTGCGGATGAACTC 4080
QY 4081 GACCTGCTCAGGAGCACTCGGAGGCTATCTGGCAGCGCTTGGCAGCGGTGCAGCTC 4140
Db 4081 GACCTGCTCAGGAGCACTCGGAGGCTATCTGGCAGCGCTTGGCAGCGGTGCAGCTC 4140
QY 4141 AAGCCTTGTTGGCAGCCTGCGCGGCGCAGCTGAGTACAGTGTGCTACCGAGGCGAG 4200
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QY 4201 GACCTGAGCTGGGCGAGAAACAGCTCTGCTGCTGTCAGCTGCTCTCCGGAAGACC 4260
Db 4201 GACCTGAGCTGGGCGAGAAACAGCTCTGCTGCTGTCAGCTGCTCTCCGGAAGACC 4260
QY 4261 CAGATCCTCATCTCGGACGAGGCTACTGCTGCGCTGGACCTGGACCGGAGCTGCAGATG 4320
Db 4261 CAGATCCTCATCTCGGACGAGGCTACTGCTGCGCTGGACCTGGACCGGAGCTGCAGATG 4320
QY 4321 CAGGCCATGCTCGGAGCTGTTTGCACAGTGCACCTGCTGCTGCTGCTGCTGCTGCTGCTG 4380
Db 4321 CAGGCCATGCTCGGAGCTGTTTGCACAGTGCACCTGCTGCTGCTGCTGCTGCTGCTGCTG 4380
QY 4381 CGCTCGCTGATGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4440
Db 4381 CGCTCGCTGATGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4440
QY 4441 GGCAGCCCGGCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4500
Db 4441 GGCAGCCCGGCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4500
QY 4501 GGCCTGTGTC 4509
Db 4501 GGCCTGTGTC 4509
```

RESULT 9

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AAD16263
ID AAD16263 standard; cDNA; 4512 BP.
XX
AC
XX AAD16263;
```

```
DT 19-NOV-2001 (first entry)
XX Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #8.
DE Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
XX Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;
KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
KW mutant; munein; ss.
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..4512
FT FT /*tag= a
FT FT /product= "Human ABCC6 (MRP6) mutant protein"
FT FT mutation replace (3940, C)
FT FT /*tag= b
FT WO200162977-A2.
XX
XX 30-AUG-2001.
XX
XX 23-FEB-2001; 2001WO-US05741.
XX
XX 23-FEB-2000; 2000US-0184269.
XX (PXE1-) PXE INT INC.
XX (UYHA-) UNIV HAWAII.
XX
XX Boyd CD, Csizsar K, Lesaux O, Urban Z, Terry S;
PI WPI; 2001-536645/59.
DR P-PSDB; AAE09370.
XX
XX Screening presence of Pseudoxanthoma elasticum mutation useful for
XX identifying homozygotes, compound heterozygotes or carriers involves
XX determining presence of mutation in MRP6 (ABCC6) nucleic acid .
XX
XX Example 2; Page -; 163pp; English.
XX
XX The invention relates to methods and compositions for diagnosing and
XX treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological
XX dysfunctions. The invention is useful for screening for the presence of
XX a PXE mutation. Mutations associated with PXE maps to the ATP-binding
XX cassette transporter ABCC6 (MRP6-Multidrug Resistance associated
XX protein-6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165
XX kDa protein located in the plasma membrane containing 17 membrane-
XX spanning helices grouped into three transmembrane domains. PXE is
XX inherited as an autosomal recessive phenotype or appears as a sporadic
XX phenotype. PXE is a heritable disorder characterised by mineralisation of
XX elastic fibers in skin, arteries and the retina, that result in dermal
XX lesions with associated laxity and loss of elasticity, arterial
XX insufficiency, cardiovascular disease and retinal haemorrhages leading to
XX macular degeneration. The method is useful for screening a population of
XX individuals in order to identify individuals with one or more PXE
XX associated MRP6 alleles who are then provided with appropriate genetic
XX counselling in view of the PXE status. The methods are useful for
XX identifying homozygotes, compound heterozygotes or carriers and thus are
XX useful in the area of genetic testing, carrier detection and prenatal
XX diagnosis. The present sequence is human ATP-binding cassette (ABC)
XX transporter, ABCC6 (MRP6) mutant cDNA. This mutant cDNA results in an
XX amino acid change from Arg to Trp at position 1314 of MRP6 protein.
XX Note: The present sequence is not shown in the specification but is
XX derived from human ATP-binding cassette transporter ABCC6 (MRP6) cDNA
XX [SEQ ID NO: 2] shown in page 130-137 of the specification (AAD16231).
XX
XX Sequence 4512 BP; 835 A; 1379 C; 1354 G; 944 T; 0 other;
XX
XX Query Match 99.8%; Score 4497.8; DB 22; Length 4512;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 4502; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```


|||||
Db 2161 TGGCTGGAGAGTACTAGAGCCTGTGCCCTGCAGCCAGATGGACAGCTTCCCTGAG 2220
QY 2221 GGAATCCACACTTCAATTTGGGGAGCAGGGAATGTAATCTCTCCGGAGGCCAGAACGCGG 2280
Db 2221 GGAATCCACACTTCAATTTGGGGAGCAGGGAATGTAATCTCTCCGGAGGCCAGAACGCGG 2280
QY 2281 CTGAGCCTGGCCGGGCTGTATACAGAAAGSCAGCTGTGTACCTGTGGATGACCCCTG 2340
Db 2281 CTGAGCCTGGCCGGGCTGTATACAGAAAGSCAGCTGTGTACCTGTGGATGACCCCTG 2340
QY 2341 GCGGCCCTGTGATGCCACGTTGGCCAGCATGTCTTCAACCAAGGTCAATTTGGGCCCTGGTGGG 2400
Db 2341 GCGGCCCTGTGATGCCACGTTGGCCAGCATGTCTTCAACCAAGGTCAATTTGGGCCCTGGTGGG 2400
QY 2401 CTACTCAGGGAACACACAGGATTTCTGTGACGACGACATCCACATTCCTGCCCCAGGCT 2460
Db 2401 CTACTCAGGGAACACACAGGATTTCTGTGACGACGACATCCACATTCCTGCCCCAGGCT 2460
QY 2461 GATTGGATCATAGTGTGGCAATGGGCCATCGCAGAGATGGTTCTTACCAGAGCTT 2520
Db 2461 GATTGGATCATAGTGTGGCAATGGGCCATCGCAGAGATGGTTCTTACCAGAGAGCTT 2520
QY 2521 CTGCAGAGGAAGGGGCCCTGTGTCTTCTGGATCAAGCCACAGACAGCCAGAGATAGA 2580
Db 2521 CTGCAGAGGAAGGGGCCCTGTGTCTTCTGGATCAAGCCACAGACAGCCAGAGATAGA 2580
QY 2581 GGAGAAGGAACACAGAACCTTGGGACAGACCAAGGACCCAGAGCAGCTCTGCAAGC 2640
Db 2581 GGAGAAGGAACACAGAACCTTGGGACAGACCAAGGACCCAGAGCAGCTCTGCAAGC 2640
QY 2641 AGGAGCCCGAGCTTAGACGCGAGAGGTCCATCAAGTCAGTCCCTGAGAGGACCCGTACC 2700
Db 2641 AGGAGCCCGAGCTTAGACGCGAGAGGTCCATCAAGTCAGTCCCTGAGAGGACCCGTACC 2700
QY 2701 ACTTCAGAACCCACAGACAGAGTTCTCTTGATGACCTCAGAGGAGGATGGCCAGCA 2760
Db 2701 ACTTCAGAACCCACAGACAGAGTTCTCTTGATGACCTCAGAGGAGGATGGCCAGCA 2760
QY 2761 GGAAGACAGCATCCATAGCGCAGGGTGAAGGCCACAGTCACCTGGCCCTACCTCGCT 2820
Db 2761 GGAAGACAGCATCCATAGCGCAGGGTGAAGGCCACAGTCACCTGGCCCTACCTCGCT 2820
QY 2821 GCGGTGGGACCCCTCTGCTCCCTAGCGACTCTTCTCTCTCTGCTGCGCAGCAAGTGCC 2880
Db 2821 GCGGTGGGACCCCTCTGCTCCCTAGCGACTCTTCTCTCTCTGCTGCGCAGCAAGTGCC 2880
QY 2881 TCCTTCTGCCGGGGCTACTGGCTGAGCCTGTGGCGGAGCAGACCTGAGCTGGCTGCTC 2940
Db 2881 TCCTTCTGCCGGGGCTACTGGCTGAGCCTGTGGCGGAGCAGACCTGAGCTGGCTGCTC 2940
QY 2941 CAGACGAGGACCCCTGGTGGGGATCTTGGGGTCTCGGGCTCTCGGCTGTCTCCAGGCCATT 3000
Db 2941 CAGACGAGGACCCCTGGTGGGGATCTTGGGGTCTCGGGCTCTCGGCTGTCTCCAGGCCATT 3000
QY 3001 GGGCTGTTGGCTCCATGGCTGGGTGCTCTAGGTGGGGCCGGCATCCAGGTTGCTC 3060
Db 3001 GGGCTGTTGGCTCCATGGCTGGGTGCTCTAGGTGGGGCCGGCATCCAGGTTGCTC 3060
QY 3061 TTCCAGAGGCTCCTGTGGGATGGTGGCATCTCCCATCAGCTTCTTTGAGCGGACACCC 3120
Db 3061 TTCCAGAGGCTCCTGTGGGATGGTGGCATCTCCCATCAGCTTCTTTGAGCGGACACCC 3120
QY 3121 ATTGGTCACTGTCTAAACGCTTCTCCAGGAGACAGACAGGTTGACGTGGACATTCGA 3180
Db 3121 ATTGGTCACTGTCTAAACGCTTCTCCAGGAGACAGACAGGTTGACGTGGACATTCGA 3180
QY 3181 GACAACTCCGGTCCCTGTGATGACGCTTTGGACTCCTTGAGCTCAGCTGTGGTG 3240
Db 3181 GACAACTCCGGTCCCTGTGATGACGCTTTGGACTCCTTGAGCTCAGCTGTGGTG 3240
QY 3241 GCAGTGGCTACCCCACTGGCCACTGTGGCCATCTCTGCCACTGTTCTCTCTACGCTGGG 3300
|||||

Db 3241 GCAGTGGCTACCCACTGGCCACTGTGGCCATCTGCCACTGTTTCTCTCTACGCTGGG 3300
QY 3301 TTTCCAGACCTGTATGTGTAGTTCATGCCAGCTCAGACGCTTGGAGTCAGCCAGCTAC 3360
Db 3301 TTTCCAGACCTGTATGTGTAGTTCATGCCAGCTCAGACGCTTGGAGTCAGCCAGCTAC 3360
QY 3361 TCGTCTGTCTGCTCCACATGGCTGAGAGTTCCAGGGCAGCAGCTGTGTCGGGGATTTC 3420
Db 3361 TCGTCTGTCTGCTCCACATGGCTGAGAGTTCCAGGGCAGCAGCTGTGTCGGGGATTTC 3420
QY 3421 CGAACCCAGGCCCCCTTTGTGGCTCAGAACAAATGTCGCGTAGATGAAAGCCAGAGATC 3480
Db 3421 CGAACCCAGGCCCCCTTTGTGGCTCAGAACAAATGTCGCGTAGATGAAAGCCAGAGATC 3480
QY 3481 AGTTTCCCGGACTGGTGGCTGACAGGTGGCTTGGGCCAAATGTGGAGTCTCTGGGGAAT 3540
Db 3481 AGTTTCCCGGACTGGTGGCTGACAGGTGGCTTGGGCCAAATGTGGAGTCTCTGGGGAAT 3540
QY 3541 GGCCTGGTGTGGACGCCGCCACAGTGTGCTGTGCTGACGAAAGCCACCTCAGTGTGCG 3600
Db 3541 GGCCTGGTGTGGACGCCGCCACAGTGTGCTGTGCTGACGAAAGCCACCTCAGTGTGCG 3600
QY 3601 CTCGTGGGCTTCTCTGCTCTGCTGCCCTCCAGGTGACAGGTGGCTTGGGCCAAATGTGGAGTCTCTGGGGAAT 3660
Db 3601 CTCGTGGGCTTCTCTGCTCTGCTGCCCTCCAGGTGACAGGTGGCTTGGGCCAAATGTGGAGTCTCTGGGGAAT 3660
QY 3661 CGCAACTGGACAGACCTTAGAACACAGCATCTGTGCTGAGTGGAGCGGATGAGGACTATGCC 3720
Db 3661 CGCAACTGGACAGACCTTAGAACACAGCATCTGTGCTGAGTGGAGCGGATGAGGACTATGCC 3720
QY 3721 TGGAGCCCCAAGGAGGCTCCCTGGAGGCTGCCACATGTGACGCTCAGCCCCCTGGCCT 3780
Db 3721 TGGAGCCCCAAGGAGGCTCCCTGGAGGCTGCCACATGTGACGCTCAGCCCCCTGGCCT 3780
QY 3781 CAGGGCGGACAGATCGAGTTCGGGACTTGGGCTTAAGATCCGACCTCAGCTCCGCGTG 3840
Db 3781 CAGGGCGGACAGATCGAGTTCGGGACTTGGGCTTAAGATCCGACCTCAGCTCCGCGTG 3840
QY 3841 GCTGTGACGGCGTGTCTTCAAGATCCACGAGAGAGAGGTGGGATCGTTGGCAGG 3900
Db 3841 GCTGTGACGGCGTGTCTTCAAGATCCACGAGAGAGAGGTGGGATCGTTGGCAGG 3900
QY 3901 ACCGGGACAGGAAGTCTCCCTGGCCAGTGGCTGCTGCGCTCCAGGAGCAGCTGAG 3960
Db 3901 ACCGGGACAGGAAGTCTCCCTGGCCAGTGGCTGCTGCGCTCCAGGAGCAGCTGAG 3960
QY 3961 GGTGGGATCTGGATCGACGGGTCCCATTTGCCACGTGGGGCTCAGACACTGCGCTCC 4020
Db 3961 GGTGGGATCTGGATCGACGGGTCCCATTTGCCACGTGGGGCTCAGACACTGCGCTCC 4020
QY 4021 AGGATCAGCATCATCCCCAGGACCCCATCTGTTCCCTGGCTCTCTCGGGATGAACCTC 4080
Db 4021 AGGATCAGCATCATCCCCAGGACCCCATCTGTTCCCTGGCTCTCTCGGGATGAACCTC 4080
QY 4081 GACCTGTGACGAGCAGCTCGGAGAGGCTATCTGGGAGCCCTTGAGACGCTGAGCTC 4140
Db 4081 GACCTGTGACGAGCAGCTCGGAGAGGCTATCTGGGAGCCCTTGAGACGCTGAGCTC 4140
QY 4141 AAAGCCTTGGTGGCAGCCTGCCCGGCGAGCTGACGTACAGTGTGCTGACCGAGCGAG 4200
Db 4141 AAAGCCTTGGTGGCAGCCTGCCCGGCGAGCTGACGTACAGTGTGCTGACCGAGCGAG 4200
QY 4201 GACCTGAGCTGGGCCAGAACAGCTCTGTGTCTGGCACGTGCCCTTCTCCGGAAGACC 4260
Db 4201 GACCTGAGCTGGGCCAGAACAGCTCTGTGTCTGGCACGTGCCCTTCTCCGGAAGACC 4260
QY 4261 CAGATCCTCATCTCGGAGGCTGTTTGGCACAGTGCATGTGCTGCTCATTTGCCACCGCTG 4320
Db 4261 CAGATCCTCATCTCGGAGGCTGTTTGGCACAGTGCATGTGCTGCTCATTTGCCACCGCTG 4320
QY 4321 CAGGCCATGCTCGGGAGCTGTTTGGCACAGTGCATGTGCTGCTCATTTGCCACCGCTG 4380
Db 4321 CAGGCCATGCTCGGGAGCTGTTTGGCACAGTGCATGTGCTGCTCATTTGCCACCGCTG 4380

QY 4381 CCTCCGTGATGGACTGCCCCGGGTCTTGCTCATGGACAAGGGCAGGTGGCAGAGAGC 4440
 DB 4381 CGCTCCGTGATGGACTGCCCCGGGTCTTGCTCATGGACAAGGGCAGGTGGCAGAGAGC 4440
 QY 4441 GGCAGCCCGGCCAGCTGCTGGCCAGAAAGGCGCTGTTTACAGACTGGCCCGCAGAGTCA 4500
 DB 4441 GGCAGCCCGGCCAGCTGCTGGCCAGAAAGGCGCTGTTTACAGACTGGCCCGCAGAGTCA 4500
 QY 4501 GGCCTGGTC 4509
 DB 4501 GGCCTGGTC 4509

RESULT 10
 AAD16264
 ID AAD16264 standard; cDNA; 4512 BP.
 XX
 AC AAD16264;
 XX
 DT 19-NOV-2001 (first entry)
 XX
 DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cDNA #9.
 XX
 KW Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
 KW Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;
 KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
 KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
 KW mutant; mutein; ss.
 XX
 OS Homo sapiens.
 OS
 XX Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..4512
 FT /tag= a
 FT /product= "Human ABCC6 (MRP6) mutant protein"
 FT mutation replace (3961, G)
 FT /tag= b
 XX
 XX W0200162977-A2.
 XX
 XX 30-AUG-2001.
 XX
 XX 23-FEB-2001; 2001WO-US05741.
 XX
 XX 23-FEB-2000; 2000US-0184269.
 XX
 XX (PXEI-) PXE INT INC.
 XX (UYHA-) UNIV HAWAII.
 XX
 XX Boyd CD, Csiszar K, Lesaux O, Urban Z, Terry S;
 XX
 XX WPI; 2001-536645/59.
 XX P-PSDB; AAE09371.
 XX
 XX Screening presence of pseudoxanthoma elasticum mutation useful for
 XX identifying homozygotes, compound heterozygotes or carriers involves
 XX determining presence of mutation in MRP6 (ABCC6) nucleic acid -
 XX
 XX Example 2; Page -; 163pp; English.
 XX
 XX The invention relates to methods and compositions for diagnosing and
 XX treating pseudoxanthoma elasticum (PXE) and PXE associated physiological
 XX dysfunctions. The invention is useful for screening for the presence of
 XX a PXE mutation. Mutations associated with PXE maps to the ATP-binding
 XX cassette transporter ABCC6 (MRP6-Multidrug Resistance associated
 XX protein-6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165
 XX kDa protein located in the plasma membrane containing 17 membrane-
 XX spanning helices grouped into three transmembrane domains. PXE is
 XX inherited as an autosomal recessive phenotype or appears as a sporadic
 XX phenotype. PXE is a heritable disorder characterised by mineralisation of
 XX elastic fibers in skin, arteries and the retina, that result in dermal

CC lesions with associated laxity and loss of elasticity, arterial
 CC insufficiency, cardiovascular disease and retinal haemorrhages leading to
 CC macular degeneration. The method is useful for screening a population of
 CC individuals in order to identify individuals with one or more PXE
 CC associated MRP6 alleles who are then provided with appropriate genetic
 CC counselling in view of the PXE status. The methods are useful for
 CC identifying homozygotes, compound heterozygotes or carriers and thus are
 CC useful in the area of genetic testing, carrier detection and prenatal
 CC diagnosis. The present sequence is human ATP-binding cassette (ABC)
 CC transporter, ABCC6 (MRP6) mutant cDNA. This mutant cDNA results in an
 CC amino acid change from Gly to Ser at position 1321 of MRP6 protein, but
 CC it is incorrectly referred as Gly to Ile in page 49 of the specification.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from human ATP-binding cassette transporter ABCC6 (MRP6) cDNA
 CC [SED ID NO: 2] shown in page 130-137 of the specification (AAD16231).
 XX
 SQ Sequence 4512 BP; 836 A; 1380 C; 1353 G; 943 T; 0 other;

Query Match 99.8%; Score 4497.8; DB 22; Length 4512;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 4502; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGGCGCGCGCTGCTGAGCCCTCGCGGGCAGGGGTCTGGAACACAGACAGAGCCCTGAA 60
 DB 1 ATGGCGCGCGCTGCTGAGCCCTCGCGGGCAGGGGTCTGGAACACAGACAGAGCCCTGAA 60
 QY 61 CCTGCGCGCCACAGCCCTGCTGAGCCCTGCTGCTTCTGAGAACACAGAGGGGTCTGGGTACCC 120
 DB 61 CCTGCGCGCCACAGCCCTGCTGAGCCCTGCTGCTTCTGAGAACACAGAGGGGTCTGGGTACCC 120
 QY 121 CCATGTACTCTGCGGTCTTGGTCCCATCTACTCTCTCTCATCCACCATCCATGGCCGG 180
 DB 121 CCATGTACTCTGCGGTCTTGGTCCCATCTACTCTCTCATCCACCATCCATGGCCGG 180
 QY 181 GGCTACCTCCGGATGTCCTCCACTCTTCAAGCAAGATGGTGTGATTCGCCCTCATATA 240
 DB 181 GGCTACCTGTGGATGTCCTCCACTCTTCAAGCAAGATGGTGTGATTCGCCCTCATATA 240
 QY 241 GTCTGTGTACCTCCAGCGTGGTGTGCTCTTTGGAATATCCACAGGGAAGCCCTGAG 300
 DB 241 GTCTGTGTACCTCCAGCGTGGTGTGCTCTTTGGAATATCCACAGGGAAGCCCTGAG 300
 QY 301 GCGCCAGAAATTCCTCATCTACTGTGTGGCTCACCACAGATGAGTTCGCGAGTGTTC 360
 DB 301 GCGCCAGAAATTCCTCATCTACTGTGTGGCTCACCACAGATGAGTTCGCGAGTGTTC 360
 QY 361 CTGATTCACCGAG 420
 DB 361 CTGATTCACCGAG 420
 QY 421 CTTCTCTGCTTTGCTTGGCAGCTACCAAGCTGCCAGAGCCCTCCGAGAGCGGCTTC 480
 DB 421 CTTCTCTGCTTTGCTTGGCAGCTACCAAGCTGCCAGAGCCCTCCGAGAGCGGCTTC 480
 QY 481 CAGAGCGACCTGTCCGCCACCTGTCCACTACTATGCTGTCTGTGGTGGGACAG 540
 DB 481 CAGAGCGACCTGTCCGCCACCTGTCCACTACTATGCTGTCTGTGGTGGGACAG 540
 QY 541 TTTGTGCTGCTGCTGCTGCGGATCAACCCCTCTTCCCTGAAGACCCCGAGAGTCT 600
 DB 541 TTTGTGCTGCTGCTGCTGCGGATCAACCCCTCTTCCCTGAAGACCCCGAGAGTCT 600
 QY 601 AACCCCTGTCAGAGACTGGGCGAGCTTCCCTCCAAAGCCAGCTTCGTTGGTGTCT 660
 DB 601 AACCCCTGTCAGAGACTGGGCGAGCTTCCCTCCAAAGCCAGCTTCGTTGGTGTCT 660
 QY 661 GGCCTGGTCTGGAGGGGATACAGAGGCGCACTGAGACCAAAAGACCTCTGTTGGTGGG 720
 DB 661 GGCCTGGTCTGGAGGGGATACAGAGGCGCACTGAGACCAAAAGACCTCTGTTGGTGGG 720
 QY 721 AGAGAAACTCTCAGAAGAACTTGTTCCTCCGCTTGAAGAGAGTGGATGAGAAACCG 780
 DB 721 AGAGAAACTCTCAGAAGAACTTGTTCCTCCGCTTGAAGAGAGTGGATGAGAAACCG 780

QY 781 AGTGCAGCCGGAGGCACACAGGCAATAGCATTTAAAGGAAAGCGGCAGTGGCATG 840
Db 781 AGTGCAGCCCGAGGCACACAGGCAATAGCATTTAAAGGAAAGCGGCAGTGGCATG 840
QY 841 AAGGCTCCAGAGACCGAGCCCTTCCCTACGGCAAGAGGAGCCAGTGGCGCCCACTGCTG 900
Db 841 AAGGCTCCAGAGACCGAGCCCTTCCCTACGGCAAGAGGAGCCAGTGGCGCCCACTGCTG 900
QY 901 AAGGCCATCGGAGAGTGTTCATTTACCTTCTCTCTGGGAGCCCTCAGGCTCATCATC 960
Db 901 AAGGCCATCGGAGAGTGTTCATTTACCTTCTCTCTGGGAGCCCTCAGGCTCATCATC 960
QY 961 AGTGATGTCCTCAGGTTCACTGTCCCAAGCTGCTCAGCCCTTTTCTCGGAGTTATGGT 1020
Db 961 AGTGATGTCCTCAGGTTCACTGTCCCAAGCTGCTCAGCCCTTTTCTCGGAGTTATGGT 1020
QY 1021 GATCCCAAGCCTCCAGCCTGGAAGGGCTACCTCTCTCGCCGTGCTGATGTTCCTCTCAGCC 1080
Db 1021 GATCCCAAGCCTCCAGCCTGGAAGGGCTACCTCTCTCGCCGTGCTGATGTTCCTCTCAGCC 1080
QY 1081 TGGCTGCAAAAGCGTGTGTGAGCAGCAGAACATGTACAGGCTCAAGGTGCTGCAGATGAGG 1140
Db 1081 TGGCTGCAAAAGCGTGTGTGAGCAGCAGAACATGTACAGGCTCAAGGTGCTGCAGATGAGG 1140
QY 1141 TTGGGTTCGCCCATCACTGGCCCTGGGTACAGAAAGTCTGCTCTGTCAGCGGCTCC 1200
Db 1141 TTGGGTTCGCCCATCACTGGCCCTGGGTACAGAAAGTCTGCTCTGTCAGCGGCTCC 1200
QY 1201 AGAAAGCCAGTGGCGGTGTGTGATGTGCTCAATCTGCTGTCGCTGGAGCTGCAGCGGCTG 1260
Db 1201 AGAAAGCCAGTGGCGGTGTGTGATGTGCTCAATCTGCTGTCGCTGGAGCTGCAGCGGCTG 1260
QY 1261 ACCGAGAGCCTCTACCTCAACGGGCTGTGGTGTGCTCTGCTGTGGATGCTGCTGCTG 1320
Db 1261 ACCGAGAGCCTCTACCTCAACGGGCTGTGGTGTGCTCTGCTGTGGATGCTGCTGCTG 1320
QY 1321 TTGCTGTATCTGTGGAGCTCTGGGCGCTCCGCGCTCTGCTGCTGCTGCTGCTGCTGCTG 1380
Db 1321 TTGCTGTATCTGTGGAGCTCTGGGCGCTCCGCGCTCTGCTGCTGCTGCTGCTGCTGCTG 1380
QY 1381 AGCCTCTCTCTGATTTCTTCTATCTCCAAAGAAAGAACCAACCATCAGGAGAGCAA 1440
Db 1381 AGCCTCTCTCTGATTTCTTCTATCTCCAAAGAAAGAACCAACCATCAGGAGAGCAA 1440
QY 1441 ATGAGGAGAAAGACTCACGGGACGGCTCACAGCTCTATCTCAGGAACCTCGAAGACC 1500
Db 1441 ATGAGGAGAAAGACTCACGGGACGGCTCACAGCTCTATCTCAGGAACCTCGAAGACC 1500
QY 1501 ATCAAGTTCCATGGCTGGAGGAGCCTTTCTGACAGAGCTCTGGGATCCGAGGCGCAG 1560
Db 1501 ATCAAGTTCCATGGCTGGAGGAGCCTTTCTGACAGAGCTCTGGGATCCGAGGCGCAG 1560
QY 1561 GAGCTGGGCGCCTTGGGACCTCCGGCCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
Db 1561 GAGCTGGGCGCCTTGGGACCTCCGGCCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
QY 1621 GTGCTACATTTCTGCTGCACTGGTGGTGTTCGTGTCCACACTCTGCTGCTGCTGCTGCTGCTG 1680
Db 1621 GTGCTACATTTCTGCTGCACTGGTGGTGTTCGTGTCCACACTCTGCTGCTGCTGCTGCTGCTG 1680
QY 1681 GCTATGAATCCAGAAAGCCTTTGTGACTCTCAGAGTCTCAGAGTCTCAGAGTCTCAGAGTCT 1740
Db 1681 GCTATGAATCCAGAAAGCCTTTGTGACTCTCAGAGTCTCAGAGTCTCAGAGTCTCAGAGTCT 1740
QY 1741 CAGGCTTTCTGCTGCT 1800
Db 1741 CAGGCTTTCTGCTGCT 1800
QY 1801 CTGGTCACTTCTCTGCTGGAAGAGTTGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
Db 1801 CTGGTCACTTCTCTGCTGGAAGAGTTGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860

QY 1861 GGAAGCGCTGCGGGAAGGATTTGCATACCATACACAGTGCCACCTTCCGCTGGTCCCAG 1920
Db 1861 GGAAGCGCTGCGGGAAGGATTTGCATACCATACACAGTGCCACCTTCCGCTGGTCCCAG 1920
QY 1921 GAAAGCCCTCCCTGCTCCACAGAAATAACCTTCACGGTGGCCCGCAGGGCTGTCTGCTGGCT 1980
Db 1921 GAAAGCCCTCCCTGCTCCACAGAAATAACCTTCACGGTGGCCCGCAGGGCTGTCTGCTGGCT 1980
QY 1981 GTTGTGCTCCAGTGGGGCAGGGAAGTCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
Db 1981 GTTGTGCTCCAGTGGGGCAGGGAAGTCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
QY 2041 TCAAGGTGGAGGGTTCGTGAGCATCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
Db 2041 TCAAGGTGGAGGGTTCGTGAGCATCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
QY 2101 TGGGTGCAAGAACACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
Db 2101 TGGGTGCAAGAACACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
QY 2161 TGGCTGGAGAGAGTACTAGAAAGCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
Db 2161 TGGCTGGAGAGAGTACTAGAAAGCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
QY 2221 GGAATCCACACTTCAATTTGGGGAGCAGGCATGAATCTCTCCGGAGGCCAGAGCAGCGG 2280
Db 2221 GGAATCCACACTTCAATTTGGGGAGCAGGCATGAATCTCTCCGGAGGCCAGAGCAGCGG 2280
QY 2281 CTGAGCCTTGGCCCGGCTGTATACAAAGGAGCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 2340
Db 2281 CTGAGCCTTGGCCCGGCTGTATACAAAGGAGCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 2340
QY 2341 CGGGCCTTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
Db 2341 CGGGCCTTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
QY 2401 CTACTCCAGGAAACAAACAGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
Db 2401 CTACTCCAGGAAACAAACAGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
QY 2461 GATTGGATCATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2520
Db 2461 GATTGGATCATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2520
QY 2521 CTGAGAGAGAGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
Db 2521 CTGAGAGAGAGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
QY 2581 GGAGAAGGAGAAACAGAACCTTGGGACCAAGCAGCAAGGAGGCCAGAGGACCTCTGCAGGC 2640
Db 2581 GGAGAAGGAGAAACAGAACCTTGGGACCAAGCAGCAAGGAGGCCAGAGGACCTCTGCAGGC 2640
QY 2641 AGGAGGCCGCGAGCTTAGACGGAGAGGTCATCAAGTCAAGTCCCTGAGAAAGACCTTACC 2700
Db 2641 AGGAGGCCGCGAGCTTAGACGGAGAGGTCATCAAGTCAAGTCCCTGAGAAAGACCTTACC 2700
QY 2701 ACTTCAGAAAGCCCGAGAGAGGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760
Db 2701 ACTTCAGAAAGCCCGAGAGAGGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760
QY 2761 GGAAGGACAGCATCCATACGGCAGGGTGAAGGCCACAGTGCACCTGCGCTTACCTGCGCT 2820
Db 2761 GGAAGGACAGCATCCATACGGCAGGGTGAAGGCCACAGTGCACCTGCGCTTACCTGCGCT 2820
QY 2821 GCCGTGGCAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
Db 2821 GCCGTGGCAGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
QY 2881 TCCCTTCCCGGGGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940
Db 2881 TCCCTTCCCGGGGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940
QY 2941 CAGACGACAGCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3000

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Db 2941 CAGACGAGCAGCCCTCGGTGGCGGATCTTCGGGCTCCTCGGCTGTCTCCAAGCCATT 3000
QY 3001 GGGCTGTTTGGCTCCATGGCTCGGTGTCTCTAGGTGGGCGCCGGGCATCCAGGTTGCTC 3060
Db 3001 GGGCTGTTTGGCTCCATGGCTCGGTGTCTCTAGGTGGGCGCCGGGCATCCAGGTTGCTC 3060
QY 3061 TTCAGAGGCTCCTGTGGATGTGGTGGATCTCCATCAGCTTCTTTAGGCGGACACCC 3120
Db 3061 TTCAGAGGCTCCTGTGGATGTGGTGGATCTCCATCAGCTTCTTTAGGCGGACACCC 3120
QY 3121 ATTGTGTACCTCTCTAAACCGCTTCTCAAGGAGACAGACACGGTTGACGTGGACATTCCA 3180
Db 3121 ATTGTGTACCTCTCTAAACCGCTTCTCAAGGAGACAGACACGGTTGACGTGGACATTCCA 3180
QY 3181 GACAACTCCGGTCCCTGCTGATGATGACGCTTTGGACTCCTGGAGTCAAGCTGTGGTG 3240
Db 3181 GACAACTCCGGTCCCTGCTGATGATGACGCTTTGGACTCCTGGAGTCAAGCTGTGGTG 3240
QY 3241 GCAGTGGCTACCCACTGGCCACTGTGGCCATCTCGCCACTGTTTCTCTACGCTGGG 3300
Db 3241 GCAGTGGCTACCCACTGGCCACTGTGGCCATCTCGCCACTGTTTCTCTACGCTGGG 3300
QY 3301 TTTACAGAGCTGTATGTGTTAGCTCATGCCAGCTGAGACGCTTGGAGTCAAGCTAC 3360
Db 3301 TTTACAGAGCTGTATGTGTTAGCTCATGCCAGCTGAGACGCTTGGAGTCAAGCTAC 3360
QY 3361 TCGTGTGTGCTGCCACATGGCTGAGAGTTCAGAGGCGAGCACAGTGGTCCGGGCAATC 3420
Db 3361 TCGTGTGTGCTGCCACATGGCTGAGAGTTCAGAGGCGAGCACAGTGGTCCGGGCAATC 3420
QY 3421 CGAACCCAGGCCCCCTTTGTGGCTCAGAACATGCTCGGCTAGATGAAGCCAGAGGATC 3480
Db 3421 CGAACCCAGGCCCCCTTTGTGGCTCAGAACATGCTCGGCTAGATGAAGCCAGAGGATC 3480
QY 3481 AGTTTCCCGCGACTGGTGGCTCAGAGTGGCTTGGCGCAATGTGGAGTCTCGTGGGAAT 3540
Db 3481 AGTTTCCCGCGACTGGTGGCTCAGAGTGGCTTGGCGCAATGTGGAGTCTCGTGGGAAT 3540
QY 3541 GGCCTGGTGTTCAGCGCCGACAGTGTGCTGTGAGCAAAAGCCACCTCAGTGTGCTG 3600
Db 3541 GGCCTGGTGTTCAGCGTCCAGCTGTGCTGTGAGCAAAAGCCACCTCAGTGTGCTG 3600
QY 3601 CTCGTGGGCTTCTGTCTCTGCTGCCCTCCAGGTGACCCACACACTGCAGTGGTGT 3660
Db 3601 CTCGTGGGCTTCTGTCTCTGCTGCCCTCCAGGTGACCCACACACTGCAGTGGTGT 3660
QY 3661 CGCAACTGGACAGACTAGAGAACAGCATCGTGTGAGTGGAGCGGATGAGGACTATGCC 3720
Db 3661 CGCAACTGGACAGACTAGAGAACAGCATCGTGTGAGTGGAGCGGATGAGGACTATGCC 3720
QY 3721 TGGAGCCCAAGGAGGCTCCCTGGAGGTGCCACATGTGACGCTCAGCCCCCTGGGCT 3780
Db 3721 TGGAGCCCAAGGAGGCTCCCTGGAGGTGCCACATGTGACGCTCAGCCCCCTGGGCT 3780
QY 3781 CAGGCGGGCAGACTGAGTCCGGGACTTGGGCTTAAGTGGCGGCTCAGCTCCGCGTG 3840
Db 3781 CAGGCGGGCAGACTGAGTCCGGGACTTGGGCTTAAGTGGCGGCTCAGCTCCGCGTG 3840
QY 3841 GCTGTGACGGGCGTCTCCTCAAGATCCACGAGGAGAGAGTGGGATCGTTGGCAGG 3900
Db 3841 GCTGTGACGGGCGTCTCCTCAAGATCCACGAGGAGAGAGTGGGATCGTTGGCAGG 3900
QY 3901 ACCGGGCGAGGAAAGTCTCCTCGCCAGTGGGCTGTGCGGCTCCAGGAGCAGCTGAG 3960
Db 3901 ACCGGGCGAGGAAAGTCTCCTCGCCAGTGGGCTGTGCGGCTCCAGGAGCAGCTGAG 3960
QY 3961 GGTGGATCTGGATCGAGGGGTCCCATTTGCCAGCTGGGGCTGCACACACTGCGCTCC 4020
Db 3961 AGTGGGATCTGGATCGAGGGGTCCCATTTGCCAGCTGGGGCTGCACACACTGCGCTCC 4020
QY 4021 AGGATCAGCATCATCCCGCAGGACCCCATCTGTTCCCTGCTCTCGGGATGAACCTC 4080
|||||

Db 4021 AGGATCAGCATCATCCCGCAGGACCCCATCTGTTCCCTGGCTCTCTCGGATGAACCTC 4080
QY 4081 GACCTCTGCAGGAGCACTCGGACAGGCTATCTGGGCAAGCCCTTGGAGAGCGGTGACGTC 4140
Db 4081 GACCTCTGCAGGAGCACTCGGACAGGCTATCTGGGCAAGCCCTTGGAGAGCGGTGACGTC 4140
QY 4141 AAGCCCTTGGTGGCCAGCCTGCGCCAGCTGCAGTACAGTGTGCTGACCCAGGCGAG 4200
Db 4141 AAGCCCTTGGTGGCCAGCCTGCGCCAGCTGCAGTACAGTGTGCTGACCCAGGCGAG 4200
QY 4201 GACCTGAGCGTGGCCAGCAAAACAGCTCCTGTGTGGCAGCTGCCCTTCTCCGGAAGACC 4260
Db 4201 GACCTGAGCGTGGCCAGCAAAACAGCTCCTGTGTGGCAGCTGCCCTTCTCCGGAAGACC 4260
QY 4261 CAGATCCTCATCTCTGACGAGGCTACTGTGCGGTGGACCCCTGGCAGCGAGTGCAGATG 4320
Db 4261 CAGATCCTCATCTCTGACGAGGCTACTGTGCGGTGGACCCCTGGCAGCGAGTGCAGATG 4320
QY 4321 CAGGCCATGCTCGGAGCTGGTTTGCACAGTGCAGTGTGCTGCCATTTGCCACCGGCTG 4380
Db 4321 CAGGCCATGCTCGGAGCTGGTTTGCACAGTGCAGTGTGCTGCCATTTGCCACCGGCTG 4380
QY 4381 CGCTCGTGTGATGACTGTGCTCGGCTTCTGTCATGACAAAGGGCGAGTGGCAGAGAGC 4440
Db 4381 CGCTCGTGTGATGACTGTGCTCGGCTTCTGTCATGACAAAGGGCGAGTGGCAGAGAGC 4440
QY 4441 GGCAGCCCGGCCAGCTGTGCTGGCCCAAGAGGGCTGTTTACAGACTGGCCCAAGAGTCA 4500
Db 4441 GGCAGCCCGGCCAGCTGTGCTGGCCCAAGAGGGCTGTTTACAGACTGGCCCAAGAGTCA 4500
QY 4501 GGCCTGGTC 4509
Db 4501 GGCCTGGTC 4509

RESULT 11
AAD16259
ID AAD16259 standard; cdna; 4511 BP.
XX AC AAD16259;
XX DT 19-NOV-2001 (first entry)
XX DE Human ATP-binding cassette transporter ABCC6 (MRP6) mutant cdna #4.
XX KW Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;
ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
mutant; mutein; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200162977-A2.
XX PD 30-AUG-2001.
XX PF 23-FEB-2001; 2001WO-US05741.
XX PR 23-FEB-2000; 2000US-0184269.
XX PA (PXEI-) PXE INT INC.
XX PA (UYHA-) UNIV HAWAII.
XX PI Boyd CD, Csiszar K, Lesaux O, Urban Z, Terry S;
XX DR WPI; 2001-536645/59.
XX PT Screening presence of Pseudoxanthoma elasticum mutation useful for
identifying homozygotes, compound heterozygotes or carriers involves
determining presence of mutation in MRP6 (ABCC6) nucleic acid -
XX

Example 2; Page -: 163pp; English.

The invention relates to methods and compositions for diagnosing and treating pseudoxanthoma elasticum (PXE) and PXE associated physiological dysfunctions. The invention is useful for screening for the presence of a PXE mutation. Mutations associated with PXE maps to the ATP-binding cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa protein located in the plasma membrane containing 17 membrane-spanning helices grouped into three transmembrane domains. PXE is inherited as an autosomal recessive phenotype or appears as a sporadic phenotype. PXE is a heritable disorder characterised by mineralisation of elastic fibers in skin, arteries and the retina, that result in dermal lesions with associated laxity and loss of elasticity, arterial insufficiency, cardiovascular disease and retinal haemorrhages leading to macular degeneration. The method is useful for screening a population of individuals in order to identify individuals with one or more PXE associated MRP6 alleles who are then provided with appropriate genetic counselling in view of the PXE status. The methods are useful for identifying homozygotes, compound heterozygotes or carriers and thus are useful in the area of genetic testing, carrier detection and prenatal diagnosis. The present sequence is human ATP-binding cassette (ABC) transporter, ABCC6 (MRP6) mutant cDNA. This mutant cDNA is obtained by the deletion of base T at position 3775 of wild-type MRP6 cDNA. Note: The present sequence is not shown in the specification but is derived from human ATP-binding cassette transporter ABCC6 (MRP6) cDNA [SED ID No: 2] shown in page 130-137 of the specification (A016231).

Sequence 4511 BP; 835 A; 1380 C; 1354 G; 942 T; 0 other:

Query Match 99.5%; Score 4487.4; DB 22; Length 4511;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4502; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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QY 1 ATGCGCGCGCTGCTGAGCCCTGCGGGGCGAGGGGCTGGAACACAGACAGAGCCCTGAA 60
DB 1 ATGCGCGCGCTGCTGAGCCCTGCGGGGCGAGGGGCTGGAACACAGACAGAGCCCTGAA 60

QY 61 CCGTGGCCACACAGCTGCTGAGCCCTGCTGCTGAGAACAGCAGGGGCTGGGTACCC 120
DB 61 CCGTGGCCACACAGCTGCTGAGCCCTGCTGCTGAGAACAGCAGGGGCTGGGTACCC 120

QY 121 CCCATGCTACCTCTGGGTCTTGGTCCCTACTACCTCTCTTATCCACACCATGGCGGG 180
DB 121 CCCATGCTACCTCTGGGTCTTGGTCCCTACTACCTCTCTTATCCACACCATGGCGGG 180

QY 181 GGTCTACCTCGGATGCTCCCACTCTTCAAGCAAGATGCTGTGATTCGCCCTCATA 240
DB 181 GGTCTACCTGATGCTCCCACTCTTCAAGCAAGATGCTGTGATTCGCCCTCATA 240

QY 241 GTCTGTGTACCTCCAGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 241 GTCTGTGTACCTCCAGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300

QY 301 GCCCGAGAAATCTCTACTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 301 GCCCGAGAAATCTCTACTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360

QY 361 CTGATTCACACGAGAGAGAAAGGAGTCCAGTCTGAGAGTCTGCTGCTGCTGCTGCTGCT 420
DB 361 CTGATTCACACGAGAGAGAAAGGAGTCCAGTCTGAGAGTCTGCTGCTGCTGCTGCTGCT 420

QY 421 CTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 CTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480

QY 481 CAGAGGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 481 CAGAGGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540

QY 541 TTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 541 TTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
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QY 601 AACCCCTGCTCCAGAGACTGGGGCAGCCCTCCCTCCAAAGCCACGCTTCTGGTGGGTTCT 660
DB 601 AACCCCTGCTCCAGAGACTGGGGCAGCCCTCCCTCCAAAGCCACGCTTCTGGTGGGTTCT 660

QY 661 GGCCTGGTCTGAGGGGATACAGGAGGACCTGAGACCAAGAGACCTCTGGTGGCTGGG 720
DB 661 GGCCTGGTCTGAGGGGATACAGGAGGACCTGAGACCAAGAGACCTCTGGTGGCTGGG 720

QY 721 AGAGAAAATCTCTCAGAGAACTTGTTCCTCCGCTTTGAAAGAGAGTGGATGAGAAACCG 780
DB 721 AGAGAAAATCTCTCAGAGAACTTGTTCCTCCGCTTTGAAAGAGAGTGGATGAGAAACCG 780

QY 781 AGTGAGCCCGGAGGACCAACAGGCAATAGCATTTAAAGGAAAGGCGGCGAGTGCATG 840
DB 781 AGTGAGCCCGGAGGACCAACAGGCAATAGCATTTAAAGGAAAGGCGGCGAGTGCATG 840

QY 841 AAGGCTCCAGAGACGAGCCCTTCTACGGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
DB 841 AAGGCTCCAGAGACGAGCCCTTCTACGGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 900

QY 901 AAGGCTCCAGAGACGAGGCTTCCATTTACCTTCTCTCTGGGAGCCCTCAGCCCTCATC 960
DB 901 AAGGCTCCAGAGACGAGGCTTCCATTTACCTTCTCTCTGGGAGCCCTCAGCCCTCATC 960

QY 961 AGTGATGCTTACAGGCTTCTACCTGCTCCCAAGGCTGCTCAGCCCTTCTCTGAGTTAT 1020
DB 961 AGTGATGCTTACAGGCTTCTACCTGCTCCCAAGGCTGCTCAGCCCTTCTCTGAGTTAT 1020

QY 1021 GATCCCAAGCCCTCCAGCCCTGGAAGGCTACCTCTCTGCGGCTGCTGATGCTTCTCAG 1080
DB 1021 GATCCCAAGCCCTCCAGCCCTGGAAGGCTACCTCTCTGCGGCTGCTGATGCTTCTCAG 1080

QY 1081 TGCTGCAAAAGCTGTTTGGAGCAGAGAACATGTACAGGCTCAAGGCTGCTGCAGATGAG 1140
DB 1081 TGCTGCAAAAGCTGTTTGGAGCAGAGAACATGTACAGGCTCAAGGCTGCTGCAGATGAG 1140

QY 1141 TTGGGTGCGGCATCAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 1141 TTGGGTGCGGCATCAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200

QY 1201 AGAAGGCGCAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
DB 1201 AGAAGGCGCAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260

QY 1261 ACCGAGAGCGTCTTACCTCAACGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
DB 1261 ACCGAGAGCGTCTTACCTCAACGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320

QY 1321 TTGCTCTATCTGCTGCGAGCTCTGCGGGGCTTCTGCGGCTGCTGCGGCTGCTGCTGCT 1380
DB 1321 TTGCTCTATCTGCTGCGAGCTCTGCGGGGCTTCTGCGGCTGCTGCGGCTGCTGCTGCT 1380

QY 1381 AGCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1381 AGCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440

QY 1441 ATGAGGCAAGAGGACTCACGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
DB 1441 ATGAGGCAAGAGGACTCACGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500

QY 1501 ATCAAGTTCCATGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
DB 1501 ATCAAGTTCCATGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560

QY 1561 GAGCTGGGCGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1620
DB 1561 GAGCTGGGCGCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1620

QY 1621 GTGTCTACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
DB 1621 GTGTCTACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
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Db 3940 GCTGTGTCAGGGGCTGCTCTTCAAGATCCACGCGAGGAGAGAGTGGGCATCGTTGGCAGG 3899
QY 3901 ACCGGGCGACGGGAAGTCTCCCTGGCGCAGTGGCTGCTGCGGTCTCCAGGAGGACAGCTGAG 3960
Db 3900 ACCGGGCGACGGGAAGTCTCCCTGGCGCAGTGGCTGCTGCGGTCTCCAGGAGGACAGCTGAG 3959
QY 3961 GGTGGGATCTGGATCGACAGGGGTCCTCCATTTGCCACGTGGGGCTGTCACACACTGCGCTCC 4020
Db 3960 GGTGGGATCTGGATCGACAGGGGTCCTCCATTTGCCACAGTGGGGCTGTCACACACTGCGCTCC 4019
QY 4021 AGGATCAGCATATATCCCGCAGGACCCATCTGTTCCCTGGCTCTCTGCGGATGAACCTC 4080
Db 4020 AGGATCAGCATATATCCCGCAGGACCCATCTGTTCCCTGGCTCTCTGCGGATGAACCTC 4079
QY 4081 GACCTGCTGCAGGACACTCGGACGAGGCTATCTGGGACGCTTGGAGCGGTGCGAGCTC 4140
Db 4080 GACCTGCTGCAGGACACTCGGACGAGGCTATCTGGGACGCTTGGAGCGGTGCGAGCTC 4139
QY 4141 AAGCCCTTGGTGCCAGCCTGCCCCGCCAGCTGCAGTACAAAGTGTGCTGACCGAGGCGAG 4200
Db 4140 AAGCCCTTGGTGCCAGCCTGCCCCGCCAGCTGCAGTACAAAGTGTGCTGACCGAGGCGAG 4199
QY 4201 GACCTGAGGTGGGCGAGAAACAGCTCTGTGTGCTGGCAGTGCCCTTCTCCGGAAGACC 4260
Db 4200 GACCTGAGGTGGGCGAGAAACAGCTCTGTGTGCTGGCAGTGCCCTTCTCCGGAAGACC 4259
QY 4261 CAGATCCTATCTGACGAGGCTACTGCTGCGTGGACCCCTGGCAGGAGTGCAGATG 4320
Db 4260 CAGATCCTATCTGACGAGGCTACTGCTGCGTGGACCCCTGGCAGGAGTGCAGATG 4319
QY 4321 CAGGCCATGCTCGGAGCTGTTTGCACAGTGCACATGTGCTGCCATTTGCCACCGCCTG 4380
Db 4320 CAGGCCATGCTCGGAGCTGTTTGCACAGTGCACATGTGCTGCCATTTGCCACCGCCTG 4379
QY 4381 CGTCCGATGATGACTGTGCGCGGGTTCTGGTCAATGACAAAGGGGAGGTGGCAGAGAGC 4440
Db 4380 CGTCCGATGATGACTGTGCGCGGGTTCTGGTCAATGACAAAGGGGAGGTGGCAGAGAGC 4439
QY 4441 GCGAGCCGCGCCAGCTGCTGCCAGAGGGCTGTTTACAGACTGGCCAGGAGTCA 4500
Db 4440 GCGAGCCGCGCCAGCTGCTGCCAGAGGGCTGTTTACAGACTGGCCAGGAGTCA 4499
QY 4501 GGCCTGGTC 4509
Db 4500 GGCCTGGTC 4508

RESULT 12
ABK62572
ID ABK62572 standard; cDNA; 5728 BP.
XX AC ABK62572;
XX AC ABK62572;
XX DT 18-JUN-2002 (first entry)
XX DE Rat sequence differentially expressed in response to a hepatotoxin #479.
XX KW Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
XX KW differential expression; centrilobular necrosis; steatosis.
XX OS Rattus norvegicus.
XX PN WO200210453-A2.
XX PN 07-FEB-2002.
XX PF 30-JUL-2001; 2001WO-US23872.
XX PR 31-JUL-2000; 2000US-222040P.
XX PR 02-NOV-2000; 2000US-244880P.
XX PR 11-MAY-2001; 2001US-290029P.
XX PR 15-MAY-2001; 2001US-290645P.
XX PR 22-MAY-2001; 2001US-292336P.
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PR 06-JUN-2001; 2001US-295798P.
PR 13-JUN-2001; 2001US-297457P.
PR 19-JUN-2001; 2001US-298884P.
PR 09-JUL-2001; 2001US-303459P.
XX (GENE-) GENE LOGIC INC.
XX PA Mendrick D, Porter MW, Johnson KR, Castile AL, Elashoff MR;
XX PI WPI; 2002-241625/29.
XX DR
XX XX
PT Predicting toxic effects of compounds or the progression of these toxic
PT effects by determining the changes in gene expression in tissues or
PT cells exposed to the toxin and comparing these to gene expression in
PT unexposed tissues or cells -
XX PS Claim 1; Seq ID No 479; 239pp; English.
XX CC The invention relates to methods for predicting toxic effects of
CC compounds or the progression of these toxic effects by determining the
CC global changes in gene expression in tissues or cells exposed to the
CC toxin and comparing these to gene expression in unexposed tissues or
CC cells. Also included are methods of predicting at least one toxic
CC effect of a compound or progression of a toxic effect, preferably the
CC hepatotoxicity of a compound, comprising detecting the level of
CC expression in a tissue or cell sample exposed to the compound of two or
CC more genes listed in the specification, where differential expression of
CC the genes is indicative of at least one toxic effect or progression.
CC The method can also be used to identify an agent which modulates the
CC toxic response and predict cellular pathways that a compound modulates
CC in a cell. The methods utilise a set of at least two probes (on a solid
CC support in kit form), where each of the probes comprises a sequence that
CC specifically hybridises to a gene listed in the specification, a computer
CC system comprising a database containing information identifying the
CC expression level in a tissue or cell sample exposed to a hepatotoxin of a
CC set of genes comprising at least two genes listed in the specification,
CC and a user interface to view the information used to present information
CC identifying the expression level in a tissue or cell of at least one gene
CC listed in the specification. The method is useful for elucidating global
CC changes in gene expression and for identifying toxicity markers in
CC tissues or cells exposed to a known toxin. The genes may be used as
CC toxicity markers in drug screening and toxicity assays. The genes and
CC gene expression information may be used as diagnostic markers for the
CC prediction or identification of the physiological state of tissue or cell
CC sample that has been exposed to a compound or agent. Hepatotoxicity
CC is characterised by centrilobular necrosis and steatosis. The present
CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene
CC which is differentially expressed in response to a hepatotoxic agent.
XX SQ Sequence 5728 BP; 1092 A; 1676 C; 1663 G; 1297 T; 0 other;
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Query Match 67.2%; Score 3030; DB 24; Length 5728;
Best Local Similarity 80.3%; Pred. No. 0;
Matches 3629; Conservative 0; Mismatches 850; Indels 39; Gaps 5;

QY 1 ATGGCGCGCTGCTGAGCCCTGCGGGGCGAGGGGTCTGGAACACAGACAGAGCTGAA 60
Db 43 ATGGCGCGCTGAGAGTCTTGGCGAGGCTGAGGGTCTGGAACACAGACAGAGAGG 102
QY 61 CCTGCGCGCCACAGCCCTGCTGAGCCTGCTCTCTGAGAACAGCAGGGGTCTGGGTACCC 120
Db 103 CCTGTGGCCTATCATTGCTCACTGCTGCTGCTGCTGAGCGCGCGGGAGCTGGGTGCC 162
QY 121 CCCATGTACCTCTGGGTCTTGGTCCCATCTACCTCTCTTATCCACACCATGGCGG 180
Db 163 CCCATGTACCTCTGGGTCTTGGCCCATCTACCTCTCTACATCCATCGCGGTGTC 222
QY 181 GGTACTCTCGGATGCCCACTCTTCAAAGCCCAAGATGGTGTGATTCGCCCTCAT 240
Db 223 TGCTACTCTCGGATGCCCGCCTTTCAAAATCAAAATGGTGTGCTCGGCTTGGCCTCATC 282
QY 241 GTCCTGTGTACCTCCAGCGTGGCTGCTCGCTCTTTGGAAATCCCAACAGGAGACCCCTGAG 300
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Db 283 CTCTCTACACCTTCAACGGCGGCGCTGCTCTCTGGAGGATCCACGGGGCATGCCCGAC 342
Qy 301 GCCCAGAAATCCCTCATTCCTACTGTGGCTCACCACGATGAGCTTCCAGTGTC 360
Db 343 GCCCAGAGCTTCTCATTCACCTACCTGCTGGCTCACCACCATGAGCTTCCACCTTC 402
Qy 361 CTGATTACACCGAGGAAAGAGAGTCCAGTCACTGGAAGTGTCTGTTGTTACTGG 420
Db 403 CTGATCCACATGGAGAGAAAGAGGGGTCCGTGCACTGGGTGTTGTTGGGTACTGG 462
Qy 421 CTCTCTGCTTGTCTTCCAGCTACCAAGCGTCCAGAGCGCTCCGGAGCGGGCTTC 480
Db 463 CTGCTCTGCTGCTGCCAGCCTACGACACTGCCAGAGCGCTCCGCGAGGAGCTTC 522
Qy 481 CAGACGACCTGTCGGCCACCTGTCACCTACCTATGCCGTCTCTGGTGTGSCACAG 540
Db 523 GCCAGGAGGCGCTCCACACCTGGCCACCTACCTGCTGTCTGCTGGTGGCGACAG 582
Qy 541 TTTGTGCTGTCTGCTGGCGGATCAACCCCTTCTTCCCTGAAGACCCCGCAGAGTCT 600
Db 583 CTGGTGTCTGTCTGCTGTAGACGACGACCCCTTCTTCTCGAAGACTCCCAAGCCATTG 642
Qy 601 AACCCCTGTCAGAGACTGGGGAGCTTCCCTCCAAAGCCACGTTCTGTTGGTGTTC 660
Db 643 AATCCATGTCCAGAGCGGAGGCTCTTTTCCCTCCAAAGGCCATGTTCTGTTGGGCTCT 702
Qy 661 GCCCTGGTCTGGAGGGGATCAGAGGCGCACTGACACCAAGACCTCTGGTTCGCTTGG 720
Db 703 GGACTGCTATGGAAGGGCTACAGGAACCTGTGGGGCCAAAGACCTCTGGTFCACCTTGG 762
Qy 721 AGAAAAAATCTCTCAGAAATCTTCTTCCCGGCTGTAAGAGAGTGGATGAGAACCGC 780
Db 763 AGAAAAAATCTCTCAGAAATCTTCTTCCAGCTGGAAGAGATGAGAGGAACTTC 822
Qy 781 AGTCAGCCCGAGGACACAAAGCAATAGCAATTAAGAAAGGCGGCACTGGCATG 840
Db 823 AGTAGCTGCGCGGGCAC-----AAAGGGCACAGTGGTATG 858
Qy 841 AAGGCTCAGAGACGAGCCCTTCTACGCAAGAGGAGCGCACTGGCGCCACTGCTG 900
Db 859 GGGACCCCGAGACAGAGGCTTCTGACGCAAGAGAGGAGCGGCGCCGCTGCTC 918
Qy 901 AAGGCATCTGGCAGGTTCATTCATCTACCTTCTTCCCTGGGACCCCTCAGCCTCATC 960
Db 919 AGGCTATCTGGCGTGTCTCCGGTCCACTTCTGCTGGGAGCCCTCAGCCTGCTCAT 978
Qy 961 AGTATGCTTCAGTTTCACGTGTCCTCCAAAGCTGCTCAGCCTTTCCTGAGTTTATGGT 1020
Db 979 AGCGATGCTTCAGGTTTGTCTTCCCAAGCTCCTCAGTCTGTTTCTGGAGTTCATGGC 1038
Qy 1021 GATCCCAAGCCTCCAGCCTGGAAGGCTACCTCCTCGCGTCTGATGTTCTCTCAGCC 1080
Db 1039 GACCTCGAGTCTCGCTGCTGAGGAGGCTGGCTCTCGGCTGCTGATGTTCTGTCGGCC 1098
Qy 1081 TGCCTGCAAGCGCTGTTTGAACAGCAGAACATGTACAGGCTCAAGGTCGCGCAGATGAG 1140
Db 1099 TGCTTACAGACACTGTTTGAACAGCAGTACATGTACAGATCAAGGTCCTGAGATGAG 1158
Qy 1141 TTGGGTGCGGCATCAGTGGCCTGGTGTACAGAAAGTCTGCGCTGTGTCAGCGGCTCC 1200
Db 1159 CTGCAACAGGCATCAGTGGCTGGTGTACAGAAAGTCTGCTGCTTCCAGTGGTTC 1218
Qy 1201 AGAAGGCGCTGCGGTGGTGTGCTGCTCAATCTGGTGTCCGTGAGCTGCGAGCGGCTG 1260
Db 1219 AGAAGTCCAGTGCAGAGGAGGAGTGTCAACCTGGTGTGAGTGGAGCTACAGCGGCTG 1278
Qy 1261 ACCGAGAGCGCTCTACCTCAAGGGGTGTGGCTGCGCTCTGCTGGATCGTGTGCTG 1320
Db 1279 GTCGAGAGCATCTCCACCTCAAGGGCTGTGGCTGCTCTTCTCTGGATCATTTGTGTC 1338
Qy 1321 TTGCTGTATCTGCGAGCTCTCGGGGCGCTCCGCGCCCTCAGTGGCATCGCTGCTTCCTG 1380
Db 1339 TTTGTGCTGCGAGCTCTCTGGGCGCTCTGGCCCTCAGACGCGTGTGCTGCTTCTCTG 1398

Qy 1381 AGCTCCTCCTCTGAATTTCTTCTATCTCAAGAAAGGAACCACTCAGGAGGACAA 1440
Db 1399 AGCTTCTCCTCCTGAACTTTCTTCAATACCAAGAGGAGCTTCCATCAGAGAAACAG 1458
Qy 1441 ATGAGCAGAAAGACTCAGGGCAGCGCTCACCAGTCTATCTCTCAGGAACTCGAAGACC 1500
Db 1459 ATGAGCAGAAAGGCTCCCGAGCAGCGCTCACCAGCTCCATGCTCAGAACTGTGAGAAC 1518
Qy 1501 ATCAAGTTCATGGCTGGGAGGAGCTTCTTGACAGAGTCTCTGGGCTCCGAGGCCAG 1560
Db 1519 ATCAAGTCCAGGCTGGGAGTGTCTTCTGAGCGACTCTCTGATATACCGGGCCAG 1578
Qy 1561 GAGCTGGGCGCTTGGGAGCTCCGCGCTCTCTCTCTGCTGCTGCTGCTCTCTTCAA 1620
Db 1579 GAGCTAGGTGGCTGAAGACCTCCGCTCTCTCTCTGCTCTCTCTGCTCTCTTCAA 1638
Qy 1621 GTGCTACATTTCTGCTCGCACTGGTGGTGTCTTCTCCACACTCTGCTGGCGCGAG--- 1677
Db 1639 GTGCTACATTTCTGCTGGCGCTGGTGTGTTGCTGTCCACACTCTGGTGGCAGAGAC 1698
Qy 1678 AATGCTATGAATGCAAGAAAGCTTTGTGACTCTCACAGTCTCTCAACATCTCTCAACAG 1737
Db 1699 AACGCCATGGATCGGAGAAAGGCTTTGTGACGCTCAGGCTGCTCAGCATCTCTTAACAAA 1758
Qy 1738 GCCAGGCTTCTCTGCGCTTCTCCATCCACTCCCTGCTCAGGCCGCGGTGCTTTGAC 1797
Db 1759 GCCAGGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTTGAC 1818
Qy 1798 CGTCTGGTCACTTCTCTGCTGGAAGAGTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTG 1857
Db 1819 CGCTAGCTGCTTCTCTGCTGGAAGAGTAGACCCCAATGGCATGGTCTTTCAGTCCC 1878
Qy 1858 TCTGAAGCGCTGCGGGAGGATTCATCACCATCAGAGTGGCAGCTTCTGCTGCTGCTGCTG 1917
Db 1879 TCCAGATGC---TCTCGAAGGATCGAATTTCTATACAAATGGCACTCTCGTGGTCTG 1935
Qy 1918 CAGGAAGCCCTCCTCTGCTCAGAAATAACCTCAGGCTGCCAGGCTGCTGCTGCTGCTG 1977
Db 1935 CAGGAGAGCCGCTGCTGCTGCAAGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1995
Qy 1978 GCTGTGCTCGTCCAGTGGGGCAGGAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2037
Db 1996 GCTGTGCTGGTCCAGTGGGGCTGGAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2055
Qy 2038 CTGTCAGAGTGGAGGGTTCGTGACATCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2097
Db 2056 CTGTTGAAGGTAGAAGGGTCTGTGAGCAITGAGGGTTCGCTGCTGCTGCTGCTGCTGCTG 2115
Qy 2098 GCTGGGTGCAGAACACCTCTGTGGTAGAATGTGTGCTGCGGAGGAGCTGAGCCCA 2157
Db 2116 GCTGGGTCCAGATACCTCTGTGGTAGAATGTGTGCTTCCAGGAGGAGCTGAGTCTG 2175
Qy 2158 CCGTGGCTGGAGAGTACTAGAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2217
Db 2176 CCATGGTTCAGGAAGTCTTAGAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2235
Qy 2218 GAGGATTCACACTTCAATTTGGGAGCAGGGCATGAATCTCTCCGAGGCCAGAGACAG 2277
Db 2236 GCAGGAGTTCACACCCAGTAGGGGAGCAGGGCATGAATCTTCTGGGGGCCAGAGACAG 2295
Qy 2278 CGGCTGAGCTGGCGGGCTGTATACAGAAAGGAGCTGTGTACCTGCTGCTGCTGCTGCTGCTG 2337
Db 2296 CGGCTGAGCTTGGCTGGCTGTGTACAGAAAGGCTGCTGTGTGCTGCTGCTGCTGCTGCTGCTG 2355
Qy 2338 CTGGCGGCTGGATGCCACGCTTGGCCAGCATGTCTTCAACAGGCTCAATTTGGGCTGCTGCT 2397
Db 2356 CTAGCAGCCCTGGATGCGCATGTACAGCAGGAAGTCTTCAACAGAGTCAATTTGGCCCCAGT 2415
Qy 2398 GGGCTACTCCAGGGAACACAGGATTCGCTGACGAGCGCATCCACATCTCTGCTGCTGCTGCTG 2457
Db 2416 GGACTTCTCCAGGTACGACTCGGATCTTGTAAACACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2475

QY 1141 TTGCGGTGGGCATCAGTCGGCTGGTGTACAGAAAGTCCCTGGCTCTGTGCAGCGCTCC 1200
DB 1146 CTGCGAAGCCATCAGTCGGCTGGTGTACAGAAAGTCCCTGGCTCTGTGCAGCGCTCC 1205
QY 1201 AGAAGGCCAGTGGCGGTGGTGTATGTGTCAATCTGGTGTCCGTGGAGCTGCAGCGGTG 1260
DB 1206 AGAAAGTCCAGCGCAGCAGAGAGAGTGTGTCAACCTGGTGTCCGTGGACATCCAGCGGTG 1265
QY 1261 ACCGAGAGCGTCCCTACCTCAACGGGCTGTGGCTGCCTCGTGTGATGTGTCTGCC 1320
DB 1266 GCCGAGAGCATCATCTAGCTCAACGGGCTGTGGCTGCCTCGTGTGATCTTTGTGTGC 1325
QY 1321 TTGCTCTATCTGTGCGACCTCTCGGGCCCTCCGGCCCTCACTGCGCTGTCTTCCTG 1380
DB 1326 TTTGTCTACCTGTGCGACCTCTTGGACCTCTGCTCTCAGCGGTGTGTCTTCCTG 1385
QY 1381 AGCTCTCTCTGTAATTTCTCATCTCCAGAAAGAACACCACTCAGGAGAGAGAA 1440
DB 1386 AGCTCTCTCTGTAATTTCTCATCAACAGAGAGAGGGCTTCCATCAGAGAAACAG 1445
QY 1441 ATGAGGAGAGAGGACTCAGCGGCAGCTCACCAGCTCTATCTCAGGAATCTGAGACC 1500
DB 1446 ATGAGGAGAGAGGCTCCAGAGCAGGCTCACCAGCTCTATCTCAGGAATCTGAGAAC 1505
QY 1501 ATCAAGTTCCATGTGCTGGAGGAGCCCTTCTGGACAGAGTCTCTGGGATCCGAGGCCAG 1560
DB 1506 ATCAAGTCCAGCGTGGAGCATGCTCTTCTGGAGGACTCTTTCACATCCGGGGCCAG 1565
QY 1561 GAGCTGGGCGCTTTCGCGACCTCCGGCTCTCTCTCTGTGTGTGTGTGTGTGTGTGTGT 1620
DB 1566 GAGCTCAGCGCCCTGAAGACCTCCACCTCTCTCTCTGTGTGTGTGTGTGTGTGTGTGT 1625
QY 1621 GTGTGTACATTTCTGTGCGACTGGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1677
DB 1626 GTGTGTACATTTCTGTGCGACTGGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1685
QY 1678 AATGCTATGAATGCAGAGAAAGCCCTTGTGACTCTCAGAGTCTCAACATCTCAACAAG 1737
DB 1686 AATGCCATGGATCAGAGAGGCGCTTGTGACGCTCAGAGTCTCAGCATCTTAACAAA 1745
QY 1738 GCCAGAGCTTTCCTGCGCTTCCATCCATCCCTCTGTGTGTGTGTGTGTGTGTGTGTGT 1797
DB 1746 GCCAGAGCTTTCCTGCGCTTCCATCCATCCCTCTGTGTGTGTGTGTGTGTGTGTGTGT 1805
QY 1798 CGTGTGTCTCCTCTGTGCTGGAAGAGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGT 1857
DB 1806 CGGTGTGTCTTCTGTGCTGGAAGAGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGT 1865
QY 1858 TCTGGAAGCGTGCAGGAGGATTTGATCACCATACAGTGTGAGTGTGTGTGTGTGTGTGT 1917
DB 1866 TCCAGGCGC---TCCCTCGAAGGATCGAATTTCTGTACACATGCGACCTTCCGCTGTG 1922
QY 1918 CAGGAAGCCCTCCTGCTCCAGAGATTAACCTCAGGTGTGTGTGTGTGTGTGTGTGTGT 1977
DB 1923 CAGGAGAGCCACCCCTGCTGCAGGGATCAACCTCAGGTGTGTGTGTGTGTGTGTGTGT 1982
QY 1978 GCTGT 2037
DB 1983 GCTGT 2042
QY 2038 CTGTCAAGGTGGAGGGGTCTGTGAGCATCGAGGTGTGTGTGTGTGTGTGTGTGTGTGT 2097
DB 2043 CTGTGTAGGTGAGAGGCTGTGTGAGCATGTGAGGTGTGTGTGTGTGTGTGTGTGTGT 2102
QY 2098 GCCTGGGTGAGAACACCTCTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2157
DB 2103 GCCTGGGTGAGAACACCTCTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2162
QY 2158 CCCTGGGTGAGAGAGT 2217
DB 2163 CCCTGGGTGAGAGAGT 2222
QY 2218 GAGGAATCCACACTTCAATTGGGAGCAGGGCATGAATCTCTCCGGAGGCCAAGCAG 2277

DB 2223 GCAGGAGTTACACCCCAATAGGGGAGAGGGCATGAATCTTTTGGGGCCAGAACAG 2282
QY 2278 CGGCTGAGCCTGGCCCGGCTGTATACAGAAAGGAGCTGTGTACCTGTGTGTGTGTGTGT 2337
DB 2283 CGGCTGAGCTTGGCTCGGGCTGTGTATACAAAAGGCTGCCATCTACTTGTGTGTGTGTGT 2342
QY 2338 CTGGCGGCTTGGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2397
DB 2343 CTGGGAGCGCTTGGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2402
QY 2398 GGGCTACTCCAGGGAACACAGGATTCGTGACGACGCTCCTCACATCTCTGCTGCTG 2457
DB 2403 GGTGTCTCCAGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2462
QY 2458 GCTGTGTGATCATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2517
DB 2463 GCTGACCGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2522
QY 2518 CTCTCTGAGAGAAAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2577
DB 2523 CTCTCTGAGAGAAAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2575
QY 2578 AGAGGAGAGGAGAAACAGAACCTGGGACACAGCACAGGACCCAGAGGACCTCTGCA 2637
DB 2576 -----TGCAGGAACACAGCATACAGTACAGTACAGTACAGTACAGTACAGTACAG 2627
QY 2638 GGCAGAGGCGCGAGCTTTAGACGCGA-----GAGTCTCATCAAGTCAAGTCAAGTCAAG 2691
DB 2628 GGTGGAGGCGCCACATGCAGACAGACAGGCGCCAGGCGCCAGGAGCAGCCCTGTGAAG 2687
QY 2692 GACCTGACCATTTAGAGGCCAGACAGAGTTCCTCTGTGTGTGTGTGTGTGTGTGTGTGT 2751
DB 2688 GGCAGAGCACATCTGAGGTACAGATGGAGGCTTCTCTGTGTGTGTGTGTGTGTGTGTGT 2747
QY 2752 TGGCCAGGAGAAAGACAGCATCCAATACGCGAGGTTGAAGCCACAGTGCACCTGGCC 2811
DB 2748 TTGACAGCAGAGAGAGT 2807
QY 2812 TACCTGT 2871
DB 2808 TACCTGT 2867
QY 2872 CAAGT 2931
DB 2868 CAAGT 2927
QY 2932 GGTGGGCGAGCAGCAGGACGCGCTGCTGCGGGGATCTTGGGCTCTCTGCGCTCTCTC 2991
DB 2928 GATGGGCGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2987
QY 2992 CAAGCATTTGGCTGT 3051
DB 2988 CAAGCATTTGGCTGT 3047
QY 3052 AGT 3111
DB 3048 GGCCTCTCTTTCCGAGGATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3107
QY 3112 CGGACACCATTTGGT 3171
DB 3108 GCGAGCCAGTGGGAAACCTGCTGAACCGCTTTTCCAGGAGACAGACAGTGTGTGTGT 3167
QY 3172 GACATTCAGACAAACTCCGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3231
DB 3168 GACATTCAGACAAACTCCGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3227
QY 3232 CTGGT 3291
DB 3228 CTGGCAGT 3287
QY 3292 TACCTGT 3351

Db	3288	TATGCTGGGTTTCAGAGCCTCTATGTGGCCACATCTTGCCAGCTGAGACGTCCTAGAGTCA	334
Qy	3352	GCCAGCTACTCGTCTCTGCTGCCACATGCGTGAGAGGTTCCAGGGCAGCACAGTGGTC	3411
Db	3348	CCCCGCTACTCATCTGTGTGTTCCCATATGGCTGAGACCTTCCAGGNAAGTCTGGTGGTC	3407
Qy	3412	CGGGCATTCGGAACCCAGGCCCCCTTTTGGCTCAGAAACAATGCTGCGGTAGATGAAGC	3471
Db	3408	AGGCGCTTCCGGGCCCAGGCGCTTACCGCTCAGCACGATGCTCTCATGGATGAGAAC	3467
Qy	3472	CAGAGGATCAGTTTCCCGGACTGGTGGCTGACAGGTTGGCTTGGGCCAATGTGGACCTC	3531
Db	3468	CAGAGGCTAGTTTCCGAAACTGGTGGCTGACAGGTGGCTTAACTCCTGGAGCTT	3527
Qy	3532	CTGGGAATGGCTGTGTTTTCAGCGCCACGCTGCTGCTGTGAGCAAAAGCCACCTC	3591
Db	3528	CTAGGNAATGGCTTGGTATTCTGTGGCTGCTACATGCTGTGTCGACGAGGCTCACCTA	3587
Qy	3592	AGTCTGGGCTCGTGGGCTTCTCTGTCTGTGCTGCCCTCCAGGTGACCCAGACACTCGAG	3651
Db	3588	AGTCTGGGCTCGTGGGCTTCTCGGCTCCGCTGCCCTCCAGGTGACACAGACTCTCGAG	3647
Qy	3652	TGGGTGTTTCGCAACTGGACAGACCTAGAGAACACCATCTGTCTAGTGGACCGGATCGAG	3711
Db	3648	TGGGTGTCGCGAGCTGGACATCTGGAGAACACATGGTAGCGGTGGAGCGGCTCGAG	3707
Qy	3712	GACTATGCTTGAGCGCCAAAGAGGGCTCCCTGGAGGCTGCCACATGTGCAAGCTACGCC	3771
Db	3708	GACTACGCTCGCATCCCAAGAGGCTCCCTGGAGGCTGCCACCTGGCAGACCCAGCCT	3767
Qy	3772	CCCTGGGCTCAGGGCGGGCAGATTCAGTTCGCGGACTTTGGGCTTAAGATGCCGACCTGAG	3831
Db	3768	CTCTGGCCTTGTGGGGACAGATTGAGTTCGCGGACTTTGGGCTCAGACACCGACACAG	3827
Qy	3832	CTCCGCTGGCTGTCAGGCGCTGCTCTCAGATTCACGACGACGAGGAGAAGTGGGCATC	3891
Db	3828	CTGCCCTTGGCTGTGACGGAATGCCCTGGAATCCCATGTCAGGAGAGAAGTGGGCATC	3887
Qy	3892	GTTGGCAGGACCGGGCAGGAAGTCTCCCTGGCGCAGTGGGGCTGTGCGGCTCCAGGAG	3951
Db	3888	GTGGCAGAACAGGGCGCGGAAGTCTCCCTTGGCTTGGGGCTGTGCGGCTTCAGGAG	3947
Qy	3952	GCAGCTGAGGTTGGGATTCGATTCGACGGGTGCCCATTTGCCACGTTGGGCTGCACACA	4011
Db	3948	GCTGCCGAGGGTAATATCTGGATCGATGGGTGCCCTATCACCCATGTGGGGCTGCACACA	4007
Qy	4012	CTGCGCTCCAGGATCAGCATCATCCCCAGGACCCCATCTGTTCCCTGGCTCTCTCGGG	4071
Db	4008	CTGAGTFCGCGAATACCATCATCCCTCAGGACCTGCTCTTTCCAGGCTCTCTCGGG	4067
Qy	4072	ATGAACCTCGACCTGCTGCAGGACGACTCGGACGAGGCTATCTGGGACGCCCTGGAGACG	4131
Db	4068	ATGAACCTGGACCTGCTTCAGGAGCACAGATGAAGGCATCTGGGCAGCGCTGGAGACA	4127
Qy	4132	GTGAGCTCAAAGCCTTGGTGGCCACGCTGCCCGGCCAGCTGCAGTACAAGTGTGCTGAC	4191
Db	4128	GTGCAGCTCAAGGCTTCTGTGACCAACGCTGCTCGTGGCCAGCTGCAATATGAGTGTGACGC	4187
Qy	4192	CGAGGCGAGGACCTGAGCCTGGGGCAGAAACAGCTTCCTGTCTCTGGCACGTCGCCCTTCTC	4251
Db	4188	CAGGAGATGACCTGAGCTGGGTATAAACAGCTCTGTGCTGGCCACGACGACGCTTCTC	4247
Qy	4252	CGGAAGACCCAGATCTCATCTCTGGACGAGGCTACTGCTCGCGTGGACCTTGGCACGGAG	4311
Db	4248	CGGNAACCCAGATCTCATCTTGACGAGGCGGACTGCTCTGTGGACCCAGGACGGAG	4307
Qy	4312	CTGCAGATCAGGCCATGCTCGGGAGCTGGTTTGGACAGTAGTGCATGCTGTGCCCATTTGCC	4371
Db	4308	ATGCAGATGCAGCGGCCCTGGAGCGCTGGTTTACACAGTGTACCTTACTGCTTATCGCT	4367
Qy	4372	CACGCTTGGCTTCCGTGATGGACTGTGCCCGGGTTCTGTGTCATGGACAAGGGCAGGTG	4431
Db	4368	CACGCTTGGCTTCCGTGATGACTGTGCGCAGAGTCTTGTTCATGGATGAGGCGAGGTG	4427

QY	4432	GCAGAGAGCGGAGCCCGCCAGCTGCTGGCCAGAGAGCGCTGTTTTACAGCTGCC	4491
Db	4428	GCAGAAAGTGGCAATCTGCTAGCTGCTGGCCAGAAAGCGCTGTTTTACAGGCTAGCC	4487
QY	4492	CAGGAGTCAAGCGCTGG	4507
Db	4488	CATGAGTCGGGCGCTCG	4503
RESULT 14			
AAZ94741			
ID	AAZ94741	standard; cDNA; 5011 BP.	
XX	AAZ94741;		
XX	01-AUG-2000	(first entry)	
XX	Human ATP binding cassette ABCCL1 (MRP1) cDNA.		
KW	ABCC1; ATP binding cassette; human; cholesterol; lipid disorder; atherosclerosis; lipid disorder; dyslipidemia; psoriasis;		
KW	lupus erythematosus; diagnosis; gene therapy; MRP1;		
KW	multidrug resistance associated protein; chromosome 16p13.12; ss.		
XX	Homo sapiens.		
OS	WO200018912-A2.		
PN	06-APR-2000.		
XX	21-SEP-1999;	99WO-EP06991.	
XX	25-SEP-1998;	98US-010706.	
PR	(FARB) BAYER AG.		
PA	Schmitz G, Klucken J;		
PI	WPI; 2000-293151/25.		
XX	Adenosine triphosphate binding proteins useful for identifying agents for treating atherosclerosis and other inflammatory disorders -		
PT	Claim 9; Page 115-117; 154pp; English.		
PS	The present sequence is that of human ATP binding cassette subfamily C protein ABCCL1 cDNA. The cDNA was identified using a		
CC	differential display method in which monocytes from peripheral blood were subjected to macrophage differentiation and cholesterol		
CC	loading with acetylated low density lipoproteins and subsequent deloading with high density lipoprotein (HDL3) to identify		
CC	cholesterol sensitive genes. The gene maps to chromosome 16p13.12		
CC	and is also termed MRP1 (multidrug resistance associated protein).		
CC	The invention provides cholesterol-sensitive ABC genes (see		
CC	AAZ94734-63). These genes, and polypeptides encoded by them,		
CC	can be used for diagnostic and therapeutic applications, and for		
CC	biochemical or cell-based assays to screen for pharmacologically		
CC	active modulator compounds useful for the treatment of lipid		
CC	disorders, atherosclerosis or other inflammatory diseases such as		
CC	psoriasis and lupus erythematosus.		
XX	Sequence 5011 BP; 1063 A; 1499 C; 1394 G; 1055 T; 0 other;		
XX	Query Match	27.3%; Score 1229.2; DB 21; Length 5011;	
XX	Best Local Similarity	55.8%; Pred. No. 1.7e-263;	
XX	Matches 2539; Conservative	0; Mismatches 1933; Indels 80; Gaps	
QY	36	GCTCTGGACACAGACAGCCCTGAACCTGCCGCCACACGCTCTGCTGAGCTGTGCTTCCT	95
Db	238	GCTCTGGGACTGGAATGTCACGTGGGAATACCAACCAACCCGCGCTTCA	297
QY	96	GAGAACAGCAGGGGTCTGGTACCCCGCTACCTCTGGGTCTGGTCTCCATCTACCT	155

Db 298 GAACACGGTCTCTGTTGGGCTGCTTTTACCTCTGGGCTGTTTCCCTCTCACTT 357
QY 156 CCTCTTCATCCACACATCGCGGGGCTACCTCCGGATGTCGCCACTTTCACAAAGCAA 215
Db 358 CCTCTATCTCTCCGGACATACCGAGGCTACATTCAGATGACACCTCTCAACAAACCAA 417
QY 216 GATGGTCTTTGGATTCGCCCTCATAGTCCCTGTGTACCTCCAGCGTGTCTGCTCTTTG 275
Db 418 AACTGCCCTTGGGATTTTGTGTGGATGCTGTCTGGGACAGCCTTCTACTCTTTCTG 477
QY 276 GAAATCCAAACAGGAACGCTGAGGCCCCAGAAATTCCTCATTCATCCTACTGTGTGGCT 335
Db 478 GGAAGAAGTGGGCAATATTCCTGGCCCGAGTGTCTGTGTCAGCCCACTCTCTTTGGG 537
QY 336 CACACAGATGAGCTTCGACGTGTTCTGTATTCACACCGAGGAGAAAGGAGTCCAGTC 395
Db 538 CATCACACGCTGCTTGTCTACCTTTTAAATTCAGCTGGAGAGGAGGAGTTCAGTC 597
QY 396 ATCTGGAGTCTGTTGGTGTACTGGCTTCTCTGCTTTGTCTTCCAGCTACCAACGCTGC 455
Db 598 TTCAGGATCATGCTACCTTTCTGGCTGTGTAGCCCTAGTGTGTGCCCTAGCCATCTCTGAG 657
QY 456 CCAGCAG-----GCCCTCCGAGCGGGCTTCCAGAGCGACCTCTGCGCCACCTGTC 506
Db 658 ATCCAAATATTACAGCCTTAAAGAGGATGCCAGTGCAGCTGTTCTGTGACATCAC 717
QY 507 CACCTAGCTATGCTCTCTGTGTGTGGACAGTTGTGTCTGTCTGCTGCTGCGGATCA 566
Db 718 TTTCTAGCTACTTTTCCCTCTTACTCATTCAGTCTGCTTGTCTGTTTTCAGATCG 777
QY 567 ACCCCCTTCTCCCTGAACACCCCGAGAGTCTTAACCCCTGTCCAGAGACTGGGGCAGC 626
Db 778 CTCACCCCTGTTCTCGGAACCATTCACGACCCCTAATCCCTGCGCCAGAGTCCAGCGCTC 837
QY 627 CTTTCCCTCCAAAGCAGTCTCTGGTGGTCTTCTGGCTGTGTGGAGGGATACAGGAG 686
Db 838 CTTTCTGTGAGGATCACTCTGTGTGGATCACAGGTTGATTTGCTCGGGGCTACCGCCA 897
QY 687 GCACCTGAGACCAAGACCTCTGTGTGGTGGAGAGAAACTCTCTCAGAGAACTTGT 746
Db 898 GCCCTTGGAGGCGAGTGCACCTCTGGTCTTAAACAAAGGAGGACACGTCGGAACAAGTCGT 957
QY 747 TTCCTGGCTTGAAGAGGATGGATAGGACGCG-----AGTGCAGCCCGGAGGACACAA 802
Db 958 GCCTGTTTGGTAAAGACTTGAAGAAGGAATGCGCCAAAGACTAGGAAGCGCGGTGAA 1017
QY 803 AGGCAATAGCATTTAAAGGAAGGCGGAGTGGCATGAAGGCTCCA----- 849
Db 1018 GGTGTGTACTCTCCAGGATCTCTGCCAGCGCGAAGAGAGTTCCAAGGTGGATGGAA 1077
QY 850 -----GAGACGAGCCCTTCTACGGCAAGAGGAGCGAGTGGGCGCCACTGCT 899
Db 1078 TGAGGAGGTGGAGGCTTTGATCTCAAGTCCCAAGTCCCAAGAGGAGTGGAAACCCCTCTCTGT 1137
QY 900 GAAGGCCATCTGCGAGGTGTTCCATCTACCTTCTCTGCTGGGACCCCTCAGCCCTCATCAT 959
Db 1138 TAGGTGTTATACAGACCTTTGGGCGCTTCTCTCATGAGTCTTCTTCAAGGCCAT 1197
QY 960 CAGTGTATGCTTTCAGTGTCTCACTGTCTCCCAAGCTGTCTCAGCCTTTTCTGGAGTTTATGG 1019
Db 1198 CCAGGACCTGATGATGTTTTCGGGCGCGAGATCTTAAAGTTGCTCATCAAGTTCGTGAA 1257
QY 1020 TGATCCCAAGCTTCCAGCTCGAAGGCTTACCTCTCTGCGGCTGCTGATGTTCTCTCAGC 1079
Db 1258 TGACACGAAGGCGCCAGACTGCGAGGCTTCTTCTACACCGTCTGCTGTTTGTCACTGC 1317
QY 1080 CTGCTGCAACGCTGTTTGGACAGCAGACATGTACAGGCTCAAGGTCGCCGAGATGAG 1139
Db 1318 CTGCTGCAAGCCCTGCTGCTGCACACAGTACTTCCACATCTGCTGCTGAGTGGCATGAG 1377
QY 1140 GTTGGCGTGGGCATCACTTGGCTGTGTACAGAAAGGCTTGGCTGTGTCTCCAGCGGCTC 1199

Db 1378 GATCAAGACCGCTGTCAATTGGGGCTGTCTATCGGAAGGCCCTGGTGATCACCATTTCAGC 1437
QY 1200 CAGAAAGCCAGTGGGTTGGTGTGATGTTGTTCAATCTGGTGTCCGTGGAGTGTGACGGGCT 1259
Db 1438 CAGAAATCCTCCAGGTCGGGGAGATTCTCAACCTCATGTCTGTGTGAGCCTCAGAGGTT 1497
QY 1260 GACCGAGAGCTCTCTACCTCAACGGGTGTGGCTGCTCTCTGCTGTGAGTGTGTCGTCG 1319
Db 1498 CATGGACTTGGCCACGTATCAATTAACATGATCTGCTGAGCCCCCTGCAAGTATCATCTTGC 1557
QY 1320 CTTGCTCTATCTCTGGCAGCTCTCGGGCCCTCCGCGCTCACTGCTCATCGCTGTCTTCTCT 1379
Db 1558 TCTCTACCTCTGTGGCTGAATCTGGGCCCTTCCGCTCTGGCTGGAGTGGCGGTGATGCT 1617
QY 1380 GAGCCTCTCTCTGTAATTTCTCATCTCCAAGAAAAGAACACCATCAGGAGGAGCA 1439
Db 1618 CTTCTATGTTGCCGCTCAATGTGTGATGGGATGAAGACCAAGAGATATCAGGTGGCCCA 1677
QY 1440 AATGAGGACAGAGGACTCACGGGACGGTCAACAGCTCTATCTCTCAGGAACTCGAAGAC 1499
Db 1678 CATGAAGACAAAGACAATCGATCAAGCTGATGAACGAAATCTCAATGGGATCAAGT 1737
QY 1500 CATCAAGTTCCATGCTGCGAGGAGCCTTTCTGACAGAGTCTCTGGGATCCGAGGCCA 1559
Db 1738 GCTAAGCTTTTATGCTGGGAGCTGGCATCAAGGACAAGGTGCTGGCCATCAGGCAGGA 1797
QY 1560 GGAGCTGGGCGCCTTGGCGAGCTCTGGGCTCTCTCTCTCTGCTGCTGCTGCTCTCTTCCA 1619
Db 1798 GGAGCTGAAGTGTCTGAAGAGTCTGCCTACCTGTCAAGGCTGGGACCTTCACTGGGT 1857
QY 1620 AGTGTCTACATTTCTGTGTCGACAGTGTGTGCTGTCTCAACACTCTGTGTGGTGGCGAGAA 1679
Db 1858 CTGACAGCCCTTTTGTGTGGCTTTGTGCACATTTGCGCGTCTACGTGACCAITGACGAGAA 1917
QY 1680 TGCTA---TGAATCAGAGAAAGCCTTTGTGACTCTCACTGTTCTCAACATCCTCAACAA 1736
Db 1918 CAACATCTGTGATGCCAGACAGCCTTCTGCTGTCTTGGCTTGTTCACATCCTCCGGTT 1977
QY 1737 GGCCAGGCTTTCCTGCGCTTCTCCACTCCCTCTGCTGAGGCGCCGGTGTCTTCTTGA 1796
Db 1978 TCCCTGAACATTTCTCCCATGGTCTATCAGCAGCATCTGTCAGGCGAGTGTCTCCCTCAA 2037
QY 1797 CCGTCTGGTCACTTCTCTGCTGGAAGAGTGTACCTGTTGTGTGTAGACTCAAGTTC 1856
Db 2038 ACGCTGAGGATCTTCTCTCCATGAGGAGTGTGAACTCTGACAGCATCGACGCGCGCC 2097
QY 1857 CTCTGGAAGCTGCTCCGGAAGGATTCATCACCATCACAGTGCACCTTCCGCTGTGTC 1916
Db 2098 TGTCAAGAGCGCGGGGCGACAGCATCACCTGAGGATGCCACATTCACCTGGGC 2157
QY 1917 CCAGGAAGCCCTCCCTGCTTCCACAGAAATAAACCCTCAGGTGCCCGCCAGGCTGTCTGCT 1976
Db 2158 CAGGAGCGACCTCCACACTGAATGGCATCACTTCTCCATCCCGAAGGTGCTTTGCT 2217
QY 1977 GGCTGTTGTGGTCCAGTGGGGGAGGAGTCTCTCTGCTGTGCTGCGCCCTCTCTTGGGGA 2036
Db 2218 GGCGTGTGGCGAGGTGGGCTCGGAAAGTCTGCTGCTCAGCGCTCTTGGCTGA 2277
QY 2037 GCTGTCAAGAGTGGAGGGTTCGTGAGCATCGAGGGTCTGCTGCTACGTGCGCCAGGA 2096
Db 2278 GATGGACAAAGTGGAGGGGCGAGTGTATCAGGGTCTCGGCTGCTGTGTGCCACAGA 2337
QY 2097 GGCTTGGGTGCAGAACACCTCTCTGTGTAGAGAAATGTGTCTGCTGCGGAGGAGCTGGAACC 2156
Db 2338 GGCTGGAATTCAGAAATCATCTCTCCGAGAAACATCCTTTTGTGATGTCAGCTGGAGGA 2397
QY 2157 ACCCTGCTGGAGAGTACTAGAGAGCTGTGCCCTGGAGCCAGATGTGGACAGCTTCCC 2216
Db 2398 ACCATTTACAGGTCCGCTGATACAGGCTGTGCCCTCTCTCCAGACCTTGAATCTCTGCC 2457
QY 2217 TGAGGGAATCCACTTCAATTTGGGAGCAGGCGATGAATCTCTCCGAGGCGGAGAGCA 2276
Db 2458 CAGTGGGATCGGACAGAGATTGGGAGAGGGCGTGAACCTGCTGGGGGCGGAGAGCA 2517

[illegible]

Db 3417 ACCGCTTCTCAAGAGAGCTGGACACAGTGGACTCCATCCCGAGGTCAATCAAGATGT 3476
QY 3197 TGCTGATCTAGCCCTTTGGACTCCTGAGAGTCAAGCTGGTGGTGGCTAGCTACCCAC 3256
Db 3477 TCATGGGCTCCTGTTCAAGCTATTGGTGGCTCCTGTTATCCTGCTGGCCACGGCCA 3536
QY 3257 TGGCCACTGTGGCCACTCCTGCCACTGTTTCTCCCTCTACGCTGGGTTCAGAGCCTGTATG 3316
Db 3537 TCGCCGCCATCATCATCCGCCCTTGGCCCTCATCTACTTCTCGTCCAGAGGTCTACG 3596
QY 3317 TGGTTACTCATGCCACTGAGAGGCTTGGAGTCAAGCAGTACTCTGCTGTCTGCTCCC 3376
Db 3597 TGGCTTCTCCCGCAGCTCAAGCGCCTCGAGTGGCTCAGCGCTCCCGGCTCTATTCCC 3656
QY 3377 ACATGGCTGAGAGCTTCCAGGGAGCAGTGGTCCGGCATTCAGAACCCAGCCCTCT 3436
Db 3657 ATTTCAAGAGACCTTCTGGGGTTCAGCGTTCATTCGAGCCTTCGAGGAGCAGGAGCGCT 3716
QY 3437 TTGTGGCTCAGAACAAATGCTCGGTAGATGAAAGCCAGAGGATCAGTTTCCCGGACTGG 3496
Db 3717 TCATCCACCAAGTGAACCTGAAGTGGACGAGAACAGAGGCTATTACCCAGCATCG 3776
QY 3497 TGGCTGACAGGTGGCTTCGGCCCAATGTGGAGCTCTCGGGGAATGGCTGTGTTCAG 3556
Db 3777 TGGCCAAACAGTGGCTGGCGCTGGGTGTGGTGTGTGGCAACTGCATCGTCTGTTG 3836
QY 3557 CCGCCAGCTGTGCTGCTGAGCAAAAGCCACCTCAGTGTGGCTCGTGGGCTTCTCTG 3616
Db 3837 CTGCCCTGTGTGGGTGATCTCCAGGCACAGCCTCAGTGTGGCTTGGTGGGCTCTCAG 3896
QY 3617 TCTCTGTGCTCCAGGTGACACACTGCAGTGGGTGTTTCGCAACTGGACAGACC 3676
Db 3897 TGCTTACTCATTTGAGGTACACCACTACTTGAATGGCTGGTTCGATGTCACTGAAA 3956
QY 3677 TAGAGAACAGATCGTGTGAGTGGAGCGGATGCAGGACTATGCCCTGGACCCCAAGGAGG 3736
Db 3957 TGGAAACCAACATCGTGGCGCTGGAGAGGCTCAAGGATATTCAGAGACTGAGAGGAGG 4016
QY 3737 CTCCTCGGAGGTGCCACATGTGCAGCTCAGCCCCCTGGCTCAGGGGGGGCAGATCG 3796
Db 4017 CGCCCTGGCAATCCAGGAGACAGCTCCCGCCACAGCTGGCCCCAGGTGGCGCGAGTGG 4076
QY 3797 AGTTCGGGACTTTGGGCTTAAGATGCCAGCTCAGCTCCGCTGGCTGTGCAGGGCGTGT 3856
Db 4077 AATTCGGAACTACTGCTCGCTACCGAGAGAGCTTGACTCTGTTCTCAGGCACATCA 4136
QY 3857 CCTTCAAGATCCAGCAGAGAGAGGTGGGCATCGTTGGCAGGACCCGGGGCAGGGAAGT 3916
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Search completed: December 18, 2002, 07:49:27
Job time : 584.826 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2002, 07:04:10 : Search time 7426.08 Seconds
(without alignments)
17670.781 Million cell updates/sec

Title: US-09-647-140A-7
Perfect score: 4509
Sequence: 1 atggcgcgcctgctgagcc.....cccaggagtcaggctggctc 4509

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl :

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- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_ph.*
- 7: gb_pl.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_on.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
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- 26: em_ro.*
- 27: em_sts.*
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- 32: em_htg_other.*
- 33: em_htg_mus.*
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- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	4509	100.0	4509	9	AF168791	AF168791 Homo sapi
2	4499.4	99.8	4512	6	AX282510	AX282510 Sequence
3	4499.4	99.8	4535	9	AF076622	AF076622 Homo sapi
4	3030	67.2	5728	6	AX400803	AX400803 Sequence
5	3030	67.2	5728	10	AB010466	AB010466 Rattus norv
6	3030	67.2	5775	10	RN073038	U73038 Rattus norv
7	3007.2	66.7	4980	6	AX282516	AX282516 Sequence
8	3007.2	66.7	4980	10	AB028737	AB028737 Mus muscu
9	1229.2	27.3	5011	9	HUMMRPX	L05628 Human multi
10	1227.6	27.2	5011	6	AR070199	AR070199 Sequence
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22	1057.6	23.5	5079	9	AF104943	AF104943 Homo sapi
23	1057.6	23.5	5142	9	AF085690	AF085690 Homo sapi
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27	1039	23.0	4762	6	A64692	A64692 Sequence 58
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34	729.8	16.2	5407	4	OC249144	Z49144 O. cuniculus
35	724.8	16.1	2969	10	RN0277881	AJ277881 Rattus no
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37	717.8	15.9	5586	6	A64635	A64635 Sequence 1
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
Homo sapiens multi-specific organic anion transporter-E mRNA,
PRI 25-AUG-1999
AF168791
Homo sapiens partial cds.
AF168791.1 GI:5764414
ACCESSION
VERSION
KEYWORDS
SOURCE
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4509)
REFERENCE
AUTHORS
TITLE
Belinsky, M.G. and Kruh, G.D.
MOAT-E (ARA) is a full length MRP/cMOAT subfamily transporter

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RESULT 2
AX282510
LOCUS AX282510 4512 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 2 from Patent W00162977.
ACCESSION AX282510
VERSION AX282510.1 GI:16609640

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Boyd,C.D., Csizsar,K., Lesaux,O., Urban,Z. and Terry,S.
Methods and composition for diagnosing and treating pseudoxanthoma
elasticum and related conditions
Patent: WO 0162977-A 2 30-AUG-2001;
Pxe international Inc. (US); UNIVERSITY OF HAWAII (US)
Location/Qualifiers
1. 4512

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BASE COUNT 835 a 1380 c 1354 g 943 t
ORIGIN

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TITLE Direct Submission
JOURNAL Submitted (14-JAN-1998) Tomoko Hirohashi, Faculty of Pharmaceutical Sciences, Tokyo University, Department of Pharmaceutics, Hongo 7-3-1, Bunkyo-ku, Tokyo 113, Japan
(E-mail:hirohashi@sei.zai.f.u-tokyo.ac.jp, Tel:81-3-5802-2045, Fax:81-3-5800-6949)

FEATURES

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||||| 4128 GTGAGCTCAAGCCCTCGTGACCAACGCTCGCTGGCCAGCTGAATATGAGTGTGAGGC 4187
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LOCUS Human multidrug resistance-associated protein (MRP) mRNA, complete
DEFINITION cds
L05628
VERSION L05628.1 GI:1833658
KEYWORDS multidrug resistance-associated protein; transporter.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo...
1 (bases 1 to 5011)
Cole, S.P., Bhardwaj, G., Gerlach, J.H., Mackie, J.E., Grant, C.E.,
Almquist, K.C., Stewart, A.J., Kurz, E.U., Duncan, A.M., and Deeley, R.G.
Overexpression of a transporter gene in a multidrug-resistant human
lung cancer cell line
Science 258 (5086), 1650-1654 (1992)
93088080
MEDLINE 2 (bases 197 to 377)
PUBMED 1360704
REFERENCE Cole, S.P. and Deeley, R.G.
AUTHORS Multidrug resistance-associated protein: sequence correction
JOURNAL Science 260 (5110), 879 (1993)
MEDLINE 93262415
PUBMED 8098549
REFERENCE 3 (bases 1 to 5011)
AUTHORS Stride, B.D., Valdimarsson, G., Gerlach, J.H., Wilson, G.M., Cole, S.P.
and Deeley, R.G.
TITLE Structure and expression of the messenger RNA encoding the murine
multidrug resistance protein, an ATP-binding cassette transporter
Mol. Pharmacol. 49 (6), 962-971 (1996)
JOURNAL 96251691
MEDLINE 8649356
PUBMED
REFERENCE 4 (bases 1 to 5011)
AUTHORS Gerlach, J.H.
TITLE Direct Submission
JOURNAL Submitted (30-JAN-1997) Cancer Research Labs, Queen's University,
Kingston, ON K7L 3N6, Canada
COMMENT On Feb 10, 1997 this sequence version replaced gi:292332.
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location/Qualifiers
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Best Local Similarity 55.8%; Pred. No. 1.4e-221;
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Db 238 GCTCTGGACTGGATGTACGTGGATATACAGCAACCCGACTTCCACGAGTCTTCA 297
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Db 298 GAACACGGTCTCTGCTGGGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTTCT 357
QY 156 CTTCTTCATCCACATGCGGGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTCT 215
Db 358 CCTCTATCTCTCCGACATGACCGAGGCTACATTCAGATGACACCTCTCAACAAACCA 417
QY 216 GATGGTCTTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 275
Db 418 AACTGCTTGGATTTTGTGCTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 477
QY 276 GAAATCCAAAGGAGACGCTGAGGCCCCAGAAATTCCTCATTCATCTACTGTGTGGCT 335
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ORIGIN

Query Match 27.2%; Score 1227.6; DB 6; Length 5011;
Best Local Similarity 55.8%; Pred. No. 2.9e-221;
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QY 96 GAGAACAGCAGGGTCTGGGTACCCCATCTACTCTGGGTCTTGTGTCCCATCTACT 155
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Qy	3077	GGGATGTGGTATCTCCCATCAGCTCTTTTGTAGCGGACACCACTATGGTCACTCTGATA	3136
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Qy	3857	CTTCA	AGAT	TC	CACG	AGAG	AGAGT	3916
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Qy	3917	CTCTCC	TG	CGAGT	GGCT	TC	CGGCT	3976
Db	4196	CGTCC	CTG	ACCT	TGGG	CTTAT	TTCG	4255
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Db	4256	ATGG	CATCA	ACAT	CGC	AGAT	CGGCC	4315
Qy	4037	CCGAG	AGCC	CACT	CTCT	TTC	CGGAT	4096
Db	4316	CCAG	AG	CCCT	TTTT	TGTTT	TCGGG	4375
Qy	4097	ACTCG	AG	CAGCT	AT	CTG	GGG	4156
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Qy	4157	GCCT	CG	CGG	CAGCT	GT	CACT	4216
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Qy	4217	AGAA	AC	AGCT	CT	GT	CTG	4276


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QY 3977 ACGGGTCCCATTTGCCACAGTGGGGTGCACACATCGGCTCCAGGTCCAGATCATCC 4036
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QY 4037 CCCAGGACCCATCTGTTCCTGCTCTCTGCGGATCAACCTCGACCTGTGTCAGGAGC 4096
Db 4316 CCCAGGACCCCTGTGTTGGGTTCCCTCCGAATGAACCTGGACCCATTCAGCCAGT 4375
QY 4097 ACTCGGACGAGCTATCTGGGCAGCCCTGGAGAGCGTGCAGCTCAAGCCCTGGTGCCA 4156
Db 4376 ACTCGATGAAGAAGTCTGGAGCTCCCTGGAGCTGGCCACCTGAGGACCTGTGTGTCAG 4435
QY 4157 CCCTGCGGGCCAGCTGCAGTACAGTGTGCTGACCGAGGCGAGACCTGAGCGTGGGCC 4216
Db 4436 CCCTTCTGACAAGCTAGACCATGAATGTGCAGAGGCGGGGAGAACCTCAGTGTGGGC 4495
QY 4217 AGAAACAGCTCTGTGTGTCGACGTGCCCTTCTCCGGAACCCAGATCTCATCTCTGG 4276
Db 4496 AGCCCGAGCTGTGTGCTGACCGCGGCCCTGTGAGAGAACGAAAGATCTGTGTGTGG 4555
QY 4277 ACAGGCTACTGTGCTGACGCTGGCAGGAGCTGCAGATGCAGGCGATGTCTCGGA 4336
Db 4556 ATGAGGCCAGGACCGCTGACCTGGAGAGGAGACCTCATCCAGTCCACCATCCGA 4615
QY 4337 GCTGGTTGCAGTGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4396
Db 4616 CACAGTTCGAGGAGTGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4675
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Db 4676 ACACAGGGTGTGCTGCTGACAGAGAGAAATCCAGGAGTACGGGCGCCCATCGGACC 4735
QY 4457 TGCTGGCCAGAGGGCTGTTTACAGACTGGCCCGAGGAGTCAAGGCTGTGT 4508
Db 4736 TCCTGCAGCAGAGAGTCTTTCTACAGCATGGCCCAAGAGCGCGGCTGTGT 4787

RESULT 12
SATHMRP LOCUS 5867 bp mRNA linear PRI 02-NOV-1994
DEFINITION Synthetic adenovirus transformed human retina cell line, MRP mRNA.
ACCESSION X78338
VERSION X78338.1 GI:563909
KEYWORDS mrp gene; multidrug resistance-associated protein.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5867)
Zaman, G.J.R., Flens, M.J., van Leusden, M.R., de Haas, M.,
Muelder, H.S., Lankelma, J., Pinedo, H.M., Scheper, R.J., Baas, F.,
Broxterman, H.J. and Borst, P.
The human multidrug resistance-associated protein MRP is a plasma
membrane drug-efflux pump
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JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (19), 8822-8826 (1994)
MEDLINE 94377445
PUBMED 7916458
REFERENCE 2 (bases 1 to 5867)
AUTHORS Zaman, G.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-1994) G. Zaman, Division of Molecular Biology,
Netherlands Cancer Institute, Plesmanlaan 121, 1066 CX Amsterdam,
NETHERLANDS
FEATURES
Location/Qualifiers
Source 1..5867
organism="Homo sapiens"
db_xref="taxon:9606"
order(1..2480,2682..5867)
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db_xref="taxon:9606"
clone="CDNA library in lambda ZapII"
haplotype="aneuploid"
cell_type="adenovirus transformed human retina"
tissue_type="retina"
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cell_line="GLC4/ADR"
cell_type="small cell lung cancer"
tissue_type="lung"
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gene /gene="MRP"
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mRNA /gene="MRP"
BASE COUNT 1263 a 1717 c 1590 g 1297 t
ORIGIN
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Query Match 27.2%; Score 1227.6; DB 9; Length 5867;
Best Local Similarity 55.8%; Pred. No. 2.8e-221;
Matches 2538; Conservative 0; Mismatches 1934; Indels 80; Gaps 7;
QY 36 GGTCTGGACACAGAGAGAGCTGAACCTGCCGCCAGCAGCTGCTGAGCCTGTGCTTCCT 95
Db 179 GCTCTGGGACTGGAAATGTACCTGGAATACCGAGCAACCCCGACTTCACCAAGTGTCTCA 238
QY 96 GAGAACAGCAGGCGTCTGGGTACCCGCCATGTACCTCGGGTCTTGGTCCCATCTACCT 155
Db 239 GAACAGGTCTCTGCTGGTGGTCCCTGTTTACCTCTGGGCTGTTTCCCTTCTTACTT 298
QY 156 CTTCTTATCCACACCATGCGCGGGGTACCTCGGATGTCCCACTCTTCAAGCCAA 215
Db 299 CTTCTATCTCTCCGACATGACCGAGGTACATTCAGATGACACCTCTCAACAAACCAA 358
QY 216 GATGTGCTTGATTCGCCCTCATAGTCTGTGTACCTCCAGCGTGGCTGCTGCTTTGG 275
Db 359 AACTGCTTGGGATTTTGTGCTGTGATGCTGTGCTGGGCGAGACCTCTTCTACTCTTTCTG 418
QY 276 GAAATCCACAGGAGAGCGCTGAGGCCCCAGAAATTCCTCATTCCTTCTGCTGTGGCT 335
Db 419 GGAAGAAGTGGGCGCATATTCCTGGCCCGCAGTGTTCGTGAGCCCACTCTCTTGGG 478
QY 336 CACACAGATGAGCTTCGAGTGTTCCTGATTCACACCGAGAGAGAAAGGGAGTCCAGTC 395
Db 479 CATCACCATGCTGCTGCTACCTTTTAATTCAGCTGGAGAGAGAGAGGGAGTTCAGTC 538
QY 396 ATCTGGAGTGTGTTGTTGTTACTGCTTCTGCTTGTTCGCCAGCTTACCAAGCTGC 455
Db 539 TTCAGGATCATGTCTACTTCTTGTGCTGTAGTGTGCTGTGCTGTGCTGTGCTGTGAG 598
QY 456 CCAGCAG-----GCTCCGGAGCGGCTTCAGAGCGGACCTGTCCGCGCCACTGTGC 506
Db 599 ATCCAAATATATGACAGCCTTAAAGAGAGATGCCCGGTGGACCTGTTTCGTGACATCA 658
QY 507 CACCTACCTATGCTCTCTGCTGGTGGTGGCAGAGTTTGTGCTGTGCTGCTGCTGGCGATCA 566
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Db 659 TTTCAGGCTACTTTTCCCTCTTACTCATTCAGTCGCTGTTGCTCCTGTTTCTCAGATCG 718
QY 567 ACCCCCTTTCTCCCTGAAGACCCCGCAGAGTCTTAACCCCTGTCCAGAGAGTGGCGAGC 626
Db 719 CTACCCCTGTTCTCGAARACCATCCAGACCCATACTCCCTGCCAGAGTCCAGCGCTTC 778
QY 627 CTTCCCTCCAAAGCCAGTCTTGTGGTGGTTTCTGGCTGGTCTGGAGGGGATACAGGAG 686
Db 779 CTTCTCTGTCAGGATCACTCTCTGTTGGTATCACAGGGTTGATTTGTCGGGGCTTACCGCCA 838
QY 687 GCACCTGAGACCAAAAGACTCTGTGCTGTGGAGAGAAACCTCTCAGAAGAACTTGT 746
Db 839 GCCCTTGGAGGGAGTGAACCTCTGGTCTTAAACAAGAGGACACGTGCGAACAAGTCGT 898
QY 747 TTCCCGGCTTGAAGAGAGTGGATGAGGAACCGC ---- AGTCAGCCCGGAGGCACAACA 802
Db 899 GCCTGTTTGGTAAAGAACTGGAAGAAGGAATCGCCCAAGACTAGGAAGCAGCGGTGAA 958
QY 803 AGCAATACATTTAAAGAAAGGCGGCGAGTGGCATGAAGGTCCA ---- 849
Db 959 GGTGTGTACTCTCTCAAGGATCTCCAGCGGAGAGAGTTCCAAGGTGGATCGAA 1018
QY 850 -----GAGACCGAGCCCTTCTACGGCAAGAGGAGCGAGTGGCGCCACTGCT 899
Db 1019 TGAGGAGTGGAGGCTTTGATCTCAAGTCCCCACAGAAGGAGTGAACCCCTCTCTGTT 1078
QY 900 GAAGGCCATCTGGCAGGTGTTCAATCTACCTTCCTCTGGGACCCCTCAGCCCTCATCAT 959
Db 1079 TAAGTGTATTACAAGACCTTTGGGCCCTACTTCTCTCATGAGTCTTCTTCAAGGCCAT 1138
QY 960 CAGTGAATCTCAGGTTCACGTCTCCCAAGCTGCTCAGCCCTTTCTGGAGTTTATGG 1019
Db 1139 CCACGACCTGATGATGTTTTCCGGGCGGAGATCTTAAAGTTGCTCATCAAGTTCTGTGA 1198
QY 1020 TGATCCAAAGCTTCCAGCTGGAAGGCTACCTCTCGCGCTCATGTTCTCTCAGC 1079
Db 1199 CGACAGAGGCCCAAGACTGGCAGGCTTACTTACACCGTCTGTTTGTCTACTGC 1258
QY 1080 CTGCTGCAAAAGCTGTTTGAAGCAGAGAACATGTACAGGCTCAAGGTCGCCAGATGAG 1139
Db 1259 CTGCTGCAAGACCTCGTGTGTCACAGTACTTCCACATCTGTTCTGTCAGTGGCATGAG 1318
QY 1140 GTTGGCGTGGCCATCACTGGCTGTGTGTACAGAAGGTCCTGGCTGTCTCAGCGGCTC 1199
Db 1319 GATCAAGACCGTGTCTATTGGGCTGTCTATCGGAAGGCGCCCTGGTATCAACCAATTCAG 1378
QY 1200 CAGAAAGCCAGTGGCGGTGATGTGGTCAATCTGGTGTCTGGCTGGACGTGACGCGGT 1259
Db 1379 CAGAAATCTCCACGCTGGGAGATTTCAACCTCATGTCTGTGGACGCTCAGAGTT 1438
QY 1260 GACCGAGAGGCTCTTACTCAACGGGTGTGGCTGCTCTGCTGGATCGTGGTCTG 1319
Db 1439 CATGGAATGGCCACGTCATTAACATGATCTGGTCAGCCCCCTGCAAGTCATCTTGC 1498
QY 1320 CTTCTGCTATCTTGGCAGCTCTGGGGGCTCCCGCCCTCAGTGCATCGTGTCTTCC 1379
Db 1499 TCTCTACCTCTCTGCTGCTGAATCTGGGCGCTTCCGCTCTGGTGGAGTGGCGGTGATGT 1558
QY 1380 GAGCCTCTCCCTCTGAATTTCTTATCTTCCAAAGAAAGAACCAATCAGGAGGAGCA 1439
Db 1559 CCTATGTTGCCGTCAATGTGTATGGGATGAGACCAAGACATATCAGTGGCCCCA 1618
QY 1440 AATGAGGCAAGAGGATCTACGCGCAGGCTACCAAGCTCTATCTCAGGAACCTCGAAGAC 1499
Db 1619 CATGAAGCAAAAGACAATCGGATCAAGCTGATGAACGAATTTCAATGGGATCAAGT 1678
QY 1500 CATCAAGTTCATGGCTGGAGGAGCCCTTTCTGGACAGAGTCTCGGCATCGGAGGCCA 1559
Db 1679 GGTAAAGCTTTATGCTGGGAGGTGGATTTCAAGGACAAGGTCTGGCCATCAGGAGCA 1738
QY 1560 GGAGCTGGCGGCTTCCGGACCTCCGGCTCTCTTCTCTGTGTCCTGTTCTTCCA 1619
Db 1739 GGAGCTGAAGAGTGTGAAGAGTCTGCCCTTACCTGTCCAGCGTGGGCACTTCACTCGGT 1798

QY 1620 AGTCTCTACATTTCTGGTTCGCACTGGTGTGTTTGTCTCCACACTCTGTGGGCGGAGAA 1679
Db 1799 CTGCACGCCCTTTCTGGTGGCCCTGTGCACATTTGCGGTCTACGTGACCATTTGAGGAGAA 1858
QY 1680 TGCTA ---- TGAATCAGAGAAAGCTTTGTGACTCTCACAGTTCTCAACATCTCTCAACAA 1736
Db 1859 CAACATCTGATGCCACGACAGCCTTCTGTTTGGCCCTTGTTCACATCTCTCCGGTT 1918
QY 1737 GGCCAGGCTTTCTGCGCTCTCATCCACTCCCTGCTCCAGGCCCGGTGCTCTTTGA 1796
Db 1919 TCCCTGAACATTTCTCCCATGGTTCATCAGCAGCATCGTGCAGGAGTGTCTCTCCCTCAA 1978
QY 1797 CCCTCTGCTACCTTCTCTGCTGGAAGAGTTGACCTGTGCTGTAGACTCAAGTTC 1856
Db 1979 ACCTCTGAGGATCTTCTCTCCCATGAGGACTGGAACCTGACAGCATCGAGCGACGCC 2038
QY 1857 CTCTGGAAGCGCTCCCGGGAAGGATTCATCACATACAGTGCACCTTTGCGCTGGTC 1916
Db 2039 TGCAAAAGAGCGGGGCGACGAACAGCATCACGCTGAGGAATGCCATTTCACTTCACTTGGC 2098
QY 1917 CCAGGAAGCCCTCCCTGCTCCACAGAAATAAACCCTCACGCTGCCCGCCAGGCTGTCTGCT 1976
Db 2099 CAGGAGGACCTCCACACTGAATGGCATCACCTTCTCCATCCCGAAGTGTCTTGGT 2158
QY 1977 GGCTGTGTCGTCAGTGGGGCAGGGAAGTCTCCTGCTGTCCGCTCTGCGCCCTCTTGGGA 2036
Db 2159 GGCGTGTGGCCAGGTGGGCTCGGGAAGTCTGCTCTCAGCCCTCTTGGCTGA 2218
QY 2037 GCTGTCAAAGTGGAGGGTTCGTGAGCATCGAGGGTCTGTGGCTTACGTGCCCCAGGA 2096
Db 2219 GATGGACAAAGTGGAGGGCACGTGGCTATCAAGGGCTCCGTGGCTATGTGCCACAGCA 2278
QY 2097 GGCTGGGTGAGAACACTCTGTGTGTAGAGAAATGTGTCTCGGGCAGGAGCTGGACCC 2156
Db 2279 GGCTGGAATCAGAAATGATTTCTCCGAGAAACATCTTTTGGATGTCTGAGTGGAGGA 2338
QY 2157 ACCCTGGCTGGAGAGACTAGTAAAGCTGTGCTCTGCGAGCCAGATGTGGACAGCTTCCC 2216
Db 2339 ACCATATTACAGGTCCGTGATACAGGCTGTGCTCTCTCCACAGCTTGGAAATCTTGC 2398
QY 2217 TGAGGGAATCCACACTTCAATTTGGGAGCAGGATGAATCTCTCGGAGGCCAAGAGCA 2276
Db 2399 CAGTGGGATCGGACAGAGATTTGGCAGAAAGGGCTGAACTCTCTGGGGCCAGAGCA 2458
QY 2277 GCGCTCAGCTTGCCCGGCTGTATACAGAAAGGAGCTGTGTACCTGTGTGATGACCC 2336
Db 2459 GCGGTGAGCTTGCCCGGCTGTACTCCACGCTGACATTTACCTCTTCGATGATCC 2518
QY 2337 CCTGGCGGCTGGATGCCACGTTGGCCAGCATGTCTTCAACAGGTCATTTGGGCGCTGG 2396
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QY 2397 TGGCTACTCCAGGGAACACAGGATTTCTGTGAGCGACGACTCCACATCTCTGCCCCA 2456
Db 2579 GGGGATGCTCAAGAAACAAAGACGCGGATTTGTGTACGACACAGCATGAGCTACTTGGCCGA 2638
QY 2457 GGCTGATTTGATCATAGTGTGGCAATGGGCCATCGCAGAGATGGTTCCTTACCAGGA 2516
Db 2639 GGTGGAGCTCATCTCATGAGTGGCGCAAGATCTCTGAGATGGGCTCTTACCAGGA 2698
QY 2517 GCTTCTCAGAGGAAGGGGCGCTCTGCTGTCTTCTGATCAAGCCAGACAGCAGGAGA 2576
Db 2699 GCTGCTGGCTCGAGACGCGCTTCG -CTGAGTCTCTGCGTACCTATGCCAGCACAGC 2757
QY 2577 TAGAGGAGAAGGAACACAGAACCTGGGACAGCAACCAAGAACCCAGAGGACCTTGC 2636
Db 2758 AGGAGCAGGATGACAGGGAACCGGGCTACCGGCGCTCAGCGGTCACGGGAAGGAAGCA 2817
QY 2637 AGCAGGAGGCCCGCTTAGACCGCAGAGGTCCATCAAGTCACTGCTCTGAGAG - ---- 2691
Db 2818 AGCAATGGAGAATGGCATGCTGTGACGACAGTGTGAGGGAAGCAACTGCAGAGACGC 2877

QY	2692	-----GACGCTACCATTCTCAGAAAGCCAGAA--	2711
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QY	2717	CAGAGTTTCTCTGGATGACCTTGACAGGCGAGGATGGCCAGCAGGAAAGGACAGCATCC	2776
Db	2938	TGCAGAAAGCTCAGGCCAAGAAAGGAGAGACCTTGGAAAGCTGATGGAGGCTGACAAGCGC	2997
QY	2777	AATACGGCAGGTGAAGGCCACAGTGCACCTGCGCTTACCTGCGTGGCTGGGACACCCCC	2836
Db	2998	AGCAGGGCAGGTCAAGCTTTCGTTGACTGGGACTACATGAAGGCCATCGGACTCTTCA	3057
QY	2837	TC TGCCCTCTACCACTCTTCTCTCTCTGCGCAGCAAGTGGCTCTCTCTGCGGGGCT	2896
Db	3058	TCTCCTCTCAGCATCTTCTCTTTCATGTGTAACCATGTGTCCGCGCTGGCTTCCAAT	3117
QY	2897	ACTGGCTGAGCCTGTGGGCGGACGACCTTGACGTAGTGGGAGCAGACAGCAGGACGCC	2956
Db	3118	ATTGGCTCAGCCTCTGGACTGATGACCCCATCGTCAACGGGACTCAGGAGCACACGAAAG	3177
QY	2957	TCGCTGGGGGGATCTCGGGCTCTCGGGCTGCTCCAGCCCATTTGGGCTGTTTGGCCTCCA	3016
Db	3178	TCCGGCTGAGCGTCTATGAGCCCTTGGGCATTTCAACGGGATCGCGGTGTTTTGGGTACT	3237
QY	3017	TGGCTGCGGTGCTCTAGTGTGGGGCCCGGGCATCCAGGTTGCTCTTCCAGAGGCTCCTGT	3076
Db	3238	CCATGGCGGTGCCATCGGGGGATCTTGGCTTCCCGCTGCTGCACGTTGGACCTGCTGC	3297
QY	3077	GGGATGTGGTGGCATCTCCCATCAGCTTCTTTGAGGGAGACCCCATTTGGTCTCACTGCTAA	3136
Db	3298	ACAGCATCTCGGGTACCCCATGAGCTTCTTTGAGCGGACCCCATCGTGGGAACTTGGTGA	3357
QY	3137	ACCGCTTCTCAAAGGAGACAGACGGTTGAGTGSAGATTTCCAGACAATCCAGACAACCTCGG	3196
Db	3358	ACCGCTTCTCCAGAGACTGACACAGTGGACTCCATGATCCCGGAGGTCTCAAGATGT	3417
QY	3197	TGCTGATGTACGCCCTTTGGACTCTCTGGAGGTGACGCTGGTGTGCGAGTGGCTACGCCAC	3256
Db	3418	TCATGGGCTCCCTGTTCAACGTCATTGGTGTGCTGTCATCTTATCCTGTGCGCACGCCCA	3477
QY	3257	TGGCCACTGTGGCCATCTCGCCACTGTTTCTCTCTAGCTGGGTTTCAGAGCGTGATG	3316
Db	3478	TCGGCGGCATCATATCCCGCCCTTGGCCCTCATCTACTTCTCTCCAGAGGTTCTAGG	3537
QY	3317	TGGTTAGTCTATGCCAGCTGAGAGCTTGGAGTTCAGCCAGCTTACTGCTGTCTGTCTGCC	3376
Db	3538	TGGCTTCTCCCGCAGCTGAAGCGCTCGAGTGGTCAAGCGCTCCCGGGTCTATTTCCC	3597
QY	3377	ACATGGCTGAGAGCTTCCAGGCGACACAGTGTGTCGGGCAATTCGAAACCCAGGCGCCCT	3436
Db	3598	ATTTCAACGAGACCTTGTGGGGTCAAGCTATTTCGAGCCTTCGAGGAGCAGGAGCGCT	3657
QY	3437	TTGTGGCTCAGAAATGCTCGCTAGATGAAGCCAGAGATCAGTTTCCGCGCACTGG	3496
Db	3658	TCATCCACGAGTGACCTGAAGTGGACGAGAACCAAGGCCATTATACCCACGATCG	3717
QY	3497	TGGCTGACAGTGGCTTCCGGCCAAATGTGGAGCTCTCGGGAATGGCCCTGGTTTTCAG	3556
Db	3718	TGGCAACAGGTGCTGSCCGTGGCGTGGAGTGTGTGGGCACTGCATCGTCTCTGTTG	3777
QY	3557	CCGCCAGTGTGTGCTGAGCAAAAGCCCACTCAGTGTGGCTCGTGGGCTTCTCTG	3616
Db	3778	CTGCCCTGTTTGGGTTGATCTCCAGGACAGCCCTCAGTGTGGTGTGGGCTCTCAG	3837
QY	3617	TCTCTGTGCCCTCCAGGTGACCCAGACACTGCACTGGGTGTTTCGCAACTTGGACAGCC	3676
Db	3838	TGCTTACTATTGCAAGGTCAACACGTACTTGAATGCGTGGTTTCGGATGTCATCTGAAA	3897
QY	3677	TAGAAACAGCATCGTGTCAGTGGAGCGGATGACGAGTATGCGCTGGAGCCCAAGGAGG	3736
Db	3898	TGGAAACCAACATCGTGGCGGTGGAGAGGCTCAGGAGTATTCAGAGCTCAGAGGAGG	3957
QY	3737	CTCCCTGGAGGCTGCCACATGTGCACTCAGCCCCCTCGCCCTCAGGGCGGACGATCG	3796

Db	3958	CGCCCTGGCCAAATCCAGGAGACAGCTCCGCCCCAGCAGCTGGCCCAAGTGGCGCGAGTGG	4017
QY	3797	AGTTCCGGGACTTTGGCTAAGATGCCAGCTCCGCGTCCGCGTGGCTGTGCACGGCGTGT	3856
Db	4018	AATTCGGGAATCTACCTGCGCTACCGAGAGACCTTGGACTTCGTCTCAGGCACATCA	4077
QY	3857	CCCTCAAGATCCACGAGGAGAGAAGTGGGCACTCTTGGCAGACCGGGGCGCAGGAAAGT	3916
Db	4078	ATGTCACGATCAATGGGGAGAAAGTCCGCATCTGGGGCGGACGGGAGCTGGAAAGT	4137
QY	3917	CCTCCTGGCAGTGGGCTGCTCGGGCTCCAGGAGCAGCTGAGGTGGGATCTGGATCG	3976
Db	4138	CGTCCCTGACCTTGGGCTTATTTCGGATCAACAGTCTGCCGAAGGAGAGATCATCATCG	4197
QY	3977	AGGGGTCCCAATTGCCACGTGGGCTGCACACACTGGCTCCAGTCCAGATCAGCATATCC	4036
Db	4198	ATGGCATCAACATCGGCCAAGATCGGGCTGCACACCTCCGCTTCAAGATCACCATCATCC	4257
QY	4037	CCAGGACCCCACTCCTGTTCCTGGCTCTCTCGGATGAACCTCGACCTGCAGGAGC	4096
Db	4258	CCCAGACCTGTTTTGGTTTTCGGGTTCCTCGAATGAACCTTGGACCATCAGCCAGT	4317
QY	4097	ACTCGACAGGCTATCTCGGCGAGCCCTGGAGACGGTGCAGCTCAAAGCCTTGGTGGCCA	4156
Db	4318	ACTCGGATGAAGAAGTCTGGACGTCCCTGGAGCTGCCCCACCTGAAGACTTCGTCTCAG	4377
QY	4157	GCTTGCCTGGCCAGCTGCAGTACAAGTGTGTGACCGAGGCGAGGACCTGAGCGTGGGC	4216
Db	4378	CCCTTCTCTGACAAGCTAGACCATGATGTGCAGAGGGCGGGGAGAACCTCAGTGTGGGC	4437
QY	4217	AGAAACAGCTCCTGTCTCGGCACGTGCCCTTCTCCGGAAGACCCAGATCCTCATCCTGG	4276
Db	4438	AGCGCCAGCTTGTGTGCTTAGCCCCGGGCGCTCTCAGGAAGACGAGAATCCTTGTGTGG	4497
QY	4277	ACGAGGCTACTGCTCGCTGGACCTGGCACGGAGTGCAGATGAGGACCATGCTCGGA	4336
Db	4498	ATGAGCCACGCGACCGCTGGACCTTGAACCGGACGACCTCATCCAGTCCACCATCCGA	4557
QY	4337	GCTGTTGTGCAGATGCACTGTGCTGCCCATTTGCCACCGCTCGGCTCCGTGATGGACT	4396
Db	4558	CACAGTTGAGGACTGCACCGTCTCCATCCATGCCCCACGGCTCAACACCATCATGGACT	4617
QY	4397	GTGCGCGGGTCTGCTCATGGAACAGGGCAGGTGGCAGAGCGGACGCCGCCGCCAGC	4456
Db	4618	ACACAAGGTTGATCGTCTTGGACAAGGAGAAATCCAGGATACGGCGCCCATCGGACC	4677
QY	4457	TGCTGGCCACGAAGGCCCTGTTTTACAGACTGGCCACGAGTCAAGCCCTGGT	4508
Db	4678	TCCTGCACGAGAGGTCTTTTACAGCATGGCCAAAGACGCCGGCTGGT	4729

[illegible]

Best Local Similarity	55.7%;	Pred. NO. 2.3e-220;
Matches 2535; Conservative	0;	Mismatches 1937; Indels 80; Gaps 7;

QY	36	GGTCTGGAACACGACAGAGCCTGAACCTTCCGCCACACAGCCTGCTGAGCCTGCTTCCT	95
DB	237	GCTCTGGGACTGGAATGTACAGCTGGAATACCAAGCAACCCGACTTCAACAACTGCTTCA	296
QY	96	GAGAACAGAGGGGTCTGGGTACCCGCCATGTACCTCTGGCTCTTGGTCCCATCTACCT	155
DB	297	GACACGGTCTCGTGGGTGCTTTGTTTTTACCTCTGGGCCGTGTTCCCTCTCTACTT	356
QY	156	CCTCTATCCACACACATGAGCGGGGTACCTCCGATGTCCGCATCTTCAAAGCAA	215
DB	357	CCTCTATCTCCGCACATACCGAGGTACATTCAGATGACACCTCTCAACAAACCAA	416
QY	216	GATGGTCTTGATTCGCCCTCATATGCTCTGTGTACTCCAGCGTGGTGTGCGCTCTTG	275
DB	417	AACCTGCTTTGGGATTTTCTGTGTGATCTGTCTGTCGGCAGACCTCTTACTCTTCTG	476
QY	276	GAAATCCAAACAGGGAACGCTTGAGSCCCAGAAATCTCATCTACTGTGTGGCT	335
DB	477	GGAAGAAGTGGGGCATATCTCTGCCCGAGTGTCTGTGTCAGCCCACTCTCTTGGG	536
QY	336	CACACAGATGAGCTTCGCAAGTTCTCTGATTCACACCAGAGAGAAAAGGAGTCCAGTC	395
DB	537	CATCACACGCTCTTGCTTACCTTTTAAATTCAGCTGGAGGAGGAGGAGTCTCAGTC	596
QY	396	ATCTGAGTGTCTTTGGTTACTGGCTTCTCTGCTTTGCTTTGCCAGCTACCAACGCTGC	455
DB	597	TTCAGGAGTATCTCTACCTTTCTGGCTGTGTAGCCCTAGTGTGTGCCCTAGCCATCTGAG	656
QY	456	CCAGCAG-----GCCTCCGAGCGGCTTCAGAGCAGACCTCTCCGACACCTGTC	506
DB	657	ATCCAAATATGACAGCCTTAAAGAGGATGCCAGGTGGACCTGTTCTGTGACATCAC	716
QY	507	CACCTACTATGCTCTCTCTGGTGGTGCACAGTTTGTGCTCTGCTCGCTGGCGATCA	566
DB	717	TTTCTAGCTACTTTTTCCTCTTACTCATTCAGCTCTGTTGCTCTTCTTCAGATCG	776
QY	567	ACCCCTCTTCCCTGAAGACCCCGACAGTCTTAACCCCTGTCCAGAGACTGGGCGAGC	626
DB	777	CTACCCCTGTTCTCGGAACCATCCAGACCTTAATCCCTGCCAGAGTCCAGCGCTC	836
QY	627	CTTCCCTCCAAAGCCAGCTTCTGTGGTGTCTTGGCTGTCTGAGGGGATACAGGAG	686
DB	837	CTTCTCTCGAGATCACCTTCTGTGGATCACAGGTTGATTCTCGGGGCTACCGCCA	896
QY	687	GCACCTGAGACCAAAGACCTCTGTGCTGGGAGAGAAATCTCTAGAAGACTTGT	746
DB	897	GCCTCTGGAGGCGATGACCTCTGTCTCTTAAACAAGGAGACAGCTCGGAACAAGTCTG	956
QY	747	TTCCCGCTTGAAGAGTGTGATGAGNACGC-----ASTGCAGCCCGGAGGCACAACA	802
DB	957	GCCTGTTTGGTAAAGACTGGAAGAAGATGCGCCAAGACTAGGAAGCAGCGGTGAA	1016
QY	803	AGCAATAGCATTTAAAGGAAGCGGCGAGTGGCATGAAGGCTCCA-----	849
DB	1017	GGTTGTGTTACTCTCAAGGATCTCTGCCAGCGCAAGAGAGTTCCRAGGTGGATGCGAA	1076
QY	850	-----GAGACCGAGCCCTTCTCTAGGCAAGAAGGAGCCAGTGGCGGCCACTGCT	899
DB	1077	TGAGGAGTGGAGGCTTTGATCGTCAAGTCCCGCCACAGAAAGAGTGGAAACCCCTCTCTGTT	1136
QY	900	GAAGGCCATCTGGCAGGTGTTCCATCTTACTTCTCTCTGGGACCTCTCAGCCTCATCAT	959
DB	1137	TAAGTGTATTACAGACCTTTTGGGCCCTACTTCTCTATGAGTCTCTTCTCAAGGCCAT	1196
QY	960	CAGTGATGCTTCAGGTTCACTGTGCCCCAAGTGCTCAGCCTTTTCTCGTGAGTTATTGG	1019
DB	1197	CCAGGACCTGATGATGTTTCCGGGCCGACATCTTAAGTTGCTCATCAGTTCGTGAA	1256
QY	1020	TGATCCCAACGCTTCCAGCCTGGAAGGGTACTCTCTCGCCGTGCTGATGTCTCTCAGC	1079

Db	1257	TGACAGCAAGGGCCCCAGACTGGCAGGGCTACTTCTACACCGTGTGCTGTTTGTCACTGC	13131
Qy	1080	CTGCGCTGCAAAACGCTCTTTTGGCAGCAGCAAGCATGTATACAGGCTCAAGGTGCCGAGATGAG	1139
Db	1317	CTGCGCTGCAGACCCCTGCTGCTGCACCAAGTACTTCCACATCTGCTTCTGTCAGTGGCATGAG	1376
Qy	1140	GTTCGGTTCGGCCATCACTTGGCTGTGTACAGAAAGGCTCTGGCTGTGTCCACAGGGCTC	1199
Db	1377	GATCAAGACCGCTGTCTATGGGGCTCTCTATCGGAAGGCCCTGTGATCACCATAATTCAGC	1436
Qy	1200	CAGAAAGCCAGTGGCGGTGGTGTGTTGTTCAATCTGTGGTGTCCGTGGAGCTGCAGCGGCT	1259
Db	1437	CAGAAATCTCCACCGTGGGAGATGTGTCAACCTCATGTCTGTGTGGACCTCAGAGGTT	1496
Qy	1260	GACCGAGAGCGTCTCTACCTCAACGGGTGTGGCTGCCCTCTGCTTGGATCTGGTCTG	1319
Db	1497	CATGACTTGGCCACGTACATTAACATGATCTGGTCAGCCCCCTGCAAGTCATCCTTGC	1556
Qy	1320	CTTCGCTATCTTGGCAGCTCCTGGGGCCCTCCGGCCCTCAGCCATCGCTCTCTTCTCT	1379
Db	1557	TCCTACTCTCTGTGGCTGAATCTGGGCCCTTCCGTCCTGGCTGGAGTGGCGGTGATGGT	1616
Qy	1380	GAGCCTCTCCCTCTGAATTTCTTTCATCTCCAGAAAGGAACCAACATCAGAGGAGCA	1439
Db	1617	CCTCATGTGGCCGTCAATGTGTGATGGCATGAAGACCAAGACGCTATCAGGTGGCCCA	1676
Qy	1440	ANTGAGGCAAGAGGACTCACGGCAGCGCTCACCAAGCTCTATCTCAGGAACCTCGAAGAC	1499
Db	1677	CATGAAGAGCAAGACAATCGGATCAAGCTGATGAACAGAAATTTCTCAATGGGATCAAAGT	1736
Qy	1500	CATCAAGTTTCCATGGCTGGGAGGGAGCCCTTCTGGACAGAGCTCTGGGCATCCGAGGCCA	1559
Db	1737	GCTAAAGCTTATGCTGGGAGCTGGCATTCAGAGACAAGGTGCTGGCCATCAGGCAGGA	1796
Qy	1560	GAGCTGGGGCCCTTGGCGACCTCCGGCCCTCTCTTCTCTGTGTGCTGGTGTCTCTTCCA	1619
Db	1797	GGAGTGAAGGTGCTGAAGAAAGTCTGCTTACCTGTGTCAGCGCTGGGACCTTCACCTGGGT	1856
Qy	1620	AGTGCTACATTTCTGGTCGCACTGGTGGTGTGCTGTGCTGTCCACACTCTGGTGCCCGAGAA	1679
Db	1857	CTGCAGGCCCTTCTGGTGGCCCTTGTGCAATTTGGCTGTAGTGCAGCATTCACAGAA	1916
Qy	1680	TGCTA---TGAATGCAGAGAAAGCCCTTGTGACTCTCACAGTTCTCAACATCTCAACAA	1736
Db	1917	CAACATCCTGGATGCCACAGACGCTTCTGTCTTTTGGCTTGTCTTCAACATCCTCCGGTT	1976
Qy	1737	GGCCAGGCTTTCCTTGGCCCTTCTCATTCACATCCCTCTGCTCAGGCCCGGGTGTCTTTGA	1796
Db	1977	TCCCTTGAACATTTCTCCCATGGTCTATCAGACATCTGTGACGGGAGTGTCTCTCCCTCAA	2036
Qy	1797	CGTCTGGTCACTTCTCTGCTGTGAAGAAGTTGACCTGGTGTGCTGAGACTCAAGTTC	1856
Db	2037	AGCCCTGAGGATCTTCTCTCCATGAGGAGCTTGAACCTGCACAGCATTCAGGCGACGGCC	2096
Qy	1857	CTCTGGAAGCGCTGCGGGAAGGATTTGCATCACCATACAGAGTGCCACCTTCGCCCTGGTC	1916
Db	2097	TGTCAAAGACGGCGGGGCAACAGACATCACCGTGGAGAAATGCCACATTCACCTGGGC	2156
Qy	1917	CCAGAAAGCCCTCCCTGGCTCCACAGAAATAACCTCAGGTGTGGTGGCCAGGGCTGTCTGCT	1976
Db	2157	CAGGAGCACCCCTCCACACTGAATGGCATCACTTCTCCATCCCGCGAAGGTGCTTTGGT	2216
Qy	1977	GGCTGTGTGGTTCAGTGGGGCAGGGAAGTCTCTCCCTGCTGTCCGCCCTCCCTCTGGGA	2036
Db	2217	GGCGTGGTGGCCAAGTGGGTTCGGAAGTGTGCTTCCCTGTCTCAGCCCTCTTGGCTGA	2276
Qy	2037	GCTGTCAAAGGTGGAGGGGTTCCTTGAGCATTCAGGGGTGCTGTGGCCCTACGTCGCCAGGA	2096
Db	2277	GATGCACAAAGTGGAGGGGACGCTGGCTATCAAGGCTCCGTGGCCCTATGTGCCACAGCA	2336
Qy	2097	GGCCTGGGTGCAGACACCTCTGTGGTGTAGAGAAATGTGTCTCGGGCAGAGCTGGACCC	2156
Db	2337	GGCCTGGATTCAGAAATGATTTCTCCGAGAAACATCTCTTTTGGATGTTCAGCTCGAGGA	2396

QY	2157	ACCCTGGCTGGAGAGAGTACTAGAAAGCCTGTGCCCTGCAGCCAGAGATGTGGACAGCTTCCC	2211
DB	2397	ACCATATTACAGTCCGTGATACAGGCCCTGTGCCCTCTCCAGACCTGAAATCTCTGCC	2456
QY	2217	TGAGGGAATCCACACTTCAATTTGGGAGCAGGCGCATGAATCTCTCCGGAGGCCACGAAGCA	2276
DB	2457	CAGTGGGATCGACAGAGATTGGCGAAGAAGCGGTGAACCTCTCTGGGGACAGAAAGCA	2516
QY	2277	GGCGCTGAGCCTGGCCCGGGCTGTATACAAAGGACGTGTGTACTCTGCTGGATGACCC	2336
DB	2517	GGCGCTGAGCCTGGCCCGGGCGGTGTACTTCCAACCGTGACATTTACCTCTTGATGATCC	2576
QY	2337	CCTGCGGCCCTGGATGCCACGTTGGCCAGCATGTCTTCAACCAAGTCAATTGGGCGCTGG	2396
DB	2577	CCTCTCAGCATGGATGCCATGTGGGAAAACACATCTTTGAAATGTGATTTGGGCCCAA	2636
QY	2397	TGGGCTACTCCAGGGAACAACACGATTCTCTGTAGCCAGCAGCTCCACATCTCTGCCCA	2456
DB	2637	GGGATGCTGAAGAAACAAGACGCGATCTTGTCACGCACACATGACTTGTGCGCA	2696
QY	2457	GGCTGATTGGATCATAGTGTCTGGGAAAATGGGGCCATTCGACAGATGGGTTCCTACAGGA	2516
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QY	2577	TAGAGGAAGGAGAAACACCTTGGACACAGCAACCAAGGACCCAGAGGCACCTCTCTGC	2636
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QY	2957	TGCGTGGGGGATCTTGGGGTCTCTGGCTGTCTCCAAGCATTTGGGCTGTTTGGCTCCA	3016
DB	3236	TCCGGCTGAGGCTCATATGAGACCCCTGGGCATTTTACAAGGGATCGCCGTGTTTGGCTACT	3295
QY	3017	TGGCTGGGTGCTCCTTAGTGGGGCCGGGCATCCAGTTGCTCTTTCAGAGGCTCTCTGT	3076
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DB	3356	ACACCATCTCGGCTCACCATGAGTCTTTTGGAGGGACCCCCAGTGGGAACCTGGGTGA	3415
QY	3137	ACCGCTTCTCAAGGAGACAGACAGGTGTGACGTGGACATTTCCAGACAACTCCGGTCCC	3196
DB	3416	ACCGCTTCTCAAGGAGCTGGACACAGTGGACTCCATCATCCCGGAGTCAATCAAGATGT	3475

QY	3197	TGCTGATGACGGCTTTGGACTCCTGGAGTGCAGCCTGGTGGTGGGACAGTGGCTACCCAC	3256
DB	3476	TCATGGGCTCCCTGTTTCAAGCTCATTTGGTGGCTGCATCGTTATCTCTGCTGCCACGCCCA	3535
QY	3257	TGGCCACTGTGGGCATCTCTGCCACTGTTTCTCCTCTACGCTGGGTTCAGAGCCTGTATG	3316
DB	3536	TCGCCGCATCATATCCCGCCCTTGGCCCTCATCTACTTCTCCTCCAGAGGTTCTTACG	3595
QY	3317	TGGTTAGCTCATGCCAGCTGAGACGTTGGAGTACAGCCAGCTACTCTGCTGTCTGCTCC	3376
DB	3596	TGGCTTCCCTCCGGCAGCTGAAGCGCTCGAGTCGGTCAGCCGCTCCCCGGTCTATTTC	3655
QY	3377	ACATGCTGAGAGGTTCCAGGGCAGACAGTGTGTCGGGCATMTCGAACCCAGGCCCCCT	3436
DB	3656	ATTTCACAGAGCCTTGCTGGGGTTCAGGCTCATTCGAGCCTTCGAGGACGAGGCGCT	3715
QY	3437	TTGTGGCTCAGAACAAATGCTCGGTAGATGAAGCCAGAGGATCAGTTTCCCGGACTGG	3496
DB	3716	TCATCCACAGAGTGACCTGAAGGTGGACGAGAACCAAGAGGCTATTACCCAGAGATCG	3775
QY	3497	TGGCTGACAGGTGGCTTGCGGCCAATGTGGAGCTCCTGGGGAATGGCTGGTGTGTTCAG	3556
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QY	3557	CGGCCAGTGTGCTGTGCTGAGCAAGCCCACTCATGCTGTGCCCTCGTGGGCTTCTCTG	3616
DB	3836	CTGCCCTGTTTGGGTGATCTCCAGGCACAGCCTCAGTGTGTGGCTTGGTGGGCTCTCAG	3895
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DB	4016	CGCCCTGGCAATTCAGGAGACACGTCGCCCCAGCAGCTGGGCCAGGTGGGCCGAGTGG	4075
QY	3797	AGTTCCGGGACTTTGGGCTAAAGTCCGACCTGAGCTCCGCTGGCTGTGCAGGGCGTGT	3856
DB	4076	TAATTCGGNACTTGTGCTTCGCCCTACCGAGAGACCTTGCATCTGTTCTCAGGCACATCA	4135
QY	3857	CTCTCAAGATCCACAGGAGAGAAGTGGGCATCTTTGGCAGGACCGGGGCGAGGAAGT	3916
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QY	3917	CTCTCCCTGGCAGTGGCTGTGCGGCTCCAGGAGCAGCTGAGGCTGGGATCTGATCG	3976
DB	4196	CGTCTCTGACCTTGGGCTTATTTCGGATCAACGAGTCTGCCGAAGGAGATCATCATCG	4255
QY	3977	ACGGGGTCCCCATTCCACAGTGGGGTGCACACACTGCGCTCCAGGATCAGCATATCC	4036
DB	4256	ATGGCATCAACATGCCAAGATCGGCCCTGCAGACCTCCGCTTCAAGATCACCATCATCC	4315
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DB	4316	CCAGGACCCCTGTTTGTGTTTTCGGGTTCCTCCGAATGAACCTGGACCATTCAGCCAGT	4375
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QY	4217	AGAAACAGTCTCTGTCTGCGACGTCCTTCTCCGGAAGACCCAGATCCTCATCTCGG	4276
DB	4496	AGCGCACGTTGTGTGCTGTAGCCCCGGGCCCTCTGAGGAAGACGAAGATCTTGTGTTGG	4555
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LOCUS AR093439 5011 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 1 from patent US 6001563.
ACCESSION AR093439
VERSION AR093439.1 GI:10020188
KEYWORDS

SOURCE

ORGANISM

Unknown.

Unknown.

Unclassified.

REFERENCE

1 (bases 1 to 5011)

Deeley R.G. and Cole, S.P.C.

Methods for identifying chemosensitizers

JOURNAL

Patent: US 6001563-A 14-DEC-1999;

FEATURES

Location/Qualifiers

1..5011

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BASE COUNT 1064 a 1497 c 1394 g 1056 t

ORIGIN

Query Match 27.1%; Score 1222.8; DB 6; Length 5011.

Best Local Similarity 55.7%; Pred. No. 2.3e-220;

Matches 2535; Conservative 0; Mismatches 1937; Indels 80; Gaps 7;

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SOURCE	Unknown.		
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AUTHORS	Deeley, R.G. and Cole, S.P.C.		
TITLE	Multidrug resistance protein		
JOURNAL	Patent: US 5489519-A 1 06-FEB-1996;		
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